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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart is described. Also described are single exon nucleic acid probes expressed in the heart and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

CROSS REFERENCE TO RELATED APPLICATIONS

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The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S.provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

FEFERENCE TO SEQUENCE LISTING AND INCORPORATION BY REFERENCE THEREOF

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The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file named pto_HEART.txt, created 24 January 2001, having 20,186,946 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

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The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome-derived single exon nucleic acid probes expressed in human

heart and single exon nucleic acid microarrays that include such probes.

Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., Proc. Natl. Acad. Sci. USA 70(4):1209-13 (1973); Gilbert et al., Proc. Natl. Acad. Sci. USA 70(12):3581-4 (1973), these techniques were used principally as tools to further the understanding of proteins — known or suspected — about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., Nature 308(5955):153-8 (1984).

More recently, however, the development of high throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences — that is, those accessible through isolation of mRNA — are of greatest initial interest. This "expressed sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,

Science 252:1651 (1991); Williamson, Drug Discov. Today

4:115 (1999)). For nucleic acids sequenced by this

approach, often the only biological information that is

known a priori with any certainty is the likelihood of

biologic expression itself. By virtue of the species and

tissue from which the mRNA had originally been obtained,

most such sequences are also annotated with the identity of

the species and at least one tissue in which expression

appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot be presumed; often the only a priori biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing approaches — and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species — there is an increasing need for methods that rapidly and effectively permit the functions of nucleic sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, Science 280:995 (1998); Pennisi, Science 283: 1822-1823 (1999), there is an important functional motivation as well.

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While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the C. elegans genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. C. elegans Sequencing Consortium, Science 282:2012 (1998). Analogously, the recently 10 completed sequence of chromosome 2 of Arabidopsis predicts over 4000 genes, Lin et al., Nature, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence — and most importantly, but not exclusively, regions that function to encode genes — to be identified.

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Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., Proc. Natl. Acad. Sci. USA 88(24):11261-5 (1991); Xu et al., Genet. Eng. 16:241-53 (1994); Uberbacher et al., Methods Enzymol. 266:259-81 (1996); GENEFINDER, Solovyev et al., Nucl. Acids. Res. 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., J. Mol. Biol. 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al., Genomics 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence.

Ansari-Lari et al., Genome Res. 8(1):29-40 (1998)

Identification of functional genes from genomic
data remains, however, an imperfect art. For example, in
reporting the full sequence of human chromosome 21, the
Chromosome 21 Mapping and Sequencing Consortium reports
that prior bioinformatic estimates of human gene number may
need to be revised substantially downwards. Nature
405:311-199 (2000); Reeves, Nature 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically — and specifically, that permit the expression of regions predicted to encode protein — readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays: A Practical Approach

25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., Genomics 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological guestion, R.S. Thomas

et al., Cancer Res. (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast Saccharomyces cerevisiae. De Risi et al., Science 178:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single exon genes, i.e., lack intrens, Lopez et al., RNA 5:1135-1137 (1999); Goffeau et al., Science 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the heart and vascular system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as causative, these disorders are for the most part believed to have polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the human heart, particularly those diseases with polygenic etiology.

Summary of the Invention

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The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the

expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 9,980 or a complementary sequence, or a portion of such a sequence.

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By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.

Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid

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probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 19,771 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and 15 bacteriophage vector sequence.

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In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most 20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single 25 exon nucleic acid probes in accordance with the first aspect of the invention is is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The 30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 35 polytetrafluoroethylene, polystyrene, polycarbonate,

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polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genomederived single exon nucleic acid probes useful for gene
expression analysis, and particularly for gene expression
analysis by microarray. In particular embodiments of this
aspect, the present invention provides human single-exon
probes that include specifically-hybridizable fragments of
SEQ ID Nos. 9,981 - 19,771, wherein the fragment hybridizes
at high stringency to an expressed human gene. In
particular embodiments, the invention provides single exon
probes comprising SEQ ID Nos. 1 - 9,980.

Accordingly, in a third aspect of the invention,

there is provided a single exon nucleic acid probe for
measuring human gene expression in a sample derived from
human heart which is a nucleic acid molecule comprising a
nucleotide sequence as set out in any of SEQ ID NOs.: 1
9,980 or a complementary sequence or a fragment thereof

wherein said probe hybridizes at high stringency to a
nucleic acid expressed in the human heart.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 9,981

35 - 19,771 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 19,772 - 29,119 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length.

20 It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition,

10 comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human heart, comprising:

contacting the single exon microarray in

20 accordance with the second aspect of the invention, with a
first collection of detectably labeled nucleic acids, said
first collection of nucleic acids derived from mRNA of
human heart; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said probe is a single exon probe having a fragment identical in

sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hypridization to single exon microarrays having a probe with said exon.

wherein a common pattern of expression of said exens in said plurality of tissues and/or cell types indicates that the exens should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 19,771 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 9,981 - 19,771, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: $1 \sim 9,980$.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 9,981 - 19,771.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set

out in any of SEQ ID NOs: 19,772 - 29,119, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

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Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), <u>DNA Microarrays: A Practical Approach (Practical Approach Series</u>), Oxford University Press (1999)

- 25 (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray"
- further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, inter alia, in Brenner et al., Proc. Natl. Acad. Sci. USA 97(4):166501670 (2000);
- 35 in such case, the term "microarray" and phrase "nucleic

acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as

PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10⁷, preferably at least 10⁸, more preferably at least 10⁹ liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual

35 display in which a single genomic sequence is annotated

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with predicted and experimentally confirmed functional information.

5 Brief Description of the Drawings

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The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray.

The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression

with signal intensity greater than 3 in at least one tissue, with: FIG. TA showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 78 showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for spering EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3

10 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (1 x 10⁻³⁰)

15 ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than 1e-30 (1 x 10⁻³⁰) ("known");

FIG. 9 presents a Mondrian of BAC AC003172 (bases 25,000 to 130,000), containing the carbamyl phosphate 20 synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming,

25 Annotating, and Displaying Functional Regions From Genomic

Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present

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invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting inter alia of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will

minimally contain as annotation a unique sequence
identifier (accession number), and will typically be
annotated further to identify the date of accession,
species of origin, and depositor. Because database 100 can
contain nongenomic sequence, each sequence will typically
be annotated further to permit query for genomic sequence.

Chromosomal origin, optionally with map location, can also
be present. Data can be, and over time increasingly will
be, further annotated with additional information, in part
through use of the present invention, as described below.
Annotation can be present within the data records, in
information external to database 100 and linked to the
records thereto, or through a combination of the two.

in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, C. elegans, C.

Databases useful as genomic sequence database 100

brigsii, Drosophila, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic

sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
are predicted to have a biological function as specified by
the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
regulating message degradation after transcription into
mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite

25 function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is

30 bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification

and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps

can be automated.

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FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to 10 encode protein can be identified inter alia using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of 15 algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of 20 algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be

identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than about 10 - 12 fragments.

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Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, infra, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added

relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods

thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent 5 analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial 10 sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the 15 genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual secuence. Such comparison can readily be done using programs well known in the art, such as CROSS MATCH, or by proprietary sequence comparison programs the engineering of 20 which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases 25 and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized

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by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those 10 nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also 15 include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, inter alia, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence 20 database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified 30 within the genomic sequence.

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As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the

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like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

5 The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genemic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not 10 hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

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Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be 25 performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when

consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genemic sequence and identifies consensus among 10 the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset 15 thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, infra, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% 25 of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

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Furthermore, consensus can be required among different approaches to identifying a chosen function. 30

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative

sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the 5 predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally 10 representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

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In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based inter alia upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that 25 have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the genespecific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses 30 amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies

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amplified product, further considerations involving hypridization stringency can be applied to identify that subset of sequences that will most readily permit sequence—specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

10 For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in

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process 200, and as further identified as suitable by process 301, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

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However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300,400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger

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fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

thus input into one or more primer design programs, such as PRIMER3 (available online for use at http://www-genome.wi.mit.edu/cgi-bin/primer/), with a goal of amplifying at least about 500 pase pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Frimers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

bs added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can

conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning: A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

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After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline

silicon or plastics. Such plastics include

polymethylacrylic, polyethylene, polypropylene,

polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate,

spolyacetal, polysulfone, celluloseacetate,

cellulosenitrate, nitrocellulose, or mixtures thereof, can

also be used. Typically, the support will be rectangular,

although other shapes, particularly circular disks and even

spheres, present certain advantages. Particularly

10 advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying

nucleic acids on support substrates can be constructed
using public domain specifications (The MGuide, version
2.0, http://cmgm.stanford.edu/pbrown/mguide/index.html), or
can conveniently be purchased from commercial sources
(MicroArray GenII Spotter and MicroArray GenIII Spotter,

Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can
also be effected by printing methods, including those using
ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids.

For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

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As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose

Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

10 certain further constraints upon the types of nucleic acid

analogs that can be generated.

For example, gene expression can be confirmed
using hybridization to lower density arrays, such as those
constructed on membranes, such as nitrocellulose, nylon,
and positively-charged derivatized nylon membranes.
Further, gene expression can also be confirmed using
nonplanar, bead-based microarrays such as are described in
Brenner et al., Proc. Natl. Acad. Sci. USA 97(4):166501670
(2000); U.S. Patent No. 6,057,107; and U.S. Patent No.
5,736,330. In theory, a packed collection of such beads
provides in aggregate a higher density of nucleic acid
probe than can be achieved with spotting or lithography
techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and

upto 10,000 - 50,000 or more nucleic acid probes of

discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the 5 array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, 10 representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and 15 advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by in situ synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for 20 study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be 25 derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the de novo construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., Cancer Res. (in press). Such 30 microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays

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based thereupon — are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, infra, the remaining population of genes identified from genomic sequence by the methods of the present invention — that is, the one third of sequences that had previously been accessioned in EST or other expression databases — are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, a priori knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays

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of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

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A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes

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disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage.

Preferably, at least about 85, 90 or more than 90% of exonincluding probes in the genome-derived single exon microarray of the present invention lack vector sequence.

With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious crosshybridization to a probe vector sequence is reduced.

As a further consequence of excision or

15 amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partiallyspliced message, probes disposed upon EST arrays will often
include multiple exons. The percentage of such exon
5 spanning probes in an EST microarray can be calculated, on
average, based upon the predicted number of exons/gene for
the given species and the average length of the immobilized
probes. For human genes, the near-complete sequence of
human chromosome 22, Dunham et al., Nature 402(6761):489-95

(1999), predicts that human genes average 5.5 exons/gene.
Even with probes of 200 - 500 bp, the vast majority of
human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the

present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genomederived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarmays, to use the genome-derived single exen microarmays of the present invention to measure tissue-specific empression of individual exens, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific empression patterns.

Furthermore, the exons that are represented in

15 EST microarrays are often biased toward the 3' or 5' end of
their respective genes, since sequencing strategies used
for EST identification are so biased. In contrast, no such
3' or 5' bias necessarily inheres in the selection of exons
for disposition on the genome-derived single exon

20 microarrays of the present invention.

Conversely, the probes provided on the genomederived single exon microarrays of the present invention
typically, but need not necessarily, include intronic
and/or intergenic sequence that is absent from EST

25 microarrays, which are derived from mature mRNA.
Typically, at least about 50, 60, 70, 80 or 90% of the
exon-including probes on the genome-derived single exon
microarrays of the present invention include sequence drawn
from noncoding regions. As discussed above, the additional
30 presence of noncoding region does not significantly
interfere with measurement of gene expression, and provides
the additional opportunity to assay prespliced RNA, and
thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from in situ

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synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on in situ synthesis 5 microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the in situ synthesis microarray requires 10 substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present 15 invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial 20 probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for in situ synthesis microarrays.

A further distinction is that the probes in in 25 situ synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on in situ microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum 35 stringency across the array as a whole.

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In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over in situ synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the in situ synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., Proc. Natl. Acad. Sci. USA 94:13057-13062 (1997).

only about 220 - 250 of the 6100 or so nuclear genes in Saccharomyces cerevisiae — that is, only about 4 - 5% — have standard, spliceosomal, introns, Lopez et al.,

Nucl. Acids Res. 28:85-86 (2000); Spingola et al., RNA

5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as Saccharomyces cerevisiae, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present

invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above-described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, infra.

mRNA can be prepared by standard techniques, see

Ausubel et al. and Maniatis et al., or purchased

commercially. The mRNA is then typically reverse
transcribed in the presence of labeled nucleotides: the

index source (that in which expression is desired to be

measured) is reverse transcribed in the presence of

nucleotides labeled with a first label, typically a

fluorophore (fluorochrome; fluor; fluorescent dye); the

reference source is reverse transcribed in the presence of

a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, infra, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a 10 Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the
genome-derived single exon microarray will identify certain
of the probes thereon as of particular interest. Thus, it
is often desirable that the user be able readily to obtain
sufficient quantities of an individual probe, either for
subsequent arrayed deposition upon an additional support
substrate, often as part of a microarray having a plurality
of probes so identified, or alternatively or additionally
as a solitary solid-phase or solution-phase probe, for
further use.

Thus, in another aspect, the present invention

25 provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and

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although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidlynoncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genomederived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such 10 as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, 15 in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, 20 etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together 25 with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable 35 media can be packaged with the microarray, with the ordered

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probe set, or with both.

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If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then 5 separate packaging of the genome-derived single exon microarray and the bicinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted 15 to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, 20 or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and 30 more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query including information on identical sequences and 35 information on nonidentical sequences that have diffuse or

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focal regions of sequence homology to the quary sequence can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical 5 or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully 10 relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are 15 well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

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FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual 35 nucleotides would rarely be readable in hard copy output of

display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically — for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 — or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping 25 nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor 30 such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to 35 computerized data, additional control over the first and

last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the putput from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired

15 function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the

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results from DICTION.

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Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, 5 and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the 10 prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such 15 measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse) -activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in 25 predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the 30 number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such 35 display makes more useful the ability of the user to select

a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and userselectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG.

3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted supra, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example,

where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 37 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 380 and 88. Rectangles 880 indicate regions

15 that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify

20 sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

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Where display 80 is used as a graphical user interface, restandles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. 5 As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

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Rectangle 85 can consist of a single rectangle, 15 thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of creen can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for 30 respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed infra, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using

normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented infra.

BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 89 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

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The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of

portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 9,980 of these ORFs in heart.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in heart is currently available for use in measuring the level of its ORF's expression in heart.

Diseases of the heart and vascular system are a

25 significant cause of human morbidity and mortality.

Increasingly, genetic factors are being found that
contribute to predisposition, onset, and/or aggressiveness
of most, if not all, of these diseases. Although mutations
in single genes have on occasion been identified as

30 causative, these disorders are for the most part believed
to have polygenic etiologies.

For example, cardiovascular disease (CVD), which includes coronary heart disease, stroke, and peripheral arterial vascular disease, is the leading cause of death in the United States and other developed countries. In

developing regions, coronary heart disease and stroke are ranked second and third, respectively, as causes of mortality. In the United States alone, about 1 million deaths (about 42% of total deaths per year) result from CVD each year. CVD is also a significant cause of morbidity, with about 1.5 million people suffering myocardial infarction, and about 500,000 suffering strokes in the United States each year. With risk for CVD increasing with age, and an increasingly aging population, CVD will continue to be a major health problem into the future.

CVD is caused by arterial lesions that begin as fatty streaks, which consist of lipid-laden foam cells, and develop into fibrous plaques. The atherosclerotic plaque may grow slowly, and over several decades may produce a severe stenosis or result in arterial occlusion. Some plaques are stable, but other, more unstable, ones may rupture and induce thrombosis. The thrombi may embolize, rapidly occluding the lumen and leading to myocardial infarction or acute ischemic syndrome.

Risk factors for CVD include age and gender. 20 addition, a family history of CVD significantly increases risk, indicating a genetic basis for development of this disease complex. Obesity, especially truncal obesity, the cause of which is suspected to be genetic, is yet another 25 risk factor for CVD. Familial disorders such as hyperlipidemia, hypoalphalipoproteinemia, hypertriglyceridemia, hypercholesterolemia, hyperinsulinemia, homocystinuria, and dysbetalipoproteinemia, all of which lead to lipid or lipoprotein abnormalities, can predispose one to the development of CVD. Both insulin-dependent and noninsulin-dependent diabetes mellitus, both of which have genetic components, have been also linked to the development of atherosclerosis.

The literature is replete with evidence for

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genetic causes of cardiovascular diseases. For example, studies by Allayee et al., Am. J. Hum. Genet. 63:577-585(1998), indicated a genetic association between familial combined hyperlipidemia (FCHL) and small dense LDL particles. The studies also concluded that the genetic determinants for LDL particle size are shared, at least in part, among FCHL families and the more general population at risk for CVD. Juo et al., Am. J. Hum. Genet. 63: 586-594 (1998) demonstrated that small, dense LDL particles and elevated apolipoprotein B levels, both of which are commonly found in members of FCHL families, share a common major gene plus individual polygenic components.

The common major gene was estimated to explain 37% of the variants of adjusted LDL particle size and 23% of the variants of adjusted apoB levels.

The atherogenic lipoprotein phenotype (ALP) is a common heritable trait, symptoms of which include a prevalence of small, dense LDL particles, increased levels of triglyceride-rich lipoproteins, reduced levels of high density lipoprotein, and increased risk of CVD, particularly myocardial infarction. Both Nishina et al., Proc. Nat. Acad. Sci. 89: 708-712 (1992) and Rotter et al., Am. J. Hum. Genet. 58: 585-594(1996) demonstrated linkage between ALP and the LDLR locus. Rotter et al., supra, also reported linkage to the CETP locus on chromosome 16 and to the SOD1 locus on chromosome 6, and possibly also to the APOA1/APOC3/APOA4 cluster on chromosome 11.

Mutations in genes identified as components of lipid metabolism, e.g., apolipoprotein E (apoE) and LDL receptor (LDLR), have been shown to be associated with predisposition to the development of CVD. For example, several apoE variants had been found to be associated with familial dysbetalipoproteinemia, characterized by elevated plasma cholesterol and triglyceride levels and an increased risk for atherosclerosis (de Knijff et al., Mutat 4: 178-

194 (1994)). Mutations in the LDLR gene have been associated with the familial hyporcholesterolemia, an autosomal dominant disorder characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL), that can lead to increased susceptibility to CVD.

To date, mutations in numerous genes have been shown to be associated with increased CVD susceptibility. However, the identified genetic associations are believed not to account for all genetic contributions to CVD.

10 As yet another example, hypertension is a major health problem because of its high prevalence and its association with increased risk of CVD. Approximately 25% of all adults and over 60% of persons older than 60 years in the United States have high blood pressure.

Material or systemic hypertension is diagnosed when the average of two or more diastolic BP measurements on at least two subsequent visits is 90 mm Hg or more, or when the average of multiple systolic BP readings on two or more subsequent visits is consistently greater than 140 mm Hg. Pulmonary hypertension is defined as pressure within the pulmonary arterial system elevated above the normal range; pulmonary hypertension may lead to right ventricle (RV) failure.

Hypertension, together with other cardiovascular risk factors, leads to atherosclerosis and other forms of CVD, primarily by damaging the vascular endothelium. In more than 40% of the U.S. population, hypertension is accompanied by hyperlipidemia and leads to the development of atherosclerotic plaques. In the absence of hyperlipidemia, intimal thickening occurs. Non-atherosclerotic hypertension-induced vascular damage can lead to stroke or heart failure.

Familial diseases associated with secondary hypertension include familial renal disease, polycystic kidney disease, medullary thyroid cancer, pheochromocytoma,

and hyperparathyroidism. Hypertension is also twice as common in patients with diabetes mellitus.

essential hypertension, that is, lack identifiable

antecedent clinical cause. Essential hypertension shows
clustering in families and can result from a variety of
genetic diseases. In most cases, high blood pressure
results from a complex interaction of factors with both
genetic and environmental components. The recent search
for genes that contribute to the development of essential
hypertension has shown that the disorder is polygenic in
origin. However, with several exceptions (such as
angiotensinogen, angiotensin receptor-1, beta-3 subunit of
guanine nucleotide-binding protein, tumor necrosis factor
receptor-2, and "-adducin), the particular genes involved
are still being sought.

Susceptibility loci for essential hypertension have been mapped to chromosomes 17 and 15q. Hasstedt et al., Am. J. Hum. Genet. 43: 14-22 (1988) measured red cell sodium in 1,800 normotensive members of 16 Utah pedigrees ascertained through hypertensive or normotensive probands, siblings with early stroke death, or brothers with early coronary disease, and suggested that red blood cell sodium was determined by 4 alleles at a single locus. This major locus was thought to explain 29% of the variance in red cell sodium, and polygenic inheritance explained another 54.6%. A higher frequency of the high red blood cell sodium genotype in pedigrees in which the proband was hypertensive rather than normotensive provided evidence that this major locus increases susceptibility to hypertension.

From a study of systolic blood pressure in 278 pedigrees, Perusse et al., Am. J. Hum. Genet. 49: 94-105 (1991) reported that variability in systolic blood pressure is likely influenced by allelic variation of a single gene, with gender and age dependence. They also suggested that a

single gene may be associated with a steeper increase of blood pressure with age among males and females.

There is strong evidence, however, for additional as yet uncharacterized, hypertension-associated loci on other chromosomes.

For example, Xu et al., Am. J. Hum. Genet. 64: 1694-1701 (1999) carried out a systematic search for chromosomal regions containing genes that regulate blood pressure by scanning the entire autosomal genome using 367 polymorphic markers. Because of the sampling design, the number of sib pairs, and the availability of genotyped parents, this study represented one of the most powerful of its kind. Although no regions achieved a 5% genomewide significance level, maximum lod scores were greater than 2.0 for regions of chromosomes 3, 11, 15, 16, and 17.

As another example, cardiac arrhythmias account for several thousand deaths each year. Arrhythmias such as ventricular fibrillation, which causes more than 300,000 sudden deaths annually in the United States alone, encompass a multitude of disorders. Another type of arrhythmia, idiopathic dilated cardiomyopathy, of which familial dilated cardiomyopathy accounts for 20-25%, is responsible for more than 10,000 deaths in the United States annually and is the predominant indication for cardiac transplantation.

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Cardiac arrhythmias can be divided into bradyarrhythmias (slowed rhythms) or tachyarrhythmias (speeded rhythms). Bradyarrhythmias result from abnormalities of intrinsic automatic behavior or conduction, primarily within the atrioventricular node and the His-Purkinje's network. Tachyarrhythmias are caused by altered automaticity, reentry, or triggered automaticity.

Bradyarrhythmias arising from suspected polygenic disorders include Long QT syndrome 4, atrioventricular block, familial sinus node disease, progressive cardiac

conduction defect, and familial cardiomycpathy.

Tachyarrhythmias with possible underlying polygenic causes include familial ventricular tachycardia, Welff-Parkinson-White syndrome, familial arrhythmogenic right ventricular dysplasia, heart-hand syndrome V, Mal de Meleda, familial ventricular fibrillation, and familial noncompaction of left ventricular myocardium.

For some of the arrhythmias, one or more of the causative genes have been identified.

For example, atrioventricular block has been 10 associated with mutations in the SCN5A gene, as well as mutations in a locus mapped to 19q13. Studies have shown linkage of familial sinus node disease to a marker on 10q22-q24. Familial ventricular tachycardia has been 15 linked to mutations in genes encoding the G proteir subunit alpha-i2 (GNAI1), and/or related genes. Examination of families with Wolff-Parkinson-White syndrome suggest an autosomal dominant pattern of inheritance and evidence of linkage of the disorder to DNA markers on band 7q3. 20 Linkage analysis shows strong evidence for localization of a gene for Mal de Meleda disease on 8qter. Familial ventricular fibrillation can be caused by mutations in the cardiac sodium channel gene SCN5A. Familial noncompaction of left ventricular myocardium has been linked to mutations 25 in the gene encoding tafazzin (TAZ), or in the FK506binding protein 1A gene (FKBP1A).

Familial dilated cardiomyopathy is characterized by an autosomal dominant pattern of inheritance with agerelated penetrance. The linkage of familial dilated cardiomyopathy to several loci indicate that it is polygenic. These loci include CMD1A on 1p11-q11, CMD1B on 9q13, CMD1C on 10q21, CMD1D on 1q32, CMD1E on 3p, CMD1F on 6q, CMD1G on 2q31, CMD1H on 2q14-q22, and CMD1I, which results from mutation in the DES gene on 2q35.

In addition, cardiomyopathy can also be caused by

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mutations in the ACTC gene, the cardiac beta-myosin heavy chain gene (MYH7), or the cardiac troponin T gene.

Familial arrhythmogenic right ventricular dysplasia is inherited as an autosomal dominant with reduced penetrance and is one of the major genetic causes of juvenile sudden death. It is estimated that the prevalence of familial arrhythmogenic right ventricular dysplasia ranges from 6 per 10,000 in the general population to 4.4 per 1,000 in some areas.

Several loci for familial arrhythmogenic right ventricular dysplasia have been mapped indicating that this disease is also polygenic in nature. These loci include ARVD1 on 14q23-q24, ARVD2 on 1q42-q43, ARVD3 on 14q12-q22, ARVD4 on 2q32.1-q32.3, ARVD5 on 3p23, and ARVD6 on 10p14-

Progressive cardiac conduction defect (PCCD), also called Lenegre-Lev disease, is one of the most common cardiac conduction diseases. It is characterized by progressive alteration of cardiac conduction through the His-Purkinje system with right or left bundle branch block and widening of QRS complexes, leading to complete atrioventricular block and ultimately causing syncope and sudden death. It represents the major cause of pacemaker implantation in the world (0.15 implantations per 1,000 inhabitants per year in developed countries). The cause of PCCD is unknown but familial cases with right bundle branch block have been reported suggesting that at least some cases are of genetic origin. Reports have linked PCCD to HB1 on 19q13.3, and to mutations in the SCN5A gene (Schott et al., Nature Genet. 23: 20-21 (1999)).

As yet a further example, congenital heart disease occurs at a rate of 8 per 1000 live births, which corresponds to approximately 32,000 infants with newly diagnosed congenital heart disease each year in the United States. Twenty percent of infants with congenital heart

disease die within the first year of life. Approximately 80% of the first-year survivors live to reach adulthood. Congenital heart disease also has economic impact due to the estimated 20,000 surgical procedures performed to correct circulatory defects in these patients. The estimated number of adults with congenital heart disease in the United States is currently about 900,000.

In 90% of patients, congenital heart disease is attributable to multifactorial inheritance. Only 5-10% of malformations are due to primary genetic factors, which are either chromosomal or a result of a single mutant gene.

The most common congenital heart disease found in adults is bicuspid aortic valve. This defect occurs in 2% of the general population and accounts for approximately 50% of operated cases of aortic stenosis in adults. Atrial septal defect is responsible for 30-40% of congenital heart disease seen in adults. The most common congenital cardiac defect observed in the pediatric population is ventricular septal defect, which accounts for 15-20% of all congenital lesions. Tetralogy of Fallot is the most common cyanotic congenital anomaly observed in adults. Other congenital heart diseases include Eisenmenger's syndrome, patent ductus arteriosus, pulmonary stenosis, coarctation of the aorta, transposition of the great arteries, tricuspid atresia, univentricular heart, Ebstein's anomaly, and double-outlet right ventricle.

A number of studies have identified putative genetic loci associated with one or more congenital heart diseases.

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Congenital heart disease affects more than 40% of all Down syndrome patients. The candidate chromosomal region containing the putative gene or genes for congenital heart disease associated with Down syndrome is 21q22.2-q22.3, between ETS2 and MX1.

DiGeorge syndrome (DGS) is characterized by

several symptoms including outflow tract defects of the heart such as teratology of Fallot. Most cases result from a deletion of chromosome 22q11.2 (the DiGeorge syndrome chromosome region, or DGCR). The 22q11 deletion is the second most common cause of congenital heart disease after Down syndrome. Several genes are lost in this deletion including the putative transcription factor TUPLE1. This deletion is associated with a variety of phenotypes, e.g., Shprintzen syndrome; conotruncal anomaly face (or Takao syndrome); and isolated outflow tract defects of the heart including Tetralogy of Fallot, truncus arteriosus, and interrupted aortic arch.

Whereas 90% of cases of DGS may now be attributed to a 22q11 deletion, other associated chromosome defects

15 have been identified. For example, Greenberg et al., Am.

J. Hum. Genet. 43:605-611 (1988), reported 1 case of DGS with del10p13 and one with a 18q21.33 deletion. Fukushima et al., Am. J. Hum. Genet. 51 (suppl.):A80 (1992) reported linkage with a deletion of 4q21.3-q25. Gottlieb et al.,

20 Am. J. Hum. Genet. 62: 495-498 (1998) concluded that the deletion of more than 1 region on 10p could be associated with the DGS phenotype. The association of the DiGeorge syndrome with at least 2 and possibly more chromosomal locations suggests strongly the involvement of several

25 genes in this disease.

Digilio et al., J. Med. Genet. 34: 188-190 (1997), calculated empiric risk figures for recurrence of isolated Tetralogy of Fallot in families after exclusion of del(22q11), and concluded that gene(s) different from those located on 22q11 must be involved in causing familial aggregation of nonsyndromic Tetralogy of Fallot. Johnson et al., Am. J. Med. Genet. (1997) conducted a cytogenetic evaluation of 159 cases of Tetralogy of Fallot. They reported that a del(22q11) was identified in 14% who underwent fluorescence in situ hybridization (FISH) testing

with the N25 cosmid probe.

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other congenital heart disease are also suspected to be of polygenic origin. For example, Holmes et al., Birth Defects Orig. Art. Ser. X(4): 228-230 (1974) described familial clustering of hypoplastic left heart syndrome in siblings consistent with multifactorial causation.

Other significant diseases of the heart and vascular system are also believed to have a genetic, 10 typically polygenic, etiological component. These diseases include, for example, hypoplastic left heart syndrome, cardiac valvular dysplasia, Pfeiffer cardiocranial syndrome, oculofaciocardiodental syndrome, Kapur-Toriello syndrome, Sonoda syndrome, Ohdo Blepharophimosis syndrome, 15 heart-hand syndrome, Pierre-Robin syndrome, Hirschsprung disease, Kousseff syndrome, Grange occlusive arterial syndrome, Kearns-Sayre syndrome, Kartagener syndrome, Alagille syndrome, Ritscher-Schinzel syndrome, Ivemark syndrome, Young-Simpson syndrome, hemochromatosis, 20 Holzgreve syndrome, Barth syndrome, Smith-Lemli-Opitz syndrome, glycogen storage disease, Gaucher-like disease, Fabry disease, Lowry-Maclean syndrome, Rett syndrome, Opitz syndrome, Marfan syndrome, Miller-Dieker lissencephaly syndrome, mucopolysaccharidosis, Bruada syndrome, 25 humerospinal dysostosis, Phaver syndrome, McDonough syndrome, Marfanoid hypermobility syndrome, atransferrinemia, Cornelia de Lange syndrome, Leopard syndrome, Diamond-Blackfan anemia, Steinfeld syndrome, progeria, and Williams-Beuren syndrome.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human heart and vascular system, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be

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expressed at detectable levels in human heart, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known 10 to be characteristic of a given heart or vascular disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the 15 patient's heart or vascular tissues to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in heart or vascular tissue of individuals with 20 known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of heart or vascular disease to be assessed through the massively parallel 30 determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human heart. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at

sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the heart has been demonstrated are useful for both measurement in the heart and for survey of expression in other tissues.

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Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

Gene expression analysis using microarrays — conventionally using microarrays having probes derived from expressed message — is well-established as useful in the biclogical research arts (see Lockhart et al. Nature 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct 10 Programs Regulating Lung Inflammation and Fibrosis," Proc. Natl. Acad. Sci. USA 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," Arch. Biochem. Biophys. 376(1):66-73 (2000)), viral infection (see for 15 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," Virology 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of 20 Replicative Senescence," Curr. Biol. 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," Proc. Natl. Acad. Sci. USA 97(6):2680-5 (2000)).

25 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," Proc. Natl.

30 Acad. Sci. USA 96(12):6745-50 (1999); Perou et al.,
"Distinctive Gene Expression Patterns in Human Mammary
Epithelial Cells and Breast Cancers, Proc. Natl. Acad. Sci.
USA 96(16):9212-7 (1999); Wang et al., "Identification of
Genes Differentially Over-expressed in Lung Squamous Cell

35 Carcinoma Using Combination of cDNA Subtraction and

Microarray Analysis," Oncogene 19(12):1519-28 (2000);
Whitney et al., "Analysis of Gene Expression in Multiple
Sclerosis Lesions Using cDNA Microarrays," Ann. Neurol.
46(3):425-8 (1999)), in drug discovery screens—see, for
example, Scherf et al., "A Gene Expression Database for the
Molecular Pharmacology of Cancer," Nat. Genet. 24(3):236-44
(2000)) and in diagnosis to determine appropriate treatment
strategies (see, for example, Sgroi et al., "In vivo Gene
Expression Profile Analysis of Human Breast Cancer
Progression," Cancer Res. 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents — whether in lead compound discovery or in subsequent screening of lead compound derivatives — the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

wo 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., Trends Biochem. Sci. 24(5):168-173 (1999) and Zweiger, Trends Biotechnol. 17(11):429-436 (1999); Schena et al.

The invention particularly provides genomederived single-exon probes known to be expressed in heart.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

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Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothicates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a

25 form and quantity suitable for amplification, where the
amplified product is thereafter to be used in the
hybridization reactions that probe gene expression.

Typically, such probes are provided in a form and quantity
suitable for amplification by PCR or by other well known

30 amplification technique. One such technique additional to
PCR is rolling circle amplification, as is described, inter
alia, in U.S. Patent Nos. 5,854,033 and 5,714,320 and
international patent publications WO 97/19193 and
WO 00/15779. As is well understood, where the probes are
to be provided in a form suitable for amplification, the

range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form

suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however — that is, for use in a hybridization reaction in which the probe is not first

bound to a support substrate (although the target may indeed be so bound) — length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message — a subset of target sequence that is much reduced in complexity as compared to genomic sequence — even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 9,981 - 19,771, respectively, for probe SEQ ID NOS. 1 - 9,980. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 9,981 - 19,771 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, inter alia, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 μg/μl poly(dA), 0.2 μg/μl human cotl DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization

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at 65°C in 6% SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in 5 temperature for hybridization and washing to room temperature (approximately $25^{\circ}\mathrm{C}$).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of 10 other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are 20 maximally about 5 kb will be used, more typically no more than about 3 kb.

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It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly 25 translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further 30 be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have 35 sequence complementary to those described herein above and

below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution

10 hybridization, the probes of the present invention can

usefully have detectable labels. Nucleic acid labels are

well known in the art, and include, inter alia, radioactive

labels, such as ³H, ³²P, ³³P, ³⁵S, ¹²⁵I, ¹³¹I; fluorescent

labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR®

15 Green and other labels described in Haugland,

Handbook of Fluorescent Probes and Research Chemicals, 7th
ed., Molecular Probes Inc., Eugene, OR (2000), or
fluorescence resonance energy transfer tandem conjugates
thereof; labels suitable for chemiluminescent and/or
20 enhanced chemiluminescent detection; labels suitable for
ESR and NMR detection; and labels that include one member
of a specific binding pair, such as biotin, digoxigenin, or
the like.

The probes, either in quantity sufficient for amplification, can be provided in individual vials or containers.

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Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

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If, as earlier mentioned, the GRF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, 5 different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen 10 for the common attribute of expression in the human heart.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

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The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid 20 amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, inter alia, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays 25 useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, supra.

The invention particularly provides genomederived single-exon nucleic acid microarrays comprising a 30 plurality of probes known to be expressed in human heart. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 9,980.

When used for gene expression analysis, the

WO 01/57274 PCT/US01/00666 cenome-derived single exon microarrays provide greater

physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. 5 At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the 15 assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 9,980 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 9,981 - 19,771, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 9,980 can be used, or that portion thereof in SEQ ID NOS. 9,981 - 19,771 used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially

that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-XTM Expression System, ClonTech Laboratories, Palo

Alto, CA; Protein Fusion & Purification (pMALTM) System, New

England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, inter alia, in Chan et al. (eds.), Fmcc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7), Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence

15 translated from SEQ ID NOS.: 9,981 - 19,771. Such amino acid sequences are set out in SEQ ID NOS: 19,772 - 29,119. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted 30 in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period

35 immediately preceding this study were downloaded from

GenBank. This corresponds to $\sim\!2200$ clones, totaling $\sim\!350$ MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

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PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the aminomodified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF

15 was passed to the primer picking software, PRIMER3

(available online for use at

http://www-genome.wi.mit.edu/cgi-bin/primer/). A first

additional sequence was commonly added to each ORF-unique

5' primer, and a second, different, additional sequence was

20 commonly added to each ORF-unique 3' primer, to permit

subsequent reamplification of the amplicon using a single

set of "universal" 5' and 3' primers, thus immortalizing

the amplicon. The addition of universal priming sequences

also facilitates sequence verification, and can be used to

25 add a cloning site should some ORFs be found to warrant

further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of

agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR 20 failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene 25 finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

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Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some

submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hypridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the abovedescribed process, reduced to 9750 discrete probes, which
were spotted in duplicate onto glass slides using

15 commercially available instrumentation (MicroArray GenII
Spotter and/or MicroArray GenIII Spotter, Molecular
Dynamics, Inc., Sunnyvale, CA). Each slide additionally
included either 16 or 32 E. coli genes, the average
hybridization signal of which was used as a measure of

20 background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified)

25 produced an exact match (BLAST Expect ("E") values less
than 1 e⁻¹⁰⁰) to either an EST (20% of sequences) or a known
mRNA (13% of sequences). A further 22% of the probe
sequences showed some homology to a known EST or mRNA
(BLAST E values from 1 e⁻⁵ to 1 e⁻⁹⁹). The remaining 45% of

30 the probe sequences showed no significant sequence homology
to any expressed, or potentially expressed, sequences
present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTK, Gish et al., Nature Genet. 3:266

(1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

5 Table 1

Function	of Predic	cted ORFs As	Deduced From Comparative
Sequence	e Analysis		
Total	V6 chip	V7 chip	Function Predicted from
			Comparative Sequence
			Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	1.4	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1)

5 Gy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 10) cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Bistech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA+ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 ug random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 uM, and 200 U Superscript II The reaction was incubated for 2 hours at 42°C. 25 After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5.

30 Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 μl hybridization solution containing 50% formamide, 5X SSC, 0.2 μg/μl poly(dA), 0.2 μg/μl human cot1 DNA, and 0.5 % SDS.

Probe was eluted using 10 mM Tris pH 8.5.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1% SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1% SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray

10 Biochip: Tools and Technology, Eaton Publishing
Company/BioTechniques Books Division (2000) (ISBN:
1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it

15 attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

30 FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues 35 tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of 15 all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data — that is, presents the results returned by query of EST, NR and SwissProt databases using 25 the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from le-05 to 1e-99; black: E values > 1e-05). 30

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the

following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more

"novel" genes among those that were up-regulated in only
one tissue, as compared with those that were down-regulated
in only one tissue. In fact, it was found that ORFs whose
expression was measurable in only a single of the tested
tissues were represented in sequencing databases at a rate
of only 11%, whereas 36% of the ORFs whose expression was
measurable in 9 of the tissues were present in public
databases. As for those ORFs expressed in all ten tissues,
fully 45% were present in existing expressed sequence
databases. These results are not unexpected, since genes
expressed in a greater number of tissues have a higher
likelihood of being, and thus of having been, discovered by
EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than 1e-30 ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since

very high signal intensity correlates with very commonlyexpressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large

5 number of even the high expressers were "unknown". Since
the genomic approach used to identify genes and to confirm
their expression does not bias exons toward either the 3'
or 5' end of a gene, many of these high expression genes
will not have been detected in an end-sequenced cDNA

10 library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic

20 sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, 30 Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as

measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and
indeed should not, be confirmed by independent assay
methods, or the high throughput, highly parallel advantages
of microarray hybridization assays will be lost. However,
in addition to the two RT-PCR results presented above, the
observation that 1/3 of the arrayed genes exist in
expression databases provides powerful confirmation of the
power of our methodology — which combines bioinformatic
prediction with expression confirmation using genome—
derived single exon microarrays — to identify novel genes
from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed

20 high (normalized) signal in brain, but which showed very
low (normalized) signal (less than 0.5, determined to be
biological noise) in all other tissues, were further
studied. There were 82 sequences that fit these criteria,
approximately 2% of the arrayed elements. The 10 sequences

25 showing the highest signal in brain in microarray
hybridizations are detailed in Table 2, along with assigned
function, if known or reasonably predicted.

Table 2

15

Function of the Most Highly Expressed Genes Expressed Only in Brain

WO 0	01/57274				PCT/US01/00666
	Microarray	Normal	Expressi	Homology	Gene Function
	Sequence	ized	on Ratio	to EST	as described by
	Name	Signal		present	GenBank
				in	
				GenBank	
	AP000217-1	5.2	T+7.7	High	S-100 protein,
					b-chain, Ca ²⁺
					binding protein
					expressed in
					central nervous
					system
	AP000047-1	2.3		High	Unknown
					Function
	AC006548-9	1.7		High	Similar to
					mouse membrane
					glyco-protein
					M6, expressed
					in central
					nervous system
	AC007245-5	1.5		High	Similar to
					amphiphysin, a
					synaptic
					vesicle-
					associated
					protein. Ref 21
	L44140-4	1.2	+2.0	High	Endothelial
				;	actin-binding
					protein found
					in nonmuscle

filamin

01/5/2/4				PC1/US01/00666
AC004689-9	2.2	+3.5	High	Protein
				Phosphatase
				PP2A, neuronal/
				downregulates
				activated
				protein kinases
AL031657-1	1.2	+3.0	High	Unknown
				function/
				Contains the
1				anhyrin motif,
				a common
				protein
				sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to
				the
				Synaptotagmin I
				protein in
				rat/present at
				low levels
				throughout rat
				brain
AP000086-1	1.0	+2.7	Low	Unknown, very
				poor homology
				to collagen
AC004689-3	1.0		High	Protein
				Phosphatase
				PP2A, neuronal/
				downregulates
				activated
				protein kinases
L			1	L

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon

giving the highest signal (APOG217-1) was found to be the gene encoding an S100B Ca²⁺ binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, Neurochem. Res. 9:1097 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., Trends Biochem. Sci. 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., J. Neurol. Sci. 134(Suppl):52-56 (1995)), a result

PCT/US01/00666 WO 01/57274

duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 18 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Ychromosome RNA-binding motif (Chai et al., Genomics 5 49(2):233-89 (1998))(ACO07320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., Mol. Genet. 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in 15 choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

10

20

Comparis	on of Expression Ra	atio, for each
tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ±0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±

Lung	-4.95	= 0.93	-3.75 ± 0.21
Placenta	-3.56	± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

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For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, 25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom): 30 red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

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The protocols set forth in Examples 1 and 2, supra, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in heart tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical

15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 9,980 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 9,980 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 9,980. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons 30 present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 9,981 - 19,771, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

10 For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more that a five-fold difference between each one of the duplicate spots raw signals.

15

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The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are

presented in Table 4, set forth respectively in Example 5.

Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human heart tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 9,981 - 19,771 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

15 The smallest in value of the BLAST (or BLASTX)
expect ("E") scores for each query sequence across the
three database divisions was used as a measure of the
"expression novelty" of the probe's ORF. Table 4 is sorted
in descending order based on this measure, reported as
20 "Most Similar (top) Hit BLAST E Value". Those sequences for
which no "Hit E Value" is listed are those exons which were
found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO:. of the exon contained within the probe: "EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The 5 pentide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each 10 prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs 15 in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for 20 each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as 25 provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about 1e-05 and 1e-100), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of 1e-05 (i.e., 1 x 10^{-5}) and 1e-100 (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, supra, a BLAST E value of 1e-30 was used as the boundary when only two classes were to be defined for 35 analysis (unknown, >1e-30; known <1e-30) (see also FIG. 8).

30

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about 1e-100 which is probative evidence that the query sequence has previously been shown to be expressed — the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 9,980) and probe exon (SEQ ID NOs.: 9,981 - 19,771, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

- the sequence was derived ("MAP TO"), thus providing a link to the chrcmosomal map location and other information about the genomic milieu of the probe sequence;
- (b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST 25 E value for the "hit";
 - (c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and
- (d) the most similar sequence provided by BLASTX 30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Heart

Table 4 (413 pages) presents expression, homology, and
functional information for the genome-derived single exon
probes that are expressed significantly in human heart.

Page 1 of 413
Table 4
Single Exon Probes Expressed in Heart

			_	_	-, -	_	_		-		-	-	- 1	т-					_				-		<u> </u>	_,_									
Snigle Excit Probes Expressed in Heart	Top Hit Descriptor																																		
Jie Exon Proi	Top Hit Database Source																																		
illo	Top Hit Acession No.																																		
	Most Similar (Top) Hit BLAST E Value																																		
	Expression Signal	4.41	17.08	2.14	76.7	1.87	4.97	1.01	0.95	7.45	0.98	3.03	262	2.34	3.7	1.52	8.97	0.87	0.99	1.71	. 5.94	0.89	0.89	1.03	1.76	0.78	5.08	207	1.92	1.92	5	5.89	4.9	2.9	1.6
	ORF SEQ ID NO:		20647		21039	21361	21381	21467		21491	21620				22875	23121	23192		23309	23781	23838	23858	23859		24402		24617	24629	24834	24835				25490	25678
	Exon SEQ ID NO:	10386		10947		İ		11596	11616	11622	ı		12008	12118	13074	13320	13387	13429	13521	14002	14064	14084	14084	14141	14616	14663	14851	14863	15140	15140	15248	15356	15248	15427	19451
	Probe SEQ ID NO:	442	871	1029	1280	1597	1619	1694	1715	1721	1848	1935	2119	2233	3149	3403	3471	3513	3607	4102	4164	4184	4184	4242	4730	4779	4976	4988	5217	5217	5328	5436	5483	2209	5668

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Table 4
Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	Top Hit Descriptor																		Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18	Haemophilus influenzae Rd section 31 of 163 of the complete genome	Mus musculus Naip3 gene, exon 1; nœuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds	Dongue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds	Mus musculus AT3 gene for antithrombin, complete cds	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds, mitochondrial gene for mitochondrial product	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
le Exon Prob	Top Hit Database Source																	•	NT	NT	NT	TN	LN	LN.	N	SWISSPROT	N	F.	EST HUMAN
Sing	Top Hit Acession No.																		9.9E+00 AJ239028.1	J32716.1	9.6E+00 AF242432.1	9.6E+00 AF242432.1	.11433.1	_11433.1	AB043785.1	9.3E+00 P11210	9.1E+00 AF095609.1	9.1E+00 AF095609.1	8.9E+00 BE971806.1
	Most Similar (Top) Hit BLAST E Value																		9.9E+00	9.8E+00 U32716.1	9.6E+00	9.6E+00	9.4E+00 L11433.1	9.4E+00 L11433.1	9.4E+00	9.3E+00	9.1E+00		8.9E+00
	Expression Signal	1.41	1.84	1.61	1.61	1.29	1.3	3.58	1.26	3.7	2.31	2.84	2.91	1.73	1.73	2.19	1.62	2.11	13.31	1.54	1.32	1.32	2.72	272	5.91	2.97	207	2.07	5.51
	ORF SEQ ID NO:	25700		26404	26405	26769	27012	27569	27758		28355				28151			25230	25701			28047	22389	22390		27271			
	Exon SEQ ID NO:	15599	15769	16244	16244	16577	16820	17364	17534	i '	19472	18266	18555	17906	17906	18606	19094	19280	15600	16549	17805	17805	12499	12499		<u></u>	15163	L	15587
	Probe SEQ ID NO:	2690	5863	6382	6382	2699	6942	7494	7684	8070	8219	8390	9998	8757	8757	8792	9464	9760	5691	6999	7955	7955	2631	2631	2893	7206	5239	5239	5678

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Oligie Lyon Flobes Lypressed III real	Top Hit Descriptor	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus	60224793BF1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5/	HYPOTHETICAL PROTEIN HVLF1	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051 5'	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IBP-1) (IGF-BINDING PROTEIN 1)	CELL DIVISION PROTEIN FTSY HOMOLOG	CYTOCHROME C OXIDASE POLYPEPTIDE III	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2A, NS2A, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1. NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMRASE (NS5);	N. tabacum chitinase gene 50 for class I chitinase C	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2	X.laevis mRNA for M4 muscarinic receptor	Homo sapiens NF2 gene	nr18a12.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMACE:1168318 similar to gb:A10416 METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN);	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'	Pseudomonas æruginosa PA01, section 8 of 529 of the complete genome	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
וופ רעסוו ו וסמפי	Top Hit Database Source	NT Pe	EST_HUMAN 60	SWISSPROT H	EST_HUMAN 60	SWISSPROT BI	Τ	SWISSPROT C	GE (E SWISSPROT NS	GI (E SWISSPROT NS		N	EST_HUMAN M	EST_HUMAN M	SWISSPROT H	H H	NT	NT	EST HUMAN MI	Ĭ L	EST_HUMAN HI	NT	EST_HUMAN 60	EST_HUMAN 60	EST_HUMAN A	NT P:	NT Pe
310	Top Hit Acession No.	4.1E+00 U57503.1	4,1E+00 BF692425.1		4.1E+00 BE885880.1	P47876				P07564		3.9E+00 AF055466.1	3.9E+00 BE814357.1	3.9E+00 BE814357.1					3.9E+00 AA661489.1	3.8E+00 AE001562.1	3.8E+00 D44725.1	3.7E+00 AL161539.2	3.7E+00 BF669279.1	3.7E+00 BF669279.1			3.6E+00 AE004447.1
	Most Similar (Top) Hit BLAST E Value	4.1E+00	4.1E+00	4.1E+00 P09716	4.1E+00	4.1E+00 P47876	4.0E+00 033010	4.0E+00 P14546	4.0E+00 P07564	4.0E+00 P07564	3.9E+00 X64518.1	3.9E+00	3.9E+00	3.9E+00	3.9E+00 P39299	3.9E+00	3.9E+00 X65865.1	3.9E+00 Y18000.1	3.9E+00	3.8E+00	3.8E+00	3.7E+00	3.7E+00	3.7E+00	3.6E+00	3.6E+00	3.6E+00
	Expression Signal	2.95	2.31	2.89	12.46	1.86	1.37	2.17	3,34	3.34	3.89	66.0	2.47	2.47	4.46	4.68	2.32	3.09	5.58	2.4	1.18	10.09	2.13	2.13	2.1	3.66	3.66
	ORF SEQ ID NO:	26684	27641			25241	26285	28164	28934	28935	23181		25454	25455	26140	26379	26913	28120	28816		26982	23622	28872	28873	20322		27091
	Exon SEQ ID NO:	16497	17427	18139	18216	19231		17917	18648	18648		14124	15391	15391	16002	16218	16719	17879	18532	12459	16789	13845	18586	18586	10516	16899	16899
	Probe SEQ ID NO:	6617	9/5/	8259	8339	9672	6266	8768	8835	8835	3459	4226	5471	5471	6108	6355	6840	8695	8715	2588	6911	3936	8730	8730	8/9	7022	7022

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Product SECT DROS SECT Sect							Jie Laulii luk	Oligie Lyol Flobes LApressed in Teals
12737 22535 1.06 3.0E+00 8923984 NT 16196 24970 1.63 3.0E+00 X67806.1 NT 16111 9.5 3.0E+00 P78406 SWISSPROT 17041 1.45 3.0E+00 P78482 SWISSPROT 18251 28501 6.51 3.0E+00 P51842 SWISSPROT 18251 28502 6.51 3.0E+00 P51842 SWISSPROT 18251 28502 6.51 3.0E+00 P51842 SWISSPROT 16146 26300 4.47 2.9E+00 P45842 SWISSPROT 16146 26301 4.47 2.9E+00 P45842 SWISSPROT 16146 26300 4.47 2.9E+00 P45842 SWISSPROT 16147 26433 5.19 2.9E+00 P45889 SWISSPROT 16149 20012 4.47 2.9E+00 P45889 SWISSPROT 16189 20012 4.63 2.7E+00 A165369 NT <t< td=""><td>Probe SEQ ID NO:</td><td>Exon SEQ ID NO:</td><td>ORF SEQ ID NO:</td><td>Expression Signal</td><td>Most Similar (Top) Hit BLAST E Value</td><td>Top Hit Acession No.</td><td>Top Hit Database Source</td><td>Top Hit Descriptor</td></t<>	Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
15196 24970 1.63 3.0E+00 X53096.1 NT 16111 9.5 3.0E+00 P18406 SWISSPROT 17041 1.45 3.0E+00 X67838.1 NT 17041 1.45 3.0E+00 X67838.1 NT 18251 28501 6.51 3.0E+00 P51842 SWISSPROT 11856 21747 2.56 2.9E+00 AF002255.2 NT 11866 26300 4.47 2.9E+00 AF002255.2 NT 16146 26301 4.47 2.9E+00 AF0849.2 SWISSPROT 16176 26501 4.47 2.9E+00 AF18528.1 NT 16179 20012 4.47 2.9E+00 AF0589 SWISSPROT 16179 2012 4.47 2.9E+00 AF0589 SWISSPROT 16179 2012 4.47 2.9E+00 AF0589 SWISSPROT 16179 2012 4.63 2.7E+00 AF0589 SWISSPROT	2807	12737	22535		3.0€+00	18	NT	Homo saplens hypothetical protein PRO0889 (PRO0889), mRNA
16111 9.5 3.0E+00 P18406 SWISSPROT 17041 1.45 3.0E+00 X67838.1 NT 18251 28502 6.51 3.0E+00 P51842 SWISSPROT 18251 28502 6.51 3.0E+00 P51842 SWISSPROT 11826 221747 2.56 2.9E+00 A77 SWISSPROT 11826 221747 2.56 2.9E+00 A78 SWISSPROT 1646 26301 4.47 2.9E+00 A7844 SWISSPROT 16716 26301 4.47 2.9E+00 A78599 SWISSPROT 16716 26301 4.47 2.9E+00 A78699 SWISSPROT 16718 26350 4.78 2.8E+00 A78699 SWISSPROT 16719 20012 4.63 2.7E+00 A16550 NT 1678 26530 4.78 2.8E+00 A165338.1 NT 1670 26532 4.63 2.7E+00 A165338.1 NT	5273	L	24970		3.0E+00		LN L	S. aureus genes encoding Sau96i DNA methyltransferase and Sau96i restriction endonuclease
17041 1.45 3.0E+00 K67838.1 NT 18251 28501 6.51 3.0E+00 P51842 SWISSPROT 18251 28502 6.51 3.0E+00 P51842 SWISSPROT 18251 28502 6.51 3.0E+00 P51842 SWISSPROT 16376 25112 1.63 2.9E+00 AE02225.2 NT 16146 26300 4.47 2.9E+00 D14514 SWISSPROT 16146 26301 4.47 2.9E+00 D14514 SWISSPROT 16147 26433 6.19 2.9E+00 D14514 SWISSPROT 16149 20012 4.77 2.9E+00 D14514 SWISSPROT 16149 20012 4.78 2.9E+00 D14514 SWISSPROT 16149 20012 4.78 2.9E+00 D4518389.1 NT 16159 20012 4.78 2.9E+00 D4518389.1 NT 16327 4.63 2.7E+00 E673306 NT	6245				3.0E+00		SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
18251 28501 6.51 3.0E+00 P51842 SWISSPROT 18251 28502 6.51 3.0E+00 P51842 SWISSPROT 18262 2.1747 2.56 2.9E+00 AE002225.2 NT 1636 2.9E+00 AE002225.2 NT NT 16146 2.6330 4.47 2.9E+00 AE014 SWISSPROT 16146 2.6330 4.47 2.9E+00 AF184 SWISSPROT 16146 2.6330 4.47 2.9E+00 AF184 SWISSPROT 16271 2.6433 5.19 2.9E+00 AF186398.1 NT 16188 2.0545 4.78 2.8E+00 AF186398.1 NT 16188 2.0556 4.78 2.8E+00 AF186398.1 NT 16189 2.0012 4.63 2.7E+00 6679306 NT 16189 2.0013 4.63 2.7E+00 AF186396.1 NT 17746 2.8E+00 AF186396.1 NT NT <td>7164</td> <td>17041</td> <td></td> <td>1.45</td> <td>3.0E+00</td> <td></td> <td>NT</td> <td>B.napus DNA for myrosinase</td>	7164	17041		1.45	3.0E+00		NT	B.napus DNA for myrosinase
18251 28502 6.51 3.0E+00 P51842 SWISSPROT 11858 21747 2.56 2.9E+00 AE002225.2 NT 16376 26112 1.63 2.9E+00 236879.1 NT 16146 26300 4.47 2.9E+00 014514 SWISSPROT 16271 26301 4.47 2.9E+00 014514 SWISSPROT 16371 26433 5.19 2.9E+00 014514 SWISSPROT 16371 26433 5.19 2.9E+00 014514 SWISSPROT 16371 26433 5.19 2.9E+00 014514 SWISSPROT 16189 26012 4.63 2.7E+00 AITSSPROT NT 16189 26012 4.63 2.7E+00 AITSS224 NT 1766 2.2 2.2E+00 AITG5306 NT 1776 2.2 2.7E+00 AITG6501 NT 16324 2.5374 1.97 2.6E+00 AITG6501 NT <t< td=""><td>8374</td><td>18251</td><td>28501</td><td>6.51</td><td>3.0E+00</td><td></td><td>SWISSPROT</td><td>RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE) F) (GC-F)</td></t<>	8374	18251	28501	6.51	3.0E+00		SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE) F) (GC-F)
18251 28502 6.51 3.0E+00 P51842 SWISSPROT 11858 21747 2.56 2.9E+00 AE002225.2 NT 15376 26112 1.63 2.9E+00 Z36879.1 NT 16146 26300 4.47 2.9E+00 O14514 SWISSPROT 16271 26433 6.19 2.9E+00 O14514 SWISSPROT 16271 26433 6.19 2.9E+00 O14514 SWISSPROT 16271 26433 6.19 2.9E+00 O14514 SWISSPROT 11549 21212 5.79 2.8E+00 P46589 SWISSPROT 11519 2.0212 6.79 AF186398.1 NT 116188 26350 4.78 2.8E+00 AA186398.1 NT 116189 2.0013 4.63 2.7E+00 AA161656.2 NT 11762 2.37 1.75 2.7E+00 A6788749.1 NT 11832 2.8E+00 A6788749.1 NT A63								RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE
11858 21747 2.56 2.9E+00 AE00225.2 NT 15976 26112 1.63 2.9E+00 Z36879.1 NT 16146 26300 4.47 2.9E+00 O14514 SWISSPROT 16271 26433 5.19 2.9E+00 P46589 SWISSPROT 11346 21212 5.79 2.8E+00 AF186398.1 NT 11519 20012 4.78 2.8E+00 AF186398.1 NT 11519 20012 4.63 2.7E+00 AF186398.1 NT 10199 20013 4.63 2.7E+00 AF186398.1 NT 10199 20013 4.63 2.7E+00 AF186390.1 NT 1079 20013 4.63 2.7E+00 AF116459.1 NT 1079 2.05 2.8E+00 AF068749.1 NT 15324 2.5373 1.97 2.6E+00 AF0683627.1 EST_HUMAN 16376 2.5574 1.97 2.6E+00 AF06836.1	8374	18251	28502		3.0E+00		SWISSPROT	F) (GC-F)
15376 26112 1.63 2.9E+00 Z36879.1 NT 16146 26300 4.47 2.9E+00 O14514 SWISSPROT 16146 26301 4.47 2.9E+00 O14514 SWISSPROT 16271 26433 5.19 2.9E+00 P46589 SWISSPROT 11346 21212 5.79 2.8E+00 AF186398.1 NT 11519 3.12 2.8E+00 AF186398.1 NT 11519 2.0012 4.63 2.7E+00 AF186398.1 NT 10199 2.0013 4.63 2.7E+00 AF186390.1 NT 10199 2.0013 4.63 2.7E+00 AF18630.1 NT 10199 2.0013 4.63 2.7E+00 AF0850.1 NT 11784 2.435 2.6E+00 AF16459.1 NT 15324 2.5374 1.97 2.6E+00 AF08502.1 NT 16576 2.6E+0 AF085502.1 NT NT 16576 </td <td>1964</td> <td>11858</td> <td>21747</td> <td>2.56</td> <td>2.9E+00</td> <td></td> <td>NT</td> <td>Chlamydophila pneumoniao AR39, section 53 of 94 of the complete genome</td>	1964	11858	21747	2.56	2.9E+00		NT	Chlamydophila pneumoniao AR39, section 53 of 94 of the complete genome
16146 26300 4.47 2.9E+00 O14514 SWISSPROT 16171 26433 5.19 2.9E+00 D4454 SWISSPROT 11346 21212 5.79 2.8E+00 AF186398.1 NT 11519 3.12 2.8E+00 AF186398.1 NT 11519 3.12 2.8E+00 AF186398.1 NT 11519 2.0012 4.63 2.7E+00 AF186398.1 NT 10199 2.0013 4.63 2.7E+00 AF186308 NT 10790 2.0013 4.63 2.7E+00 AF08700 NT 10790 2.0013 4.63 2.7E+00 AF08500 NT 17846 2.377 1.75 2.7E+00 AF08500 NT 15324 2.5373 4.35 2.6E+00 AF08501 NT 15324 2.5374 1.97 2.6E+00 AF08501 NT 16576 2.676 AF08502 NT NT 16576 2.	6129	15976	26112		2.9E+00		LN	F.pringlei gdcsPA gene for P-protein of the glycine cleavage system
16146 26301 4.47 2.9E+00 O14514 SWISSPROT 16271 26433 5.19 2.9E+00 P46589 SWISSPROT 11346 21212 5.79 2.8E+00 AF186398.1 NT 11519 20550 4.78 2.8E+00 AR161552.2 NT 10199 20012 4.63 2.7E+00 6679306 NT 10199 20013 4.63 2.7E+00 6679306 NT 1079 20013 4.63 2.7E+00 6679306 NT 17846 2.7E+00 4679306 NT NT 17846 2.7E+00 48679306 NT NT 17846 2.7E+00 48679306 NT NT 17846 2.7E+00 48679306 NT NT 16524 2.5374 1.97 2.6E+00 AF08549.1 NT 16576 2.5374 1.97 2.6E+00 AF085502.1 NT 16576 2.676 AF235502.	6282	16146	26300		2.9E+00		SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
16271 26433 5.19 2.9E+00 P46589 SWISSPROT 11346 21212 5.79 2.8E+00 AF186398.1 NT 11519 2.0550 4.78 2.8E+00 A8161552.2 NT 10199 2.0012 4.63 2.7E+00 6679306 NT 10199 2.0013 4.63 2.7E+00 6679306 NT 17062 2.21 2.7E+00 6679306 NT 17846 2.21 2.7E+00 6679306 NT 17845 2.453 2.7E+00 6679306 NT 17846 2.7E+00 1416459.1 NT NT 15324 2.435 2.6E+00 AF068749.1 NT 15324 2.5574 1.97 2.6E+00 AF068749.1 NT 15324 2.5574 1.97 2.6E+00 AF068749.1 NT 16576 2.5577 1.2 2.6E+00 AF05550.1 NT 17418 2.768 2.6E+00	6282	16146	26301	4.47	2.9E+00		SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
11346 21212 6.79 2.8E+00 AF186398.1 NT 11519 3.12 2.8E+00 AL16155.2 NT 16188 2.6350 4.78 2.8E+00 AL16155.2 NT 10199 2.0012 4.63 2.7E+00 G679306 NT NT 10199 2.0013 4.63 2.7E+00 G679306 NT NT 17062 2.01 1.75 2.7E+00 G679306 NT NT 17846 2.21 2.7E+00 G679306 NT NT 17846 2.21 2.7E+00 G679301 NT NT 15324 2.435 2.6E+00 G679301 NT NT 15324 2.5373 1.97 2.6E+00 G75601 NT NT 15324 2.5374 1.97 2.6E+00 G75601 NT NT 16576 2.6E+00 G75601 NT NT NT 16576 2.6E+00 G75601 NT NT NT 1771 2.6E+00 G75601 NT NT NT 17718 2.7640 G7640 G7141540.2 NT NT 17777 1.52 2.6E+00 G71415250.1 <td>6410</td> <td>16271</td> <td>26433</td> <td></td> <td>2.9E+00</td> <td></td> <td>SWISSPROT</td> <td>ADHERENCE FACTOR (ADI IESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)</td>	6410	16271	26433		2.9E+00		SWISSPROT	ADHERENCE FACTOR (ADI IESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
11519 3.12 2.8E+00 AL16155.2 NT 16188 26350 4.78 2.8E+00 8393724 NT 10199 20012 4.63 2.7E+00 6679306 NT 10199 20013 4.63 2.7E+00 6679306 NT 17062 2.21 2.7E+00 6679306 NT 17846 2.21 2.7E+00 14005.1 NT 17847 2.4253 4.35 2.6E+00 AL116459.1 NT 15324 2.5373 1.97 2.6E+00 AF068749.1 NT 15324 2.5373 1.97 2.6E+00 AF068749.1 NT 16576 2.56+00 AF068749.1 NT NT 16576 2.6E+00 AF088749.1 NT 16576 2.6E+00 AF05560.1 NT 16576 2.6E+00 AJ132180.1 NT 17418 2.7634 2.9E+00 AJ132180.1 NT 17777 1.52 2.	1441	11346	21212		2.8E+00		TN	Buxus harlandii maturase K (matk) gene, partial cds; chloroplast gene for chloroplast product
16188 26350 4.78 2.8E+00 8393724 NT 10199 20012 4.63 2.7E+00 6679306 NT 10199 20013 4.63 2.7E+00 6679306 NT 15327 2.21 2.7E+00 6679306 NT 17062 2.21 2.7E+00 BE06352.1 NT 17846 2.71 2.7E+00 BE06352.1 ST HUMAN 14467 24253 4.35 2.6E+00 BE06352.1 NT 15324 25373 1.97 2.6E+00 BE06352.1 NT 16374 25373 1.97 2.6E+00 BE06352.1 NT 16576 25676 1.27 2.6E+00 BF06352.1 NT 16576 26676 1.27 2.6E+00 BF06350.1 NT 1771 27634 2.95 2.6E+00 BF0350.1 NT 17777 1.52 2.6E+00 BF0350.1 NT 17777 1.52 2.6E+00 BF0350.1 NT 19649 2.31 2.6E+00 BF03513.1 NT 11353 21216	1615	11519			2.8E+00		LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
10199 20012 4.63 2.7E+00 6679306 NT 10199 20013 4.63 2.7E+00 6679306 NT 15327 2.21 2.7E+00 6679306 NT 17062 2.21 2.7E+00 L14005.1 NT 17846 2.16 2.7E+00 BE063527.1 EST_HUMAN 14467 24253 4.35 2.6E+00 AF068749.1 NT 15324 25373 1.97 2.6E+00 AF068749.1 NT 16324 25373 1.97 2.6E+00 AF068749.1 NT 16576 2557 1.97 2.6E+00 AF068749.1 NT 16576 2567 1.2 2.6E+00 AF23550.1 NT 16576 2660 AJ132180.1 NT NT 1771 2.6E+00 AJ132180.1 NT NT 17777 1.52 2.6E+00 AJ132180.1 NT 19649 2.31 2.6E+00 AJ132180.1 <td< td=""><td>6325</td><td>16188</td><td>26350</td><td></td><td>2.8E+00</td><td>8393724</td><td>Ę</td><td>Mus musculus endomucin (LOC53423), mRNA</td></td<>	6325	16188	26350		2.8E+00	8393724	Ę	Mus musculus endomucin (LOC53423), mRNA
10199 20013 4.63 2.7E+00 6679306 NT 15327 2.577 1.75 2.7E+00 L14005.1 NT 17062 2.21 2.7E+00 L14005.1 NT 17846 2.16 2.7E+00 BE063527.1 EST_HUMÁN 14467 24253 4.35 2.6E+00 AF068749.1 NT 15324 25373 1.97 2.6E+00 AF068749.1 NT 16324 25373 1.97 2.6E+00 AF068749.1 NT 16376 25670 1.97 2.6E+00 AF068749.1 NT 16576 25670 1.2 2.6E+00 AF235502.1 NT 16576 26676 1.2 2.6E+00 AJ132180.1 NT 17718 27634 2.95 2.6E+00 AJ132180.1 NT 17777 1.52 2.6E+00 AJ132180.1 NT 19649 2.31 2.6E+00 AJ1419220 NT 11353 21216	230	10199	20012		2.7E+00		LN	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
15327 25377 1.75 2.7E+00 L14005.1 NT 17062 2.21 2.7E+00 AL116459.1 NT 17846 2.16 2.7E+00 BE063527.1 EST_HUMÁN 14467 24253 4.35 2.6E+00 AF068749.1 NT 15324 25373 1.97 2.6E+00 AF068749.1 NT 16324 25373 1.97 2.6E+00 AF068749.1 NT 16324 25374 1.97 2.6E+00 AF068749.1 NT 16576 266+00 AF235502.1 NT NT 16576 26767 1.2 2.6E+00 AJ132180.1 NT 17418 27634 2.95 2.6E+00 AJ132180.1 NT 17777 1.52 2.6E+00 AJ132180.1 NT 19649 2.31 2.6E+00 AJ132180.1 NT 152 2.6E+00 AJ132180.1 NT 152 2.6E+00 AJ132180.1 NT 152 2.6E+00 AJ132180.1 NT 153 2.6E+00 AJ1419220 NT 11353 21216 2.31	230	10199	20013		2.7E+00		LN	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
17062 2.21 2.7E+00 AL116459.1 NT 17846 2.16 2.7E+00 BE063527.1 EST_HUMAN 14467 24253 4.35 2.6E+00 AF068749.1 NT 15324 25373 1.97 2.6E+00 AF068749.1 NT 16324 25374 1.97 2.6E+00 AF068749.1 NT 16376 2567 1.97 2.6E+00 AF23560.1 NT 16576 2676 1.2 2.6E+00 AJ132180.1 NT 17418 27634 2.95 2.6E+00 AJ132180.1 NT 17777 1.52 2.6E+00 AJ132180.1 NT 17777 1.52 2.6E+00 AJ132180.1 NT 19649 2.31 2.6E+00 AJ132180.1 NT 17777 1.52 2.6E+00 AJ132180.1 NT 19649 2.31 2.6E+00 AJ132180.1 NT 17777 2.6E+00 AJ132180.1 NT 1363 2.26E+00 AJ1419220 NT	5408	15327	25377	1.75	2.7E+00		LN	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
17846 2.16 2.7E+00 BE063527.1 EST_HUMAN 14467 24253 4.35 2.6E+00 AF068749.1 NT 15324 25373 1.97 2.6E+00 6755601 NT 15324 25374 1.97 2.6E+00 6755601 NT 16391 5.42 2.6E+00 6755601 NT 16576 28767 1.2 2.6E+00 AJ132180.1 NT 16576 266+0 AJ132180.1 NT NT 17418 27634 2.95 2.6E+00 AJ132180.1 NT 17777 1.52 2.6E+00 AJ132180.1 NT NT 17777 1.52 2.6E+00 AJ132180.1 NT NT 19649 2.31 2.6E+00 AJ1419220 NT 11353 21216 2.08 2.5E+00 AJ271844.1 NT	7185	j		2.21	2.7E+00		NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
14467 24253 4.35 2.6E+00 AF068749.1 NT 15324 25373 1.97 2.6E+00 AF068749.1 NT 16324 25374 1.97 2.6E+00 AF28560.1 NT 16391 5.42 2.6E+00 AF285502.1 NT 16576 26767 1.2 2.6E+00 AJ132180.1 NT 17418 27634 2.95 2.6E+00 AJ132180.1 NT 17777 1.52 2.6E+00 AJ132180.1 NT 19649 2.31 2.6E+00 AJ132180.1 NT 1352 2.6E+00 AJ132180.1 NT 17777 1.52 2.6E+00 AJ132180.1 NT 19649 2.31 2.6E+00 AJ132180.1 NT 11353 21216 2.31 2.6E+00 AJ1419220 NT	7996			2.16	2.7E+00	BE063527.1	EST_HUMAN	CM0-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
15324 25373 1.97 2.6E+00 6756601 NT 16324 25374 1.97 2.6E+00 6756601 NT 16391 5.42 2.6E+00 6756601 NT 16576 26F+00 AL32180.1 NT 16576 26F+00 AJ132180.1 NT 17418 27634 2.95 2.6E+00 AJ132180.1 NT 17777 1.52 2.6E+00 AJ132180.1 NT 19649 2.31 2.6E+00 AJ132180.1 NT 11353 2.1216 2.31 2.6E+00 AJ132180.1 NT	4576		24253		2.6E+00		FN	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
16324 25374 1.97 2.6E+00 6756601 NT 16391 5.42 2.6E+00 AF235502.1 NT 16576 26767 1.2 2.6E+00 AJ132180.1 NT 17418 27634 2.95 2.6E+00 AJ132180.1 NT 17777 1.52 2.6E+00 AJ132180.1 NT 19649 2.31 2.6E+00 AJ132180.1 NT 1353 2.6E+00 AJ132180.1 NT 1354 2.9E+00 AJ1419220 NT 1364 2.31 2.6E+00 AJ271844.1 NT	5405		25373		2.6E+00	6755601	LN	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
16391 5.42 2.6E+00 AF235502.1 NT 16576 26767 1.2 2.6E+00 AJ32180.1 NT 16576 26768 1.2 2.6E+00 AJ32180.1 NT 17418 27634 2.95 2.6E+00 AJ132180.1 NT 17777 1.52 2.6E+00 AJ161540.2 NT 19649 2.31 2.6E+00 AJ271844.1 NT 11353 21216 2.08 2.5E+00 AJ271844.1 NT	5405	1	25374		2.6E+00	6755601	L	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
16576 26767 1.2 26E+00 AJ132180.1 NT 16576 26768 1.2 2.6E+00 AJ132180.1 NT 17418 27634 2.95 2.6E+00 AJ13180.2 NT 17777 1.52 2.6E+00 AJ13180.2 NT 19649 2.31 2.6E+00 AJ271844.1 NT 11353 21216 2.08 2.5E+00 AJ271844.1 NT	6533			5.42	2.6E+00	-	LN	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
16576 26768 1.2 2.6E+00 AJ132180.1 NT 17418 27634 2.95 2.0E+00 AL161540.2 NT 17777 1.52 2.6E+00 OD55193 NT OD55193 NT 19649 2.31 2.6E+00 OD55193 NT OD55193 NT 11353 21216 2.0E+00 OD571844.1 NT	9699		26767	1.2	2.6E+00		LN	faba bean necrotic yellows virus C2-Eg gene, Isolate Egyptian EV1-93
17418 27634 2.95 . 2.6E+00 AL161540.2 NT 17777 1.52 2.6E+00 S055193 NT 19649 2.31 2.6E+00 AJ271844.1 NT 11353 21216 2.08 2.5E+00 AJ271844.1 NT	9699		26768		2.6E+00		FN	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
1777 1.52 2.6E+00 9055193 NT 19649 2.31 2.6E+00 11419220 NT 11353 2.1216 2.08 2.5E+00 AJZ71844.1 NT	7567	17418	27634		2.6E+00		L	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
19649 2.31 2.6E+00 11419220 NT 11353 21216 2.08 2.5E+00 AJZ71844.1 NT	7927	17777		1.52	2.6E+00		TN	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpst3), mRNA
11353 21216 2.08 2.5E+00 AJ271844.1 NT	9711	_ 1			2.6E+00	11419220	LZ	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
	1448		21216		2.5E+00		뉟	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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Single Exon Probes Expressed in Heart

	Top Hit Descriptor	se, exons 1-4			<u> </u>		sapiens cDNA		Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds	Ţ	DOC2A) mRNA	TEIN 1)	ACTIVATION ANTIGEN CD27) (T14)	ACTIVATION ANTIGEN CD27) (T14)	2 of the complete genome	sapiens cDNA						:DNA clone IMAGE:3133187 3'	:DNA clone IMAGE:3133187 3'	degrees: glpPFKD operon and downstream	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds	ne (L3)		ublquitous (Atp2a3), mRNA	CENTROMERE PROTEIN B) (CENP-B)	ding for DhaK and DhaJ	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)	12 dE 20001 70 11 1 111	JNA clone IMAGE:4068173 5	JNA clone IMAGE:4068173 5'
Single Exon Probes Expressed in hear	F	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4	TEICHOIC ACID BIOSYNTHESIS PROTEIN F	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA	Rice DNA for aldolase C-1, complete cds	Mus musculus EIF4H gene, partial cds; LIMK1	Chicken alpha-3 collagen type VI mRNA, 3' end	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA	ENDOCHITINASE B PRECURSOR (CHN-B)	SKIN GRANULE PROTEIN PRECURSOR	SKIN GRANULE PROTEIN PRECURSOR	Hisapiens CTGF gene and promoter region	XYLULOSE KINASE (XYLULOKINASE)	hr63f06.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:3133187 3'	hro3f06.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFKD operon and downstream	Fragaria x ananassa cytosolic ascorbate peroxi	G.domesticus artificial single chain antibody gene (L3)	Bos taurus partial cytb gene for cytochrome b	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)	M.mazei dnaK and dnaJ genes homologues coding for DnaK and Dna.	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GA	(FUCOSYLIRANSPERASE 4) (FUCT-IV)	602069121F1 NIH MGC 58 Homo sapiens cDNA clone IMAGE:4068173 5	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5			
gie Exon Pro	Top Hit Database Source	ZI	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	LN	LN	NT	NT	SWISSPROT	SWISSPROT	SWISSPROT	LN	EST HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	LN	SWISSPROT	EST_HUMAN	EST HUMAN	NT	LZ	FZ	Ę	NT	SWISSPROT	TN		SWISSPROT	EST HUMAN	EST_HUMAN
	Top Hit Acession No.	2.5E+00 AJ271844.1	713485	213485	713485	73485	2.5E+00 AW949158.1	D50307.1	2.5E+00 AF289665.1	M24282.1	4503352 NT	P02843	26842	P26842	2.4E+00 AE001486.1	2.4E+00 AW875126.1	P24091	P13673	P13673	X92511.1	P09099	2.4E+00 BE326702.1	BE326702.1	Y14079.1	2.4E+00 AF158652.2	246724.1	2.3E+00 AJ401081.1	6978554 NT	P07199	X60265.1		011127	2.3E+00 BF541987.1	2.3E+00 BF541987.1
	Most Similar (Top) Hit BLAST E Value	2.5E+00	2.5E+00 P13485	2.5E+00 P13485	2.5E+00 P13485	2.5E+00 P13485	2.5E+00	2.5E+00 D50307.1	2.5E+00	2.4E+00 M24282.1	2.4E+00	2.4E+00 P02843	2.4E+00	2.4E+00 P26842	2.4E+00	2.4E+00	2.4E+00 P24091	2.4E+00 P13673	2.4E+00 P13673	2.4E+00 X92511.1	2.4E+00 P09099	2.4E+00	2.4E+00	2.4E+00 Y14079.1	2.4E+00	2.3E+00 Z46724.1	2.3E+00	2.3E+00	2.3E+00 P07199	2.3E+00 X60265.		2.3E+00 Q11127	2.3⊏+00	2.3E+00
	Expression Signal	2.08	2.33	2.33	1.71	1.71	1.34	1.75	2.26	0.86	7.62	4.19	2.14	2.14	2.63	1.71	9.45	2.5	2.5	2.18	6.49	1.67	1.67	1.77	2.52	9.36	1.28	2.22	2.3	1.53		1.81	2.6	2.6
	ORF SEQ ID NO:	21217	25537	25538	25537	25538	26598	27334		22707	24485	25664	26802	26803			27194	27853	27854	27911		28002	28003	28558	28839	20392		26431		26613		27364	29083	29084
	Exon SEQ ID NO:	11353	15468	15468	15468	15468	16419	17141	18861	12907	14599	15569	16613	16613	16659	16903	17002	17621	17621	17670	17731	17764	17764	18302	18554	11140	13934	<u> </u>	19766	16431	l _			18793
	Probe SEQ ID NO:	1448	5225	5552	5886	5886	6561	7264	9086	2980	4816	5657	6733	6733	6780	7026	7125	7771	7771	7820	7881	7914	7914	8428	8665	1233	4031	6408	6479	6573		7289	8988	8988

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Single Exon Probes Expressed in Heart

					ביים ס	אסו ויוסערו סול	Sligle Lyon Flores Expressed III lear
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9304	19002	25333	4	2.3E+00	2.3E+00 BE895237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5
9836	19405		1.37	2.3E+00	2.3E+00 AF281862.1	NT	Neurospora crassa G protein alpha subunit GNA-3 (gna-3) gene, complete cds
4216	14114	23891	3.82		2.2E+00 D67071.1	IN	Rat gene for regucalcin, exon1 (non-coding exon)
4216	14114	23892	3.82		2.2E+00 D67071.1	TN	Rat gene for regucalcin, exon1 (non-coding exon)
5276	15198	24973	10.08	2.2E+00 O88307	088307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEP FOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS)
							SORTH IN BELATED RECEDTOR PRECHIRSOR (SORTING PROTEIN BELATED RECEPTOR
						TOddoolwo	CONTRING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR REPEATS) (LD
5276	15198	249/4	10.08		2.2E+00 000307	EST HUMAN	60094340171 NIH MGC 17 Homo sapiens cDNA clone IMAGE:2959777 3'
0600					00000	1000000	MINIOD MIDION STELL IDAL DEOTEIN MILO
5835	- 1				G00335	SWISSPROI	MINOR VIRION STRUCTURAL PROTEIN MO-2
5978	١	26005			P51459	SWISSPROI	INSULIN-LINE GROW IN FACTOR II PRECENSOR (FGT-11) COMPANIA A)
6155	15113				2.2E+00 AA594574.1	EST_HUMAN	ni95b02.s1 NCI_CGAPC010 Homo sapiens cUNA clone IMAGE:10583.9 3
6486	16344	26514	51.56		2.2E+00 AA449012.1	EST_HUMAN	zx05g10.r1 Soares, total fetus_NbZHF8_9w Homo sapiens cDNA clone IMAGE:785634 5
7381	17250		11.83		2.2E+00 BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
7518	19468		2.1		2.2E+00 Q04706	SWISSPROT	TRANSPOSON TY1 PROTEIN A
7783	17633	27865	1.58		2.2E+00 AI290373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8tc9weeks_ZNbHP8tc9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
7783			1.56		2 2E+00 AI290373.1	EST HUMAN	qm69b03.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
7812					2.2E+00 BF246782.1	EST_HUMAN	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
7975	1				2.2E+00 AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
8739	1			2.2E+00 P07911	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
8889	18700		4.87	L	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
557	12670		18.9		2.1E+00 AF132612.2	TN	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3539	13455		1.19		2.1E+00 AW 449366.1	EST_HUMAN	UI-H-Bi3-aki-e-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6074	16057	26206	3.72		2.1E+00 070159	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
6195	15955	26087	7.4		2.1E+00 N29575.1	EST_HUMAN	yy08a10.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654 TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN);
6948	16826		1.99		2.1E+00 AU123630.1	EST_HUMAN	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5'
1178	_	20934	1.23		2.0E+00 AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds

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		7	1	T	T	$\overline{}$	T	$\overline{}$	7	7	7	7	-	Т	T	$\overline{}$	T	Т	7	1	7	Т	_	7-	7	Т	7			7	7	_	7-	7
	Top Hit Descriptor	VIRULENCE FACTOR MVIN HOMOLOG	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP bgenes	M.musculus COL3A1 gene for collagen alpha-l	M.musculus COL3A1 gene for collagen alpha-l	ph6b6_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV	QV4-LT0016-090200-100-d07 LT0016 Homo saplens cDNA	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA	Homo sapiens transglutaminase type I (Tgasel) gene, promoter region	Homo sapiens unknown mRNA	AV764043 MDS Homo sapiens cDNA clone MDSDAH08 5	Rattus norvegicus jun dimerization protein 2 (idp-2) mRNA, complete cds	Chlamydophila pneumoniae AR39, section 32 of 94 of the complete genome	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (meterridin) (Adam15) mDNA	Potato virus A RNA complete genorne, isolate U	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1) mRNA	Potato virus A RNA complete genome, isolate U	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1	yg10e02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693.5'	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR	HYPOTHETICAL 118.4 KD PROTEIN IN BATZ-DAL5 INTERGENIC REGION PRECURSOR	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA	602035771F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183865 5'	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381306 5'	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'	DKFZp547P243_s1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547P243 3'	Malze mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA	Thermoplasma acidophilum complete genome; segment 3/5	Raftus norvegicus 5 - Lipoxygenase (Alox5), mRNA	Homo sapiens DKFZP586W0122 protein (DKFZP586W0122), mRNA	Homo sapiens DKF2P586M0122 protein (DKF2P586M0122), mRNA	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
310	Top Hit Database Source	SWISSPROT	N	NT	N-	EST HUMAN	EST_HUMAN	EST_HUMAN	E	N	EST HUMAN	NT	N	Z L	N	F	N	Z	EST_HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	Ę	Z-	7	77	トフ	NT
	Top Hit Acession No.	246378	1.6E+00 AJ297131.1	X52046.1	X52046.1	141290.1	1.6E+00 AW835644.1	1.6E+00 AW835644.1	1.6E+00 AF005631.1	1.6E+00 AF104313.1	1.6E+00 AV764043.1	J53449.1	1.5E+00 AE002201.2	6752961 NT	1.5E+00 AJ131402.1	6678350 NT	1.5E+00 AJ131402.1	1.5E+00 AE001945.1	317879.1	1.5E+00 BE785356.1	47179				_		1.		6753287 NT	1.5E+00 AL445065.1	6978492 NT	7661685 NT	51685	1.4E+00 AF053357.1
	Most Similar (Top) Hit BLAST E Value	1.6E+00 Q46378	1.6E+00	1.6E+00 X52046.1	1.6E+00 X52046.1	1.6E+00 T41290.1	1.6E+00	1.6E+00	1.6E+00	1.6E+00 /	1.6E+00	1.5E+00 U53449.1	1.5E+00/	1.5E+00	1.5E+00 /	1.5E+00	1.5E+00 /	1.5E+00/	1.5E+00 R17879.1	1.5E+00 E	1.5E+00 P47179	1.5E+00 P47179	1.5E+00 BF376754.	1.5E+00 E	1.5E+00 A	1.5E+00 AA017689.	1.5E+00 A	1.5E+00 X07380.1	1.5E+00	1.5E+00 A	1.5E+00	1.4E+00	1.4E+00	1.4E+00[A
	Expression Signal	1.21	3.56	1.3	1.3	1.29	1.25	1.25	5.86	3.25	1.65	4.29	1.76	1.79	2.46	2.02	2.22	0.82	2.71	1.42	29.13	29.13	7.56	1.71	1.96	1.96	3.91	10.73	1.5	2.89	1.42	1.28	1.28	0.95
<u> </u>	ORF SEQ ID NO:		26958	26646	26647	27879	27946		25601			19812	20014		22135	22237	22135	23054	25880		26268	26269	27747		27951	27952	28802					19808	19809	
	Exon SEQ ID NO:	16561	16760	19465	19465	17462	17702	17702	15520	18752	19379	10017	10200	10541	12239	12344	12239	13249	15762	16096	16116	16116	17521	17632	17706	17706	18520	18641	18946	19178	19243	10014	10014	12116
	Probe SEQ ID NO:	6681	6881	7444	7444	7611	7852	7852	8217	8944	9902	30	231	605	2359	2468	3099	3329	5856	6230	6250	6250	7671	7782	7856	7856	8702	8828	9223	9596	0696	27	27	2231

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Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds zr36e09.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665512.5' similar to contains element PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA) yg33f12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34345 5' wt45g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3 601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3' 601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE: 3845805 3' 602156687F1 NIH MGC 83 Homo sapiens cDNA clone IMAGE:4297556 5' Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12 Chlamydia muridarum, section 55 of 85 of the complete genome Chlamydia muridarum, section 55 of 85 of the complete genome Top Hit Descriptor CM0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA CM0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA RC1-BT0313-301299-012-f05 BT0313 Homo sapiens cDNA Homo sapiens APECED mRNA for AIRE-1, complete cds Homo sapiens mRNA for KIAA0905 protein, complete cds Homo sapiens Xq pseudoautosomal region; segment 1/2 Homo sapiens mRNA for KIAA1157 protein, partial cds Homo sapiens Mad4 homolog (MAD4) mRNA WSB1 protein (WSB1) genes, complete cds WSB1 protein (WSB1) genes, complete cds Ovis aries prion protein gene, complete cds Human papillomavirus type 7 genomic DNA DNA TOPOISOMERASE III ALPHA Single Exon Probes Expressed in Heart MER22 repetitive element; SYNAPSIN II SYNAPSIN II EST HUMAN EST_HUMAN EST HUMAN EST HUMAN HUMAN EST_HUMAN **EST HUMAN** EST_HUMAN EST HUMAN SWISSPROT SWISSPROT SWISSPROT SWISSPROT Database TopH≝ Source EST 둗 눋 F þ þ 눋 눋 Z z b F 눋 눋 5453733 NT Top Hit Acession AW900455.1 AW900455.1 1.4E+00 AW054976.1 BE962107.2 1.4E+00 AE002324.2 1.4E+00 AL161500.2 1.4E+00 AF064564.2 1.4E+00 AF064564.2 AE002324.2 BE962107.2 1.4E+00 BF681547.1 1.4E+00 AA195528.1 1.4E+00 AB006682.1 1.4E+00 AB032983.1 1.4E+00 AB020712.1 1.4E+00 AJ133269.1 1.4E+00 AJ271735.1 1.4E+00 BE064667. å R20459.1 1.4E+00 U30790.1 1.4E+00 U30790.1 U67922.1 X74463.1 1.4E+00 Q13472 1.4E+00 Q92777 1.4E+00 Q07869 Q92777 1.4E+00 **Most Similar** (Top) Hit BLASTE Value 1.34 5.15 1.86 1.88 1.94 2.68 1.09 1.53 2.39 9.38 1.63 3.29 0.87 1.09 0.8 5.21 3.37 4.97 1.0 107 7.5 5.17 271 Expression Signal 28548 28695 28868 22755 22756 25812 27325 28808 28809 22500 23835 25884 25885 27381 28867 22394 22501 26341 ORF SEQ 23836 25026 ID NO: 18526 18583 18583 17133 17179 18294 18426 12169 12608 12962 12962 13213 15313 19765 15766 16181 18526 19604 12501 14062 15702 15766 SEQ ID 14062 14376 15004 16222 16984 Exo ë 6318 8727 2286 2634 2746 3034 3034 4162 4482 5394 5796 5802 5860 7107 7256 7303 8420 8556 8709 8709 8727 3291 4162 5137 5301 5860 9221 SEQ ID ö

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	Top Hit Descriptor	M.mucedo gene encoding 4-Dihydromethyl-trisporate dehydrogenase	Cantharellus sp. partial 25S rRNA gene, isolate Tibet	Homo sapiens putative psihHbA pseudogene for hair keratin, exons $2 \ \mathrm{to} \ 7$	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA	Homo sepiens zinc finger protein 157 (HZF22) (ZNF157) mRNA	Coix lacryma-jobi dihydrodipicolinate synthase (dapA) gene, complete cds	Chlamydia muridarum, section 66 of 85 of the complete genome	Oyprinus carpio MRPb and MASPb genes for mannosc-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA	Fugu rubripes gamma-amInobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMIP-1), procollagen C-proteinase	enhancer protein (PCOLCE) genes, complete c>	Mus musculus alpha-spectrin 1, enythroid (Spna1), mRNA	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1	PM0-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA	PM0-CT0289-291199-004-f08 CT0289 Homo saplens cDNA	D.melanogaster no-on-transient A gene product, complete cds	Sus scrofa plp gene	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3	Homo sapiens GL004 protein (GL004), mKNA	Homo sapiens heparan glucosaminy N-deacetylase/N-sulfotransferase-2 gene, complete cds	S.alba phr-1 mRNA for photolyase	S.alba phr-1 mRNA for photolyase	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)	wo85a07.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2462100 3'	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome	Campylobacter Jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)	MRNA 3'-END PROCESSING PROTEIN RNA15
	Top Hit Database Source	NT	N	NT			N	N L	O NT	T_HUMAN		<u> </u>					HUMAN	T_HUMAN			T_HUMAN				S	SWISSPROT A	EST_HUMAN W	T_HUMAN			\neg	SWISSPROT
	Top Hit Acession No.		1		4507998 NT	TN 8667054	U61730.2	2	Υ.	1.3E+00 BE966735.2	6755621 NT		Ψ,	6755621 NT	1	.1	4.1	4.1			1.3E+00 BE963379.2	9910247 NT	1.3E+00 AF042084.1				1.3E+00 AI927629.1	1.3E+00 BE963379.2	1.3E+00 AE004392.1	.1		P25299
-	Most Similar (Top) Hit BLAST E Value	1.3E+00 Z73640.1	1.3E+00 AJ271192	1.3E+00 Y19213.1	1.3E+00	1.3E+00		1.3E+00 AE002338	1.3E+00 AB030447	1.3E+00	1.3E+00		1.3E+00 AF016494	1.3E+00	1.3E+00 AJ252087	1.3E+00 AJ252087	1.3E+00 AW36283	1.3E+00 AW36283	1.3E+00 M33496.1	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00 X72019.1	1.3E+00 X72019.1	1.3E+00 000754	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00 Q14117	1.3E+00 P25299
	Expression Signal	1.67	2.74	16.5	10.9	10.9	1.62	2.09	2.1	2.19	1.12		1.03	0.82	86.0	86.0	7.76	7.76	1.33	1.25	3.06	1.55	5.44	2.31	2.31	1,45	1.27	4.9	1.6	1.39	4.3	2.34
	ORF SEQ ID NO:		20659		21033	21034					22632		23258			24608	25674	25675	25889	26901	26988				27561	27639				27968		28398
-	Exon SEQ ID NO:	10498	10810	11028	11183	11183	11241	11497	12083	12378	12835		13463	12835	14839	14839	15576	15576	15770	16707	16795	16931	17350	17357	17357	17425	17471	17525	17716	17724	17969	18157
-	ш	1			1275		1	1	2196	2503	2909)	_	1	┸	4964	5995	5665	5864	6828	┸	7054	7480	7487	7487	7574	7620	7675	7866	7874	8078	8277

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Top Hit Descriptor	E.faecalis pbp5 gene	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'	qd85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3'	Herpes simplex virus type 1 (strain KOS) UL41 gene	Herpes sImplex virus type 1 (strain KOS) UL41 gene	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5	Homo sapiens mRNA for KIAA0934 protein, partial cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA	Klebsormidium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding	mitochondrial protein, partial cds	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA	Petroselinum crispum cytosolic gluccse-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds	wf76e11.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'	LOW TEMPERATURE ESSENTIAL PROTEIN	Taenia solium immunogenic protein Ts76 mRNA, partial cds	Dictyostelium discoideum isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds	Xenopus laevis rhodopsin gene, complete cds	Cavia cobaya mRNA for serine/threoine kinase, complete cds	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA	Girardia tigrina mRNA for homeodomain transcription factor (so gene)	Homo sapiens chromosome 21 segment HS21C018	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds	V.carteri Algal-CAM mRNA	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds		DNA GYRASE SUBUNIT B
Top Hit Database Source	NT E.		EST_HUMAN 60	EST_HUMAN qo		H.	NT	T HUMAN	NT	NT						NT	NT P.	EST_HUMAN W	SWISSPROT L	TN T	NT	X IN	NT		NT IN	I I	NT A	NT	TN	ISSPROT	SWISSPROT
Top Hit Acession No.		FN 0538530	1.1E+00 BE960184.1				1.1E+00 AL161588.2	1.1E+00 BF693996.1	1.1E+00 AB023151.1	1.1E+00 AL161515.2	6754021 NT	11067364 NT		1.1E+00 AF068942.1	8922973 NT	1.1E+00 AF012862.1	1.1E+00 AF012862.1	1.1E+00 Al809699.1		1.1E+00 AF216596.1	1.1E+00 AF234169.1	1.0E+00 U23808.1		1.1	1.0E+00 AJ251660.1	1.0E+00 AL163218.2	1.0E+00 AF125984.1	1.0E+00 X80416.1	1.0E+00 AB006531.1		P48355
Most Similar (Top) Hit BLAST E Value	1.1E+00 X78425.1	1.1E+00	1.1E+00	1.1E+00/	1.1E+00 Z72338.1	1.1E+00 Z72338.1	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00		1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00	1.1E+00 P07866	1.1E+00	1.1E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00 P48355
Expression Signal	1.16	1.57	12.04	1.29	1.93	1.93	7.53	3.22	1.65	4.39	20.08	2.65		3.41	5.73	4.41	4.41	4.73	4	2.13	1.54	3.49	1.14	2.16	1.14	4.51	0.95	1.04	1.32	1.4	1.4
ORF SEQ ID NO:	24638	24945	25426	25440	28444	26445	26458		27733	27791	27815					28581		28835		25310			19904		20308				21492		22209
Exen SEQ ID NO:	14874	15172	15370	15380	16283	16283	16296	16608	17508	17565	17594	17934		17981	13426	18323	18323	18551	18999	19056	19570	10077	10089	10358	10502	10595	10597	<u> </u>	11623	_	Ш
Probe SEQ ID NO:	4999	5249	5449	5460	6422	6422	6435	6728	7658	7715	7744	8043		8090	8447	8450	8450	8662	9300	9402	9523	92	108	412	562	661	663	1364	1722	2435	2435

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SEQ ID NO: NO: 2846 2846 28378 3327 3327 3327 4951 4951 5568 5568 5568 5568	Exon SEQ ID NO: NO: 12518 12774 13087 13385 14828 15626 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 15627 1562	ORF SEQ ID NO: 22408 22562 23328 23328 24919 24777 24777 24777 25557 25557 25568 25573 25573 25573 25574	Signal Signal Signal 1.09 1.09 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109 1.109	Wos BLI B	No. o. o	Top Hit Database Source Source Source Source SWISSPROT SWISSPROT SWISSPROT NT SWISSPROT SWISSPRO	Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Datbase Source Null Problem-16 (Nain-1406), and neuronal apoptosis inhibitory protein-15 (Nain-1406), and neuronal apoptosis inhibitory protein-16 (Nain-1406), and neuronal apoptosis inhibitory neuronal apoptosis inhibitory protein-16 (Nain-1406), and neuronal apoptosis inhibitory
6546	16404	26583	5.99		1.0E+00 AA775191.1	EST_HUMAN	ac79b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868791 3'
6641	16521	26713	1.71		1.0E+00 BE868267.1 1.0E+00 BE868267.1	EST HUMAN EST HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5' 601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
6734	14828		1.38		1.0E+00 D10852.1	Z	Rattus norvegicus mRNA for N-acety/glucosaminytransferase III, complete cds

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Table 4
Single Exon Probes Expressed in Heart

Top Hit Descriptor	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) {INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE }	RC1-HT0229-181099-011-e06 HT0229 Homo sapiens cDNA	Human immunodeficiency virus type 1 (HIV-1), Isolate SF33,	601497581F1 NIH_MGC_70 Horno sapiens cDNA clone IMAGE:3899421 5'	Mus musculus chloride channel calcium activated 1 (Cica1), mRNA	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA	AV689554 GKC Homo sapiens cDNA clone GKCCYA11 5'	Xenopus laevis zona pellucida C glycoprotein precursor (XIZPC) mRNA, complete cds	Xenopus laevis zona pellucida C glycoprotein precursor (xIZPC) mRNA, complete cds	AV758825 BM Homo sapiens cDNA clone BMFAWC04 5'	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)	EST388293 MAGE resequences, MAGN Homo saplens cDNA	Homo sapiens mRNA for KIAA1517 protein, partial cds	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C102	Apple mosaic virus RNA 2 putative polymerase gene, complete cds	SERINETHREONINE PROTEIN KINASE MINIBRAIN	Lycopersicon esculentum putative Mi1 copy 1 nematode-resistance gene	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL- like protein, isolate JM983
Top Hit Database Source	SWISSPROT D	SWISSPROT D	EST HUMAN R		EST_HUMAN 6			EST HUMAN A	X	X	EST_HUMAN A	EST_HUMAN Z	EST_HUMAN Z	SWISSPROT	EST HUMAN E	N IN	N	D IN	H L	NT A	SWISSPROT	LN LN	SWISSPROT B	NT	SWISSPROT	EST_HUMAN 6		NT NT
Top Hit Acession No.	002207	Q02207	1.0E+00 BE147331.1	1.0E+00 M38427.1	1.0E+00 BE907592.1	6753429 NT	6753429 NT	1.0E+00 AV689554.1	1.0E+00 U44952.1	1.0E+00 U44952.1	1.0E+00 AV758825.1	1.0E+00 AA004982.1	1.0E+00 AA004982.1	P15306	1.0E+00 AW976184.1	1.0E+00 AB040950.1	9.9E-01 AF245455.1	9.9E-01 AF245455.1	9.9E-01 AL163302.2	9.9E-01 AF174585.1	P49657	9.9E-01 U65667.1	028642	9.9E-01 AJ005029.1	P22567	9.8E-01 BE957439.2	9.8E-01 BE957439.2	9.8E-01 AJ302158.1
Most Similar (Top) Hit BLAST E Value	1.0E+00 Q02207	1.0E+00 Q02207	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00 P15306	1.0E+00	1.0E+00	9.9E-01	9.9E-01	9.9E-01	9.9E-01	9.9E-01 P49657	9.9E-01	9.9E-01 Q28642	9.9E-01	9.8E-01 P22567	9.8E-01	9.8E-01	9.8E-01
Expression Signal	2.7	2.7	2.01	1.9	1.76	1.28	1.28	2.03	1.2	1.2	2.83	17.08	17.08	2.05	1.51	1.67	0.84	0.84	6.0	1.18	9.22	1.38	2.43	2.92	2.32	0.82	0.82	4.61
ORF SEQ ID NO:	26932	26933		27133	27405	27526	27527	27607	27609	27610	28005	28075	28076				21315	21316	22360		25441			28237	20265	23429	23430	26292
Exon SEQ ID NO:	16740	16740	19466	16941		17320		17395			17766	17835	17835	18928		19350	11458	11458	12467	13468	15381		17298	17988	10454	13644	13644	16137
Probe SEQ ID NO:	6861	6861	2969	7064	7339	7460	7460	7544	7546	7546	7916	7985	7985	9193	9513	9859	1553	1553	2598	3553	5461	7336	7510	8097	512	3732	3732	6272

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	. Top Hit Descriptor
6272	16137	26293	4.61	9.8E-01	9.8E-01 AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL- like protein, isolate JM983
8362	18239	28487	4.43		9.8E-01 BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
8362	18239	28488	4.43	9.8E-01	9.8E-01 BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
9408	19061		1.62	9.8E-01	9.8E-01 U52111.2	L Z	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoloukodystrophy protein >
5108	14974		1,01	9.7E-01	9.7E-01 AI660384.1	EST_HUMAN	we62e04.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:23456943'
				1	0	<u> </u>	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d
6052	16830	20702	2.37	9.75-01	9.7E-01 026/16.1	Z L	and e, partial cds Trificim acctiving trick resistance protein V/40 (V/40)
5050				1	0.7E 04 MODEA 4	T.V	niconi accessimi super user cassicative de la contrata del la contrata de contrata del la
8510					9.7E-01 RE511209 1	EST HIMAN	Common Spring and the second of the second o
9956			1 39		9.7E-01 Al 114281 1		Borndis cinerea strain T4 cDNA library under conditions of nitronan dentivation
4337		24016			9.6E-01 AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4337	14234	24017	6.8	Ĺ	9.6E-01 AF197825.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4355	14251	24036	1.3		9.6E-01 AW 799674.1	EST HUMAN	PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5083	14953	24729	0.92	9.6E-01	7662375 NT	Į	Homo sapiens KIAA0914 gene product (KIAA0914), mRNA
5517	15435	25498	3.46		9.6E-01 Z70556.1	TN	Parvovirus B19 DNA, patient C, genome position 2448-2994
5517	15435	25499	3.46		9.6E-01 Z70556.1	LN	Parvovirus B19 DNA, patient C, genome position 2448-2994
6890	16769		1.37	9.6E-01	9.6E-01 X95275:1	IN	P.falciparum complete gene map of plastid-like DNA (IR-A)
8808	18622		4.15		9.6E-01 AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
8808	18622	28913	4.15		9.6E-01 AV752605.1	EST_HUMAN	AV752805 NPD Homo sapiens cDNA clone NPDBAG06 5'
		İ					Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial
9709	19646		1.52	9.6E-01	9.6E-01 U91423.1	NT	protein, partial cds
3715	13627	23410	1.6		9.5E-01 BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3715	13627	23411	1.6			EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5
7266	17143	27336	1.17	9.5E-01	9.5E-01 AW861102.1	EST_HUMAN	RC1-CT0295-241199-011-b02 CT0295 Homo sapieris cDNA
3165	13090		3.37	9.4E-01	9.4E-01 AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3181	13106		191	9.4E-01	9.4E-01 AF080595.1	N	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
9354	19029		1.64	9.4E-01	9.4E-01 BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_67 Hamb sapiens cDNA clone IMAGE:3869929 5'
9708			1,43	9.4E-01	11419857 NT	TN	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1700	11601		1.11	9.3E-01	9.3E-01 AF242382.1	LN	Homo saplens phylanoyi-CoA hydroxylase (PHYH) gene, exon 5

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Juga Extra Flores Expressed III lear	Top Hit Descriptor		Bovine papillomavirus type 2, complete genome	Bovine papillomavirus type 2, complete genome	Equus caballus microsatellite LEX013	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds		Aedes triseriatus putative large subunit ribosomal protein rpL34 mRNA, complete cds	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B); melanoma antigen family A3 (MAGEA3), caltractin (CAI T) NAD(P)H dehydrogense-like protein (NSDHI) and 15	T	Т	Mus musculus carbonic anhydrase 4 (Car4), mRNA	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA	7058e06.x1 NO_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219.3' similar to SW:NU5M_TRYBB P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5		Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'	Rattus norvegicus mucin (MUC2) gene, partial cds	Г		Г	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA	Homo sapiens neurexin III-alpha gene, partial cds	Oryctolagus cuniculus Rad51 (RAD51) mRNA, complete cds	Xenopus laevis gene for aldolase, complete cds
פופ רייחוו ביו	Top Hit Database Source	EST HUMAN	N N	NT	NT	TN	N	EST_HUMAN	TN	L Z	EST HUMAN		L _Z	N L	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	님	SWISSPROT	EST_HUMAN	LN	NT	ΓN	TN	TN	Z
	Top Hit Acession No.	9.3E-01 BE071172.1	9.3E-01 M20219.1	9.3E-01 M20219.1	9.3E-01 AF075615.1	AF213884.1	9.3E-01 L36189.1	9.3E-01 AA847040.1	9.3E-01 AF271207.1	9.3E-01 (182671.2	BE622702.1	9.2E-01 BF037586.1	6671677 NT	11430963 NT	9.2E-01 BF593251.1	9.2E-01 BF132402.1	9.2E-01 BF680047.1	8923056 NT	9.1E-01 T26418.1	9.1E-01 T26418.1	9.1E-01 U68172.1	Q61704	9.1E-01 AA806623.1	9.1E-01 U72995.1	9.1E-01 AF050113.1	7661625 NT	9.0E-01 AF099810.1	9.0E-01 AF017729.1	9.0E-01 D38621.1
	Most Similar (Top) Hit BLAST E Value	9.3E-01	9.3E-01	9.3E-01	9.3E-01	9.3E-01	9.3E-01	9.3E-01	9.3E-01	9.38-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.1E-01	9.1E-01	9.1E-01	9.1E-01	9.1E-01	9.1E-01	9.1E-01	9.1E-01	9.0E-01	9.0E-01	9.0E-01	9.0E-01
	Expression Signal	1.13	0.82	0.82	1.54	1.62	3.84	1.88	1.56	1.38	3.04	4.23	1.38	3.63	1.73	1.85	2.01	1.43	0.97	76.0	98.0	2:92	15.99	2.2	30.05	0.89	2.37	0.82	1.45
	ORF SEQ ID NO:		23630	23631		25410		26771				25649			28041	53053	29101		22898	22899	23991	25950	26498	26587			23959	24589	
	Exon SEQ ID NO:	12464	13857	13857	15022		15402	16581	19325	19418	L	15556	17469	17740	17802	18767	18809	11967	13094	13094	14207	15824	16331	16409		13095			16250
	Probe SEQ ID NO:	2594	3949	3949	5155	5434	5482	6701	9822	9954	3201	5643	7618	7890	7952	8960	9006	2077	3169	3169	4310	5919	6472	6551	9445	3170	4282	4945	6388

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Single Exon Probes Expressed in Heart	Most Similar Top Hit Acession (Top) Hit Descriptor Source Source	2.52 8.5E-01 11418543 NT Homo sapiens human immunodeficiency virus type enhancer-binding protein 1 (HIVEP1) mRNA	2.63 8.5E-01 9507008 NT Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Pton5) mRNA	1 NT	8.4E-01 AF143509.1 NT	8.4E-01 L78726.1 NT	2.7 8.4E-01 L78726.1 NT Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7	8.4E-01 AJ248287.1 NT	LN.	2 NT	9.1 NT	8.3E-01 Y19177.1 NT	8.3E-01 U46916.1 NT	8.3E-01 U46916.1 NT	8.3E-01 U46916.1 NT	8.3E-01 U46916.1 NT	2.13 8.3E-01 AL161540.2 NT Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40	4.2 R 3E-01 A1201052.1 EST HIMAN reportifice algorithms against CDAP C09 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR.	8.3E-01 AF098070 1 NT	8.3E-01 AF108133.1 NT	8.3E-01 AE000903.1	8.3E-01 7212472 NT		8.3E-01 AF020503.1 N.	8.ZE-01 AB000489.1	8.2E-01 AF145589.1 NT	8.2E-01 AW3/6990.1 EST HUMAN	8.2E-01 AB000489.1 NT	8.2E-01 AW379433.1 EST_HUMAN	S.cerewisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isoproplymalate (alpha-IPM) 8.2E-01/212126.1 NT synthetase (partial), and DNA polymerase alpha (partial)	8.2E-01 AF052659.1 NT	8.2E-01 Q9JI70 SWISSPROT
		8.5E-01	8.5E-01	8.5E-01 AB030	8.4E-01 AF143	8.4E-01 L7872	8.4E-01 L7872	8.4E-01 AJ248	8.3E-01 M9343	8.3E-01 AL161	8.3E-01 AB010	8.3E-01 Y1917	8.3E-01 U4691	8.3E-01 U4691	8.3E-01 U4691	8.3E-01 U4691	8.3E-01 AL161	8.3F-01 A17910	8.3E-01 AF098	8.3E-01 AF108	8.3E-01 AE000	8.3E-01	100 C	8.3E-01 AF020	8.ZE-01 AB000	8.2E-01 AF145	8.2E-01 AW3/t	8.2E-01 AB000	8.2E-01 AW378	8.2E-01 212126	8.2E-01 AF0520	8.2E-01 Q9JI70
	Expression Signal	2.52	2.63	1.29	0.84				2.31	2.64	-	3.11	1.12	1.12	0.95	0.95	2.13	4	1.23	3.1	2.46	2.46	C	2.03	2.38	1.91	41.14	-	3.26	3.58	1.53	99.9
	ORF SEQ ID NO:						25146										24839		27914		28204			24.780					26154	26330		28028
	S]						- 1	Ì		\perp		_	_	15145	17424	1.		17953	17967	18486		\perp			1	15016	19462		17787
	Probe SEQ ID NO:	9430	9436	9683	4108	5378	378	7721	724	3056	3739	3930	4917	4917	5177	5177	5222	7573	7822	7867	8062	8076	RECAR	2000		20.00	2040	245	7710	6309	7788	7937

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Single Exori Propes Expressed in Heart	Top Hil Descriptor	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA	OVARIAN TUMOR LOCUS PROTEIN	w14d02.r1 Soares, placenta, 8to9weeks, 2NbHP8to9W Homo sapiens cCNA clone IMAGE:252195 5 similar to gb:M36072,60S RIBOSOMAL PROTEIN L7A (HUMAN):	Mus musculus mRNA for NIPSNAP2 protein	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds	Homo sapiens MHC class 1 region	Homo sapiens MHC class 1 region	NEURONAL MEMBRANE GLYCOPROTEIN M6-B	NEURONAL MEMBRANE GLYCOPROTEIN M6-B	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA	Thermotoga maritima section 23 of 136 of the complete genome	Staphylococcus aureus partial pta gene for phosphate actyfransferase allele 15	Bos taurus futb and rtlf genes	602072473F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215091 5'	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds	Mus musculus gene for oviductal glycoprotein, complete cds	Neisseria meningitidis serogrcup A strain Z2491 complete genome, segment 7/7	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit	RC0-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds	Ureaplasma urealyticum section 31 of 59 of the complete genome	Homo sapiens mRNA for KIAA1452 protein, partial cds	Haemophilus influenzae Rd section 54 of 163 of the complete genome	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'	Mus musculus embigin (Emb), mRNA	Mus musculus embigin (Emb), mRNA	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
e Exori Prope	Top Hit Database Source	SWISSPROT	N-	SWISSPROT	EST HUMAN S	T	N-	TN LN	T L	SWISSPROT		EST_HUMAN R	EST_HUMAN R	Г	NT	NT	EST_HUMAN 6	NT	NT	N LN	NT	EST_HUMAN R	NT	U	NT	H		NT	NT	EST_HUMAN 6				NT
guic	Top Hit Acessian No.					<u>-:</u>	AF191839.1	8.1E-01 AF055066.1	8.1E-01 AF055066.1			8.1E-01 BE938558.1	8.1E-01 BE938558.1	8.1E-01 AE001711.1	8.0E-01 AJ271510.1	1	8.0E-01 BF530962.1	8.0E-01 AF127897.1	8.0E-01 AB006193.1	8.0E-01 AL162758.2		8.0E-01 AW901489.1		.1	7.9E-01 AB040885.1		.1	7.9E-01 AF130459.1	7.9E-01 AF228684.1	7.9E-01 BE263612.1	6753745 NT	6753745 NT		
	Most Similar (Top) HIt BLAST E Value	8.2至-01 (8.2E-01 L10127.1	8.2E-01 P10383	8.2E-01 H87398.1	8.2E-01	8.1E-01	8.1E-01	8.1E-01	8.1E-01 Q13491	8.1E-01 Q13491	8.1E-01	8.1E-01	8.1E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01 X83739.2	8.0E-01	7.9E-01 D11476.1	7.9E-01	7.9E-01	7.9E-01 U32739.1	7.9E-01 AB004816	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01 Z47210.1	7.9E-01
	Expression Signal	99'9	2.81	9	6.65	1.73	1.29	2.81	2.81	2.49	2.49	1.94	1.94	1.84	3.02	3.76	1.83	2.73	1.14	1.8	5.65	284	3.78	1.16	65.97	1.37	5.24	2.29	2.75	0.92	1.02	1.02	0.84	0.84
	ORF SEQ ID NO:	28029	29011	. 29064	29069	25284		23130	23131	26020	26021	28879	28880	25343		20070		22761	22993		24115		20211				22006	22007	23193		24188	24189	24720	24721
	Exon SEQ ID NO:	17787	18717	18772	18777	19083	12593	13329	13329	15897	15897	18592	18592	18909	10142	10250	11884	12967	13194	13557	14327	16541	10390	10631	11491	11538	12102	12103	13388	14103	14401	14401	14945	14945
	Probe SEQ ID NO:	7937	8809	8966	8971	9451	2731	3412	3412	5992	5992	8775	8775	9166	170	285	1990	3039	3273	3643	4432	6661	446	869	1587	1634	2216	2217	3472	4204	4508	4508	5075	5075

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Origin Explication Explication	Top Hit Descriptor	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17	P.sativum GR gene	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds	SMALL HYDROPHOBIC PROTEIN	Homo sapiens KIAA1072 protein (KIAA1072), mRNA	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04	EST371637 MAGE resequences, MAGF Homo sapiens cDNA	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds	Sphenodon punctatus alpha enolase mRNA, partial cds	D.discoideum racGAP gene	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha	chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds:	butyrophilin-like (NG9), butyrophilin-li>	CITRATE SYNTHASE	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNAC-T7), mRNA	Homo sapiens PRO1975 mRNA, complete cds	Coturnix coturnix Japonica sub-species japonica beta-actin mRNA, partial cds	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds	RAFFINOSE INVERTASE (INVERTASE)	RAFFINOSE INVERTASE (INVERTASE)	yf24b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3'	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds	Archaeoglobus fulgidus, complete genome	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete ods	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
מסו וווסעד מופ	Top Hit Database Source	Į.	NT	NT	SWISSPROT		SWISSPROT	EST_HUMAN	EST_HUMAN	Į.	IN.	Į.	TN ,	NT			LN L	SWISSPROT		L L	IN	F	SWISSPROT	SWISSPROT	EST HUMAN	F		Ľ	
5	Top Hit Acession No.	7.9E-01 M29930.1	X90996.1	7.9E-01 U01912.1	P19719	7662471 NT	P19022	7.8E-01 Z43785.1	7.8E-01 AW959567.1	7.8E-01 U87305.1	7.8E-01 AF115856.1	7.8E-01 Y10159.1	L29260.1	7.7E-01 AF184345.1			7.7E-01 AF050157.1	033915	8393408 NT	AF118085.1	7.7E-01 AF199488.1	7.7E-01 AF199488.1	P16553	P16553	7.7E-01 R08600.1	7.7E-01 AF184345.1	11497621 NT	7.6E-01 AF059510.1	7.6E-01 AF059510.1
	Most Similar (Top) Hit BLAST E Value	7.9E-01	7.9E-01	7.9E-01	7.9E-01 P19719	7.9E-01	7.9E-01	7.8E-01	7.8E-01	7.8E-01	7.8E-01	7.8E-01	7.8E-01	7.7E-01			7.7E-01	7.7E-01 033915	7.7E-01		7.7E-01	7.7E-01	7.7E-01 P16553	7.7E-01 P16553	7.7E-01	7.7E-01	7.7E-01	7.6E-01	7.6E-01
	Expression Signal	1.01	2.43	4.78	3.95	2.30	2.48	1.75	3.2	0.79	2.32	1.27	1.42	6.33			1.85	2.8	8.0	4.45	2.88	2.88	1.44	1.44	1,95	2.6	6.14	4.04	4.04
	ORF SEQ ID NO:		26790	27582	27864		28682		22016	24278	25709	27399		19932	_			22436		23259	23979	23980	25386		25630	19932		25720	25721
	Exon SEQ ID NO:	14954	16601	17373	17631	18249	18415	10784	12114	14491	15607	17199	19623	10112			10641	12545	13234	13464	14195	14195	15335	15335	15541	10112	19004	15618	15618
	Probe SEQ ID NO:	5084	6721	7504	7781	8372	8543	828	2229	4603	2698	7323	9424	138			209	2680	3313	3549	4297	4297	5415	5415	5626	9212	9311	5710	5710

Page 26 of 413 Table 4 Single Exon Probes Expressed in Heart

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| Top Hit Descriptor | Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; and H5AR (H5ar) gene, complete cds | Mus musculus advillin (Advil-pending), mRNA | Mus musculus advillin (Advil-pending), mRNA | Mus musculus cytochrome P450, 2b9, phenobarbitol inducible, type a (Cyp2b9), mRNA | MUSCARINIC ACETYLCHOLINE RECEPTOR M2 | MUSCARINIC ACETYLCHOLINE RECEPTOR M2 | H.aspersa mRNA for neurofilament NF70 | H. aspersa mRNA for neuroflament NF70 | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88 | Homo sapiens mRNA for KIAA0895 protein, partial cds

 | Homo sapiens chromosome 21 segment HS21C101 | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 | C14203 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-037E11 5 | Homo sapiens hypothetical protein FLJ10793 (FLJ10793), mRNA | Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds | Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885 | Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
 | tn14b09.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' slmllar to contains Alu | repetitive element contains element Milk repetitive element | Maka nisilla actin (AcH) mRNA complete cds | Homo saciens chromosome 21 segment HS21C048 | 601573026F1 NIH MGC 9 Homo ganiens cDNA clane IMAGE 3834174 F
 | Mus musculus complement component 1 inhibitor (C1nh), mRNA | ta13h01.x1 NCI_CGAP_Lym5 Homo saplens cDNA clone IMAGE:2043985 3' | Borrelia burgdorferi (section 52 of 70) of the complete genome | Homo sapiens HT017 mRNA, complete cds | Homo sapiens growth arrest-specific 7 (GAS7), transcript variant b, mRNA
 | Mus musculus antigen (CD72) gene | Mus musculus anligen (CD72) gene |
| Top Hit
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Source | LΝΤ | IN | NT | NT | SWISSPROT | TORISSIMS | NT | IN | NT | NT

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No. | 4F146793.2 | 6857752 | 6857752 | 6753577 | | | X86347.1 | X86347.1 | AL161592.2 | 4B020702.1

 | AL163301.2 | AF020503.1 | C14203.1 | 8922672 | | 1 | 4E000823.1
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 | 6753217 | 41472641.1 | AE001166.1 | AF225421.1 |
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 | 7.46-01 | 7.4E-01 | 7.3E-01 | 7.3E-01 | 7.3E-01
 | 7.3E-01 | 7.3E-01 |
| Expression
Signal | 1.41 | 2.04 | 2.04 | 1.28 | 7.52 | 7.52 | 2.31 | 2.31 | 4.81 | 2.74

 | 1.52 | 2.23 | 0.88 | 13.92 | 3.57 | 1.87 | 1.42
 | | 1.23 | 1 22 | 4 43 | 7 23
 | 3.28 | 1.59 | 0.95 | 4.76 | 1.1
 | 5.61 | 5.61 |
| ORF SEQ
ID NO: | 26770 | 26796 | 26797 | 27252 | 27414 | 27415 | 28837 | 28838 | |

 | | 20315 | 23040 | 19900 | | 25209 | 25190
 | | | 23366 | 23889 |
 | | | 24194 | 24277 |
 | | 26011 |
| Exon
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NO; | 16579 | 16606 | 16606 | 17061 | 17215 | 17215 | 18553 | 18553 | 18756 | 18850

 | 10444 | 10508 | 13236 | 10083 | 19042 | 19329 | 19368
 | , | 11029 | 13570 | 14111 | 17135
 | 18828 | 18901 | 14408 | 14490 | 14994
 | 15889 | 15889 |
| Probe
SEQ ID
NO: | 6699 | 6726 | 6726 | 7184 | 7347 | 7347 | 8664 | 8664 | 8948 | 9073

 | 505 | 569 | 3315 | 4573 | 9381 | 9828 | 9884
 | | 1114 | 3665 | 4213 | 725R
 | 9041 | 9150 | 4515 | 4602 | 5127
 | 5984 | 5984 |
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Table 4
Single Exon Probes Expressed in Heart

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	ORF SEQ ID NO:	26480	26481	28870	28871		21687	22186	22748	23124					24706		70786				28256			22/45	23793			25626	26162	27746			20967
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Page 28 of 413 Table 4 Single Exon Probes Expressed in Heart

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 | 1.63 | 0.85
 | 2.73 | 2.73 | 3.56 | 3.56 | 2.37 | 1.03 | 1.16 | 1.58 | 1.26
 | 0.83 | 1.52 | 2.34 | 2.34 | 2.59
 | 2.59 | 1.79 |
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 | 22911 | 23117
 | 26726 | 26727 | 28719 | 28720 | | 20713 | | 21362 | 24153
 | 24420 | 27622 | 28566 | 28567 | 28593
 | 28594 | 28757 |
| Exon
SEQ ID
NO: | 12277 | 12277 | 14864 | 16759 | 18336 | 18336 | 10878 | 10878 | 11196

 | 13107 | 13316
 | 16532 | 16532 | 18450 | 18450 | 19543 | 10866 | 12506 | 11502 | 14363
 | 14634 | 17407 | 18311 | 18311 | 18331
 | 18331 | 18485 |
| Probe
SEQ ID
NO: | 2399 | 2399 | 4989 | 6880 | 8463 | 8463 | 954 | 954 | 1288

 | 3182 | 3399
 | 6652 | 6652 | 8582 | 8582 | 9016 | 941 | 2639 | 2799 | 4469
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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds	zx12g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE.786310 3' similar to contains element TAR1 repetitive element;	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription fector (Relish) nene complete cds, alternatively spliced.	Mus musculus Wiskoft-Aidrich syndrome profess in Residence on a series of spices	S.tuberosum mRNA for alucose-6-phosphate dehydrogenase	x895g12x1 NCI CGAP Co17 Homo sepiens cDNA clone IMAGE-25745g8 31	Dendrobium fimbriatum mRNA for phosphoenolovruvate carhoxydase partial	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome	Gallid herpesvirus 2. complete denome	Gallid herpesvirus 2. complete genome	Pseudomonas aerudinosa PA01 section 167 of 529 of the complate ganging	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome	CM3-HT0769-010600-197-c03 HT0769 Homo saplens cDNA	N-ACETYLGLUCOSAMINYL-PHOSPHATIOYLINOSITOL RIOSYNTHETIC PROTEIN CPI	Homo sapiens SLIT1 protein (SLIL2) mRNA, partial cds	Homo sapiens lens epitrelium-derived growth factor gene, alternatively spliced complete cots	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semanhorin) 54 (SEMA5A) mRNA	Calbicans random DNA marker, 282bp	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis	in LA-r1) gene, Korket gene, and sodium phosphate transporter (NPT3) gene, complete cds	Mus musculus kinesin light chain 2 (Kic2), mRNA	AV660506 GLC Homo sapiens cDNA clone GLCGID04 3'	Homo sapiens chromosome 21 segment HS21C078	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome	H.vulgaris Na, K-ATPase alpha subunit mRNA, complete cds	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
gle Exon Pro	Top Hit Database Source	LΝ	NT	EST_HUMAN	IN	IN	FN	EST HUMAN		NT L	F	N-	LZ LZ	F	EST HUMAN	SWISSPROT	ZI.	LΝ	L	IN	. 1			HUMAN		NT		
	Top Hit Acession No.	6.7E-01 AF213884.1	6.7E-01 AF213884.1	6.7E-01 AA451864.1	AF186073.1	TN 082829		6.7E-01 AW079110.1	6.7E-01 AJ252942.1	AE001486.1	9635035 NT	9635035 NT	6.7E-01 AE004506.1	\E001486.1	6.7E-01 BF354649.1			6.6E-01 AF199339.1	4506880 NT	Y07669.1	043084	111111111111111111111111111111111111111						
	Most Similar (Top) Hit BLAST E Value	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01 X74421.1	6.7E-01	6.7E-01	6.7E-01 AE00148	6.7E-01	6.7E-01	6.7E-01	6.7E-01 AE00148	6.7E-01	6.7E-01 014357	6.6E-01 AF075240	6.6E-01	6.6E-01	6.6E-01	8 119		0.00-01	6.55-01	6.6E-01 /	6.6E-01	6.5E-01 M75140.1	6.5E-01 M75140.1
	Expression Signal	29.34	19.53	1.57	3.59	3.7	96.0	0.85	0.89	1.62	1.42	1.42	3.98	1.46	2.23	3.69	0.87	1.29	1.04	3.05	78.0	90.6	0.30	3.63	2.41	1.35	1.37	1.37
	ORF SEQ ID NO:	20080	20110	21887	21908	22692	24032	24538	24811	25631	25836	25837		26367	28449	28147	22227	22422	23168	23310		25840	25040	50007	-	25256	20352	20353
	Exon SEQ ID NO:	10259	10295	11989	12713	12893	14246	14762	15046	15542	15723	15723	16192	16205	18200	17903	12329	12532	13362	13522	13924	15728	16387	1000	1/422	19197	10544	10544
	Probe SEQ ID NO:	295	336	2100	2120	2966	4350	4881	5182	5627	5817	5817	6328	6342	8323	8754	2452	2867	3445	3608	4020	5822	6525	0353	(5/1	9619	800	809

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Table 4
Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	D melanogaster mRNA for metabotropic glutamate receptor	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5	glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]	Variola virus, complete genome	Variola virus, complete genome	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome	nr09h06.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 002916 HLARK;	CM-BT043-090299-046 BT043 Homo saplens cDNA	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds	C.limicola pscD gene	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds	ys01e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3'	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23	NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIGI. PROTEASE P3C ; HELICASE (2C LIKE PROTEIN).	NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL DECTEASE DAY HE DECTEMBED CONTENDS	Mus musculus secreted acidic exsteine rich alvonordein (Sparc) mRNA	Rattus norvogicus dihydroxyoolyprenybenzoate methytransferase mRNA complete cds	Rattus norvegicus dihydroxypolyprenybenzoate methyltransferase mRNA, complete cds	Rat TRPM-2 gene, complete cds	Rat TRPM-2 gene, complete cds	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds	Homo saplens G-protein coupled receptor EDG-7 mRNA, complete cds
21 1104 216	Top Hit Database Source	NT	EST_HUMAN	LN	LN	. IN	NT	EST HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	Ę	F	Z	SWISSPROT	N	EST_HUMAN	EST_HUMAN	LN	TN	SWISSPROT	FORGONIA	NT NT	Į.	LN	Z L	Ę	N N	Z	N	NT	NT
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	Most Similar (Top) Hit BLAST E Value	6.3E-01 X99675.1	6.3E-01 BE90204	6.3E-01 S62927.1	6.3E-01	6.3E-01	6.3E-01	6.3E-01	6.3E-01 Al904160	6.3E-01 P47003	6.3E-01 P36073	6.3E-01	6.3E-01 AF10522	6.3E-01 X83528.1	6.2E-01 Q10135	6.2E-01	6.2E-01 H72255.1	6.2E-01 BE56268	6.2E-01 M24461.1	6.2E-01 AL16151	6.2E-01 P27410	70	6 1F-01	6 1F-01 20427 1	6 1F-01 20427 1	6.1E-01 M64733.1	6.1E-01 M64733.1	6.1E-01	6.1E-01	. 6.1E-01	6.1E-01 AF23611	6.1E-01 AF23611
	Expression Signal	1.38	3.17	1.67	2.72	272	4.1	2.27	11.72	1.94	1.98	9.21	1.54	1.58	2.12	3.06	5.45	1.71	2.56	7.14	5.02	20	20.02	06 0	66.0	3.78	3.78	3.72	1.75	1.75	19.47	19.47
	ORF SEQ ID NO:	23668	}	27223	27495	27496	28095	28543	28791	28865	28969	24899			25569		26903	26638		27886	28099	00.00	70107	24577	24578			26863	27175	27176	27492	27493
	Exon SEQ ID NO:	13892	16837	17027	17288	17288	17854	18288	18511	18581	18680	19697	18944	19619	15493	16287	16710	16448	17336	17649	17857	<u> </u>	17225		\perp	L	1	l	16985	16985	17286	17286
	Probe SEQ ID NO:	3985	6928	7150	7421	7421	8004	8413	8647	8725	8868	9128	9220	9435	5578	6426	6831	7435	7476	7799	8007	1000	2345	4031	4931	6104	6104	6792	7108	7108	7419	7419

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	Top Hit Descriptor	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain U7-71	D(2) DOPAMINE RECEPTOR	UI-H-BI1-aeb-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE: 27 Ico 19 3	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	SEGMENTATION PROTEIN FUSHI JAKAZU	SEGMENTATION PROTEIN FUSHI TARAZU	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)	Gailus gallus mRNA for Hyperion protein, 419 kD isoform	Gallus gallus mRNA for Hyperion protein, 419 kU isotorm	#08f07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE::2095621 3	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (INTERLS), mirally	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mKNA	RC1-HT0375-030500-015-c03 H10375 Homo sapiens cDNA	Haemophilus influenzae Kd section 16 of the complete genome	Homo capiens chromosome 21 segment HS21CU6/	Homo sapiens chromosome 21 segment H241cJo7	Raftus norvegicus cenexin 2 mKNA, partial cds	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds	THYMIDYLATE KINASE (DTMP KINASE)	PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA	Mus spretus strain SPRET/El CD48 antigen (Cd48) gene, partial cds	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region	Aspergillus oryzae pyrG gene for orolidine-5'-phosphate decarboxylase, complete cds	MICROTUBULE-ASSOCIATED PROTEIN 14 [CONTAINS: MAPT LIGHT CHAIN LOZ]	SIMTPROTEIN
Single Evel 1 19893 Expressed	Top Hit Database Source	H	NT		H			EST_HUMAN U			SWISSPROT	SWISSPROT		SWISSPROT	NT D	NT	T_HUMAN			THUMAN	L			_ L	 	ISSPROT	EST HUMAN	F	N			SWISSPROT
ה ה ה	Top Hit Acession No.	6.1E-01 AF119117.1		5802999 NT	6.0E-01 AF065253.1	6.0E-01 AJ233396.1		6.0E-01 AW139713.1	6.0E-01 U38813.1	6.0E-01 AJ277661.1			6.0E-01 AB008193.1	Q01497	6.0E-01 AJ131892.1	6.0E-01 AJ131892.1	6.0E-01 AI420623.1	11421663 NT	9055303 NT	6.0E-01 BE157617.1	5.9E-01 U32701.1	5.9E-01 AL163267.2	5.9E-01 AL163267.2	5.9E-01 AF162756.1	5 9F-01 AF065440.2	5.9E-01 Q9X0I3	5.9E-01 AW937175.1	5.9E-01 AF064626.1	5.9E-01 L42320.1	5.9E-01 AB017705.1	P34926	5.8E-01 P40472
	Most Similar (Top) Hit BLAST E Value	6.1E-01	6.0E-01 D87675.1	6.0E-01	6.0E-01	6.0E-01	6.0E-01 P20288	6.0E-01	6.0E-01	6.0E-01	6.0E-01 P02835	6.0E-01 P02835	6.0E-01	6.0E-01 Q01497	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	5.9E-01			5.9E-01	5 QF_01	5.9层-01	5.9E-01					
	Expression Signal	1.59	0.92	2.64	1.76	1.02	1.56	2.58	2.61	6.2	4.19	4.19	1.69	1.43	1.78	1.78	2.74	1.64	2.1	2.18	1.25	4.85	4.85	4.12	2.1	2.67	3.1	,			4.15	1.44
	ORF SEQ ID NO:	27860	20243		21103	23438	24918	25086	25968	26375			27727		28541			_	25065	_	20752		22955		25047				25342			3 21637
	Exon SEQ ID NO:	17628	10429	10490	11245	13656	15151	15260	15845	1_	١.	1_			18286	18286		<u> </u>	19554	上	L	<u>l</u> _	<u> </u>	L		17057			1		19193	11763
	Probe SEQ ID NO:	7778	486	549	1330	3744	5227	5339	5940	6350	6725	6725	7653	7894	8411	8411	8838	9500	9787	9809	984	3232	3232	4129		2003	0000	8520	9165	9404	9614	1867

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Homo sapiens protein tyrosine phosphalase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA

Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds

Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds

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12617

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3205

5.3E-01 AF087658.1

5.3E-01 AF019413.1 5.3E-01 AF113919.1 5.3E-01 AF113919.1

Single Exon Probes Expressed in Heart Page 34 of 413 Table 4

					ט. טיי	יאון בייטים פול	טוופוס בעמון ווספס בעלו סססס וווין ומווי
	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8	11103	20949	1.09	5.5E-01	8393912 NT	IN	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
-	12533	22423	2.88	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
1 ~	12533		2.88	5.5E-01 P03341		SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
8	12815		1.34	5.5E-01	5902085 NT	LN	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
12	12955		1.39		H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5HB55Y Homo saplens cDNA clone IMAGE:178266 3'
10	13121	22926	3.1		5.5E-01 AF227240.1	LN	Rabbit oral papillomavirus, complete genome
+	13548	23335	1.29		5.5E-01 P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
6	10113	19933	3.74	5.4E-01	7657266 NT	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
- 0	10113	19934	3.74	5.4E-01	7657266 NT	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
$\overline{}$	10509	20316	2.61		5.4E-01 AF232006.1	TN	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes
	10509	20317	2.61	5.4E-01	5.4E-01 AF232006.1	LN TN	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes
C	11157	21006	2.24		5.4E-01 AW896087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
l Co	11949		2.78		5.4E-01 AE002247.2	NT	Chlamydophila pneumoniae AR39, section 74 of 94 of the complete genome
8	12095	21998	2.23		5.4E-01 AJ276682.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
8	17588		2.01		5.4E-01 BF572536.1	EST_HUMAN	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
l N	18301	28557	2.87		5.4E-01 P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
2	18702	28996	4.51		5.4E-01 Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
2	18702	28997	4.51	5.4E-01	5.4E-01 Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
	18862		2.12		5.4E-01 AI858398.1	EST_HUMAN	wI37g04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
_							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P453 21-
- 1						!	hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B
எ	10447	-			_	Z !	(b1), and complement component CZ (CZ) genes.
പ്	11982	21877	0.91		5.3E-01 AF113919.1	2	brassica deracea var. capitata phosphotipase $UZ(PLUZ)$ gene, complete cds
í		-		LOR		!	

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Probe SEQ ID NO:

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	Top Hit Descriptor	Mycoplasma genitalium section 9 of 51 of the complete genome	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE::/40/11 5	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'	7e73c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783	TROTEIN DISOLFIDE ISOME, WELL TREGISCON (FROM 17).	76/3612.X1 NOT_CGAP_P126 north Septents CDNA dura InnASE.32331.15 3 311116 to 92:321.33 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for	chloroplast product	601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5	og30e05.s1 NCI_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611 APOLIPOPROTEIN D PRECURSOR (HUMAN);	Drosophila melanogaster helix-loop-helix mRNA, complete cds	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFATS)	Homo sapiens phospholipid scramblase 1 gene, complete cds	Homo sapiens chromosome 21 segment HS21C085	Homo sapiens mRNA for KIAA0740 protein, partial cds	Chlamydophila abortus strain S26/3 POMP91A and POMP90A precursor, genes, complete cds	Azotobacter vinelandii icd gene for isocitrate dehydrogenase, complete cds	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	am77g05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding	chloroplast protein, complete cds	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12	(MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin	(CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>	Mus musculus vanilloid receptor-like protein 1 (Vrl1), mRNA	Homo sapiens PELOTA (PELOTA) gene, complete cds	UI-H-BI1-acp-a-08-0-Ui.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714799 3'	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-	DELTA)	Human adrenodoxin reductase gene, exons 3 to 12	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
	Top Hit Database Source	NT	EST_HUMAN	EST_HUMAN		EST HOMAN	FST HUMAN		NT	EST HUMAN	EST HUMAN	F		SWISSPROT	Z	닏	Z L	Z	LN L	NT	EST_HUMAN		NT			뉟	NT	F	EST HUMAN		SWISSPROT	N	NT
)	Top Hit Acession No.			1820921.1		E645620.1	3E645620 1		01950.2	3E566291.1	5.3E-01 AA916053.1	20770.1			2.1	5.2E-01 AL163285.2	5.2E-01 AB018283.2	J65942.1	5.2E-01 D73443.1	5.2E-01 AL116780.1	5.2E-01 AA984165.1		5.2E-01 AF020269.1			U82671.2	7106444 NT	5.2E-01 AF143952.2	5 2F-01 AW137066 1		P18516	5.1E-01 M58509.1	5.1E-01 AJ233944.1
30 4	Most Similar (Top) Hit BLAST E Value	5.3E-01 U39687.1	5.3E-01 AI820921	5.3E-01 AI820921		5.3E-01 BE645620	5 2E-04 RE645620	12.0	5.3E-01 L01950.2	5.3E-01 BE56629	5.3F.01	5.2F-01 L20770.1		5.2E-01 Q9WV30	5.2E-01 AF224493	5.2至-01/	5.2E-01	5.2E-01 U65942.1	5.2E-01				5.2月-01			5.2E-01 U82671	5.2E-01				5.2E-01 P18516		
	Expression Signal	1.29	1.75	1.76		1.91	5	16:1	2.15	5.62	2 4R	1131		7.69	2.83	5.04	2.75	1.9	1.22	1.76	1.9		1.13			1.06	1.29			2	3.43	1.89	
	ORF SEQ ID NO:		25098	25089		25447	07.730			28946		20568		20904				22798			23114					23287		27837				20347	
	Exon SEQ ID NO:	14017	15270	15270		15387	1000	19391	17038	18658	10551	10704	27.0	11061	I_{-}	11739	11988	13008			L		13494	1_		13496	1_	1		_L	19370		Ш
	Probe SEQ ID NO:	4117	5350	5350		5467	i i	240/	7161	8846	4,00	2007	667	1148	1174	1843	2090	3084	3100	3350	3397		3580			3582	4949	7764	0240	9/19	9887	601	632

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Table 4
Single Exon Probes Expressed in Heart

oligie Lydin Tobes Lypressed in Teal	dit Top Hit Descriptor . Top Hit Descriptor	Polyangium vitellinum (strain P1 vt1) 16S rRNA gene	R.novegicus mRNA for manmalian fusca protein	Г		NOT TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)	MAN yi94a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1458/23'	Г			nec51f10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element AAN TAR1 repetitive element;	Homo sapiens postmelotic segregation increased 2-like 9 (PMS2L9), mRNA	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L.9), mRNA	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes.	complete cds; and termination factor Rho (rho) gene>	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (dridA) genes	complete cds; and termination factor Rho (rho) gene>	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibooy 363p. 138, partial cds	Homo sapiens mRNA for KIAA1184 protein, partial cds	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds		GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE		GLUCANOTERANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE	Т	Oryzias latipes gene for membrane guanyly cyclase OIGC1, complete cds	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds		OT NUCLEAR ENVELOPE PROTEIN CUT11
igie LAUI	Top Hit Database Source	뉟	N.	EST_HUMAN	EST_HUMAN	SWISSPROT	EST HUN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	노		NT		뉟	N	IN	N	EST_HUMAN	TOGGOOMS	200 40	SWISSPROT	EST HUMAN	ΙΝ	TN	TN	SWISSPROT
5	Top Hit Acession No.	5.1E-01 AJ233944.1	5.1E-01 X87885.1	5.1E-01 BF683095.1	5.1E-01 AI858495.1	P96380	5.1E-01 R80873.1		5.1E-01 W22302.1	5.1E-01 BF030207.1	5.1E-01 BF439982.1	4885552	4885552 NT		5.0E-01 AF008210.1		5.0E-01 AF008210.1	J55574.1	5.0E-01 AB033010.1	5.0E-01 M92304.1	5.0E-01 BF317212.1	D25572	2,000	³ 35573	180	5.0E-01 AB021490.2	5.0E-01 AF029215.1	02.2	J13961
	Most Similar (Top) Hit BLAST E Value	5.1E-01	5.1E-01	5.1E-01	5.1E-01	5.1E-01 P96380	5.1E-01	5.1E-01	5.1E-01	5.1E-01	5.1E-01	5.0E-01	5.0E-01		5.0E-01		5.0E-01	5.0E-01	5.0E-01	5.0E-01	5.0E-01		2	5.0E-01 P35573	5.0E-01	5.0E-01	5.0E-01	5.0E-01	5.0E-01 013961
	Expression Signal	3.28	1.06	1.44	3.84	2.86	1.57	4.54	3.57	3.62	2.03	1.37	1.37		1.32		1.32	0.84	3.44	5.62	3.61	0.05		2.25	1.27	9.32	2.26	2.02	2.94
	ORF SEQ ID NO:	20382			23667	23771	26116	27650	27653			21871	21872		21882		21883	23388	23495		26644	27614		27615		29099			
	Exon SEQ ID NO:	10569	11536	11870	13891	13994	15980	17435	17437	19478	19100	11977	11977		11986		11986	13601	13709	16839	16455	17401		17401	17791	18806	18913	19349	19358
	Probe SEQ ID NO:	632	1632	1977	3984	4094	6133	7584	7586	9230	9473	2087	2087		2097		2097	3688	3797	6961	7442	7550		7550	7941	9003	9170	9858	6986

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Table 4
Single Exon Probes Expressed in Heart

					3	and in the control of the	
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
772	10702		1.98	4.9E-01	4.9E-01 BF571462.1	EST_HUMAN	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1864	11760	21634	1.39	4.9E-01	4.9E-01 U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5679	15588	25688	2.46		4.9E-01 AF020931.1	NT	Homo saplens diacylglycerol kinase 3 (DAGK3) gene, exon 10
5679	15588	25689	2.46	4.9E-01		NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6406	16267	26429	1.76			NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7197	17074		1.41	4.9E-01	4.9E-01 BF209791.1	EST_HUMAN	601874964F1 NIH_MGC_54 Horno saplens cDNA clone IMAGE:4102503 5'
7359	19768		2.2	4.9E-01	10946863 NT	LN.	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
3065	18846		1.43	4.9€-01	4.9E-01 AF176912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
9851	19733		3.55		4.9E-01 AA613562.1	EST_HUMAN	nq22e11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144652 3'
							Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated
4577	14136		1.12	4.8E-01	4504850JNT	NT	products
5381	15300	25153	70 8	4 RE-01	4 RF-01 102987 1	L	Saccharomyces cerevisiae) sporulation protein (SPO11) gene required for melotic recombination, complete cds
6018	15922			4.8E-01	4.8E-01 AA659878.1	EST HUMAN	nu85f09.s1 NCI CGAP Aiv1 Homo sapiens cDNA clone IMAGE:1217513
6330	16193		1.98		5031650 NT	LZ	Homo sapiens reproduction 8 (D8S2298E) mRNA
6563	16421	26601	3.82		4.8E-01 AL161492.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6563	16421	26602	3.82		4.8E-01 AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6613	16493	26679	1 16		4 8F-01 A1820744 1	EST HUMAN	yj77f10 y5 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER6 repetitive element:
8111	1				4.8E-01 X83502.1	N-	S.cerevisiae ORFs from chromosome X
9369	19511		2.52		4.8E-01 AF227565.1	LN	Trypanosoma cruzi transposon VIP II SIRE repeat region
9870	19359		2.26		4.8E-01 BE790632.1	EST_HUMAN	601584324F1 NIH_MGC_7 Horno sapiens cDNA clone IMAGE:3938909 5'
5925	15830	25953	8.36		4.7E-01 BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
8221	18103		5.77	4.7E-01	4.7E-01 AF102673.1	N⊤	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds
8434	18308		2.06		4.7E-01 U41069.1	NT	Human collagen alpha2(刈) (COL11A2) gene, exons 6 through 16, and partial cds
8682	18570	28853			4.7E-01 AW889448.1	EST HUMAN	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
9390	19049		1.36		4.7E-01 AW341561.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE::2909198 3'
3674	13588	23375	1.27		4.6E-01 AW818638.1	EST_HUMAN	RC1-ST0278-040400-018-b06 ST0278 Hcmo sapiens cDNA
3683	13597		1.28		4.6E-01 BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3683	13597	23384	1.28		4.6E-01 BF693300.1	EST HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5087	14957		76.0		4.6E-01 M11267.1	TN	Bovine steroid 21-hydroxy/ase gene (P-450-c21) gene, complete cds
5360	15280	25111			4.6E-01 Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5360	15280	25112	3.38		4.6E-01 Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5404	15323	25372	1.78		4.6E-01 BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
:							

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•					6 -		
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
	1	25387	3 20		4 6E-01 AI247679.1	EST HUMAN	qh59h02.x1 Soares_feta_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:015338 015338 BUTYROPHILIN.;
5414					4 6E-01 AI247679 1		qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA cicne IMAGE:18490 3 Similar to TR:015338 015338 BUTYROPHILIN.;
5414	15334	25393			4.6E-01 P20050	П	MEIOSIS SPECIFIC PROTEIN HOP1
7303	1		1.47		4.6E-01 U62332.1	L	Emericella nidulans NEMPA (nempA) gene, minoci oriuna gene en cocani gene en cocani gene en complete cds
6057	1				4.6E-01 U62332.1		Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitocholdral protein, complete cds
6843	Ī	_	13.48		4.6E-01 BF697399.1	EST HUMAN	602/30803F1 NIH MICC_30 HOLD SAPELIS CONTROLLED TO THE CONTROLL TO THE MATERIAL NATERIAL PROPERTY (GC-B) (GUANYLATE)
7363	17230	0 27430	26.48		4.6E-01 P55202	SWISSPROT	ATMAL MATERIAL PETTING PETTING RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE
7363	17230	0 27431	1 26.48		4.6E-01 P55202	SWISSPROT	A I KIAL I A I RICHAEL I OLI TICLI I LICE I CONTROL SADIAN CON CONTROL SADIAN CON CONTROL SADIAN CON CONTROL SADIAN CONTROL SA
7730	17580	27802	1.33		4.6E-01 AI915634.1	EST HUMAN	Wg/361ZXI Soales NSI 19 3W OT PA P S1 Homo sapiens cDNA clone IMAGE:2370766 3'
7730	17580				4.6E-01 AI915634.1	EST HUMAN	Wg/3elz.xi soales Not 1 0 3 1 7 1 2 2 1 1 2 2 1 2 1 2 1 2 1 2 1 2 1
8359	18236	9	2.86		4.6E-01 P98163	SWISSPROI	FORMULA TO THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE
8368	3 18245	5 28495	5 4.78		4.6E-01 BE185449.1		## ### ###############################
8368	3 18245	15 28496			4.6E-01 BE185449.1	FOI TOWAIN	Limen thioninine methyltransferase (TPMT) gene, exon 10 and complete cds
8766	3 17915				4.6E-01 AF019369.1	į.	Turner thionings mathytransferase (TPMT) gene, exon 10 and complete cds
8766	5 17915	15 28161	1 5.45		4.6E-01 AF019369.1	Z	Hulling of Bright Hills of Bright Brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-105F03
9313	3 19005	35	1.43		4.6E-01 D53316.1	EST_HUMAN	5
9266	19491	1	2.21		4.6E-01 AF120134.1	TN	Linanthus jamauensis maturase (matk) gene, chloroplast gene encoding chloroplast protein, partial cds
1869	L	65 21639	1.73		4.5E-01 AE001931.1	NT	Deinococcus radiodulfans R. i. secucii loo di 229 di die complete chromosome 1
1869	9 11765	55 21640	1.73		4.5E-01 AE001931.1	ŁZ	Definococcus rational is N1 section to 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 a
2841	_		58 4.87		4.5E-01 AA677086.1	EST_HUMAN	ASSENTENT MENAPPANE SPECIFIC HEPARAN SUI FATE PROTEOGLYCAN CORE PROTEIN
3275	75 13196	96 223	3.97		4.5E-01 Q05783	SWISSPROT	BASEMENT MEMBER VICE CONTROL OF THE PRESENCE OF THE PRESENCE OF THE PRESENCE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
3331	_		1.05		4.5E-01 AF126378.1	LN L	Mus musculus DINA polytiletase epolici catalytic subuliit (1 old) gairs, oxolo z micray.
3942			1.41		4.5E-01 Q28247	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN COLLAGEN A Barriard 2042 HDI RRE Home saniens cDNA clone IMAGE 2353480 3
3982		89 23665			4.5E-01 AI708908.1	EST HUMAN	HAGINDO X1 Soares, NFL T GBC S1 Homo sapiens cDNA clone IMAGE:3041810 3'
4085	35 15079	79	4.02		4.5E-01 AW873495.1	EST HOMAIN	יייייייייייייייייייייייייייייייייייייי

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Table 4
Single Exon Probes Expressed in Heart

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Dalabase Source	Top Hit Descriptor
4862	14742	24522	0.94	4.5E-01	4.5E-01 BE983445.2	EST_HUMAN	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5406	15325	25375	1.45		4.5E-01 AW608814.1	EST_HUMAN	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
5983	15888		1.47	4.5E-01	4.5E-01 Q00956	SWISSPROT	COAT PROTEIN
6488	16346	26515	2.49	4.5E-01	4.5E-01 AI858849.1	EST HUMAN	wi32e02.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923 SWI/SNF COMPLEX 170 KDA SUBUNIT.;
6897	16776		3.14	4.5E-01	AI648596.1	EST_HUMAN	tz56g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3'
7100	16977		1.54	4.5E-01	11444786 NT	Z	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
7991	17841	28082		4.5E-01		EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBCY17
7991	17841	28083	25.09	4.5E-01	4.5E-01 M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
8237	18117	28369	2.42	4.5E-01	4.5E-01 AW591271.1	EST_HUMAN	xo14h01.x1 NCI_CGAP_Uß Homo sapiens cDNA clone IMAGE:2703986 3' similar to SW:INT6_MOUSE_Q84252 VIRAL INTEGRATION SITE PROTEIN INT-6. [1];
9036	19724		2.25	4.5E-01		EST_HUMAN	601449201F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3852961 5'
9694	19245		1.44	4.5E-01	4.5E-01 BF337531.1	EST_HUMAN	602035275F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183290 5'
9763			2.15	4.5E-01	11422099 NT	N	Homo saplens testis-specific kinase 2 (TESK2), mRNA
9974	19652	24987	1.83	4.5E-01	4.5E-01 AF238234.2	IN	Entamoeba histolytica diaphanous protein (dia) gene, partial cds
1991	11885		2.47	4.4E-01	F680503 NT	TN	Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA
2340	12220	22118	3.59	4.4E-01	4.4E-01 P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3274	13195			4.4E-01	4.4E-01 AF058790.1	N	Rattus norvegicus SynGAP-b mRNA, complete cds
3274		22995	66.0	4.4E-01	4.4E-01 AF058790.1	IN	Rattus norvegicus SynGAP-b mRNA, complete cds
3277	13198		1.87	4.4E-01	4.4E-01 BF056726.1	EST_HUMAN	7j91402.y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4141	14041		1.33	4.4E-01	4.4E-01 BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5
4924	14803		0.93	4.4E-01	4.4E-01 BE141396.1	EST HUMAN	MR0-HT0078-131299-007-g05 HT0078 Homo sapiens cDNA
5326			1.99	4.4E-01 P04929	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5326			1.99	4.4E-01	4.4E-01 P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5490		25474	1.3	4.4E-01	S65019.1	NT	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5499	15418		1.98	4.4E-01	4.4E-01 AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5
5624	15539	25627	1.6	4.4E-01	4.4E-01 AI198413.1	EST_HUMAN	qi62h11x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN;
1001	7			L		1	qi62h11x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
5624	15539	25628	1.6	4.4E-01	4.4E-01 AI198413.1	EST_HUMAN	UNKNOWN PROTEIN:
5782		25798	1.79	4.4E-01	5.1	EST_HUMAN	xc27e08.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:095154 095154 AFLATOXIN B1-ALDEHYDE REDUCTASE.;
6582	16462		10.84	4.4E-01	4.4E-01 Z11679.1	N	S.tuberosum mRNA for induced stolon tip protein (partial)

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Single Exon Probes Expressed III near	Top Hit Descriptor	ZINC FINGER X-CHROMOSOMAL PROTEIN	4039f09.x1 NCI_CGAP_Lub Homo sapiens culvA clotle IMAGE. 19 1092.13	YCOPROLEIN B PRECORSON (GLICOTING)	TYROSINE-PROTEIN KINASE KECEPTON TIE-LIFNECONSON	beta -HKA=H,K-A I Pase beta-subumitinas, Certonius, Oscorni, Segiment 2 of 2	beta -HKA=H,K-A I rase beta-subulin [lass, Genomic, 3500 m, 359 mm, 25]	Mus musculus sodium diamilier, type A, apria polycomod, comod,	Homo sapteris difformice at legitical trace of the complete genome	Adulgiaphia Candrillo Archer PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)	OV EACISION INEL AIR CONTINUE MANAIL M. Onesin gene upstream flanking region	Cellin III (Section Wife Commission of Commission Commission of Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Commission Co	Callul IX Jacob Liu S MVVIII - 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Sing	Top Hit Acession No.		1.00		P35590		S76404.1	77874	4.4E-01 AL183282.2	962//42				Ī		-	8.1	4.3E-01 J00306.1	4.3E-01 AF155218:1	4.3E-01 AF155218.1	4.3E-01 AL161502.2	9635250 NI	4.3E-01 AF179825.1	4.3E-01 AJ001678.1	033367	4.3E-01 BF348001.1			4.3E-01 AW630048.1	4 3E_01 AW170559 1	4 3E-01 AE075629 1	4 3E 04 AWOO3658 1	4.3F-01 AW993658.1	4 3E-01 A Inn3022 1	
	Most Similar (Top) Hit BLAST E Value	4.4E-01 O62836	4.4E-01	4.4E-01 P28922	4.4E-01	4.4E-01		4.4E-01	4.4E-01		4.4E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01													╽
	Expression Signal	1.29	1.99	2.45	4.67	1.33	1.33	2.29	3.29	5.34	1.75	1.98	1.98	1.1	96.0	0.93	1.53	1.15	1.02	1.02	1.11				4.01	2.54	2.83	1.65	1.65						2.02
	ORF SEQ ID NO:	27422	27798		27903	28025	28026	25329		25224		20178	20179			22742		23737		20179											26106				
	Exon SEQ ID NO:	17992	17573	17574	17663	17785	17785	18996	19663	19267	19326	10351	10351	11489	12771	12950	13145	13961	10351	10351	14755	14929	15514	15933	15996	16255	16787		1_	1_	77//		┸		5 19390
	Probe SEQ ID NO:	7354	7723	7724	7813	7935	7935	9536	9306	9731	9824	405	405	1585	2843	3022	3221	4059	4306	4306	4875	5059	2600	6029	6102	6393	6069	7608	7608		7/8/	8307	8537	8237	9916

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	. Top Hit Descriptor
1335	12691	21099	1.04	4.2E-01 Q39102	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
1904	11800		0.89	4.2E-01	4.2E-01 AA761653.1	EST_HUMAN	nz24a09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'
3558	13472	23263	4.78		4.2E-01 AE003947.1	NT	Xylella fastidiosa, section 93 of 229 of the complete genome
3585	13499		1.09	4.2E-01	4.2E-01 AI280338.1	EST_HUMAN	ql94b01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3803	13715	23503	96'0		4.2E-01 AW835527.1	EST_HUMAN	QV0-LT0015-180200-127-h01 LT0015 Homo sapiens cDNA
3900	13810		1	4.2E-01 Q04886	Q04886	SWISSPROT	SOX-8 PROTEIN
4545	14438		3.63	4.2E-01	4.2E-01 BE073574.1	EST_HUMAN	RC5-BT0559-020300-013-E06 BT0559 Homo sapiens cDNA
4500	14487	27040	4 06		4 2E-01 A 4 53 4 0 93 1	HST HIMAN	nj69b01.st NCL_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN. DR-1 BETA CHAIN (HUMAN):
4671	14557	24350	3.13		4.2E-01 R13467.1	EST HUMAN	y777e01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28278 5'
5503	15422	25484	1.5		4.2E-01 BF242055.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5533	15450	25518	1.56		4.2E-01 AW854162.1	EST_HUMAN	RC3-CT0254-060400-029-g04 CT0254 Homo sapiens cDNA
6151	16024	26164	9.1	4.2E-01	4.2E-01 AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6151	16024	26165	9.1	4.2E-01	4.2E-01 AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sepiens cDNA clone PLACE2000470 3'
6184	19461	26219	2.1	4.2E-01	4.2E-01 S82504.1	NT	Brca1=breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
6217	16083	26233	5.91	4.2E-01	4.2E-01 AL161547.2	TN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
6999	16543			4.2E-01	4.2E-01 AW957448.1	EST HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
6663	16543	26740	2.1	4.2E-01	4.2E-01 AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
6776	16655	PPBSC	1 10	4 2E-01	4758039 NT	<u> </u>	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial prolein, mRNA
7992	17842		1.48		4.2E-01 AW863666.1	EST HUMAN	MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
8400	18276		2.2		4.2E-01 AB023489.1	N	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
8699	18517		2.04		4.2E-01 BE966485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
9863	19353		1.66		4.2E-01 AV731815.1	EST HUMAN	AV731815 HTF Homo sapiens cDNA clone HTFBHH05 5'
1078	10994	20835	1.88		4.1E-01 AI905481.1	EST_HUMAN	RC-BT091-210199-142 BT091 Homo sapiens cDNA
1087	11003	20844	2.4			EST HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1087	11003	20845				EST HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5
1592	11496	21356	1.03		4.1E-01 Al905949.1	EST_HUMAN	PM-BT103-270499-684 BT103 Homo sapiens cDNA
2678	12543	22434	1.52	4.1E-01	7705283 NT	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2910	12836		1.76		4.1E-01 AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2910	12836	22634	1.76		4.1E-01 AL161536.2		
3263	13186				4.1E-01 AA906344.1	EST_HUMAN	oj94b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
4177	14077	23852			4.1E-01 AJ249207.1	N	Rhodococcus sp. AD45 isoC, isoH, isoI, isoA, isoA, isoB, isoC, isoD, isoE and isoF genes
4208	14107		1.07		4.1E-01 AA909257.1	EST_HUMAN	om33d02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819.3'

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Single Exoll riones Lypiessed in reduction	Top Hit Descriptor	yg11b03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31814.3'	AV747880 NPC Homo sapiens culviv done in Court to 3	Bacilius subtitis complete genome (section z.t.or.z.). Itorii 35992201 to 42,14014	602130590FI NIT MIGG 63 TUTIN SEPTEMBER CONTRIBITE GENOME	Mentanococcus jailitasciili secucii 17 or 100 or 110	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Sitpec-pending), mRNA	ampylobacter Jeuni IVC I CT I Tod Complete generality, segment of	CM2-H1013/-Z00899-U10-E00 H1013/ Troilin septens control	Zea mays ZMITMOS gene to 19 MOS Zeil Protein.	VOL I AGE-CATIED FOL ASSIGNIA CITAMINEET INCLES AND CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CON	tomo saplens DINA lot alligible precarsor process, compress case	Laglest Tubelles International Company Systems	Drosophila metanogaster Dalillarari (Crity III M.M., Composito C.C.)	Mus musculus pialeter delived growing action coopers, soon profession and a second coopers and a second coopers and a second coopers and a second coopers and a second coopers are a second coopers and a second coopers are a second coopers and a second coopers are a second coopers and a second coopers are a second coopers and a second coopers are a second coopers and a second coopers are a second coopers and a second coopers are a second coopers are a second coopers and a second coopers are a second coopers are a second coopers and a second coopers are a second coopers are a second coopers and a second coopers are a second coopers and a second coopers are a second coopers are a second coopers are a second coopers and a second coopers are a second coopers and a second coopers are a second coopers are a second coopers are a second coopers are a second coopers are a second coopers are a second coopers are a second coopers are a second coopers are a second coopers are a second coopers are a 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coopers are a second coopers are a second coopers ar	SECONDIAL HILLIES OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE 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STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE	Ascobolus immersus masoz gene	Mus musculus upiquiuri-protein ligase es component recognin (com), mission appropriate transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and 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transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer and transfer	Homo sapiens chromosomie z I segment HS21C080	Homo sapieris cili di ilosuine et i sagina in 1721 coco.	Streptococcus pneumoniae YIIC (yIIC), YIID (yIID), peniciliir-birdiilig protein 24 (pup.zx), and anacoccing of paper protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein and protein a	spo	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST	FST382691 WAGE resequences, MAGK Homo saplens cDNA	Company the condition of Court transmission of the complete cds	Sylled Roysus sp. 1 od 3110 um sprougesterner HS21C100	TOTAL TITLE A TANDENTE IN GINS STEE INTERGENIC REGION	Community Inc. 101 TC 1168 complete genome: segment 2/6	CampyAbdacer Jeguin NO 101 102 compact gament and Appendix and Appendix CNA LHThrase 15090a 0.14-f09 HT0136 Home sapiens cDNA	Corilla mailla carboxol-ester libase (CEL) gene, complete cds		
e Exon Plone	Top Hit Database Source	HUMAN	EST_HUMAN /		T HUMAN	Т	EST HOMAN			T HUMAN	П	ISSPROT								N	LN.		L	LN	LN	SWISSPROT	EST HIMAN	AND LOUIS	Z	I N	SWISSPROI	IN FOR	ES HOMAN	<u>N</u>
Builo	Top Hit Acession No.	R41726.1	1		<u></u>		4.1E-01 BF574604.1	55521	2	4.1E-01 BF349382.1	(58700.1	209470	387675.1	8404656 NT	AF203478.1	6679258 NT	4.0E-01 Z96933.1	4.0E-01 Z96933.1	6678490 NT	4.0E-01 AL163280.2	4.0E-01 AL163280.2		4 OF-01 AF068903-1	4 OF-04 A 1277511 1	A 1077544 4	4.0E-01 A341151	0.51049	4.0E-01 AW9/0610.1	4.0E-01 L76080.1	4.0E-01 AL163300.2	P36049	4.0E-01 AL 139075.2	3.9E-01 AW352188.1	3.9E-01 AF 205518.1
	Most Similar (Top) Hit BLAST E Value	4.1E-01	4.1E-01 AV747880.	4.1E-01 Z99124.1	4.1E-01 E	4.1E-01 U67535.1	4.1E-01	4.1E-01	4.1E-01 /	4.1E-01	4.1E-01 X58700.1	4.1E-01 Q09470	4.1E-01 D87675.1	4.0E-01		4.0E-01	4.0E-01	4.0E-01	4.0E-01	4.0E-01	4.0E-01		4 OF-01	A OF-04	10-01	4.05-01	4.0E-01	4.0E-0.1	4.0E-01	4.0E-01	4.0E-01 P36049			3.9E-01
	Expression Signal	0.83	1.26	0.87	4.13	291	1.3	1.23	1.3	1.58	164	2.79	1.72	1.27	96.0	4.06	1.17	1.17	1.09	2.24	2.24		7	10.6	3.24	3.24	7.34	1.31	3.24	2.22	1.33			2.1
	ORF SEQ ID NO:		24247		25650	26418	26757	27323			28349			ŀ	21079		21742		L	22665						23452		7 25596	1		1			21119
	Exon SEQ ID NO:	14269	14459	15049	15557	16257	16563	17130	1_		1_	17880	19702		l.	<u></u>	12709	1_	10110	1	12866	1		1	- [-{		15517	18766	19567	19327	19387	1	11262
	Probe SEQ ID NO:	4373	4567	5185	5644	6395	6683	7253	7888	8018	8213	8696	9624	1023	1316	1469	1960	1960	2774	2939	2939			3637	3755	3755	4712	5603	8929	9312	9825	9910	227	1356

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	Top Hit Descriptor	ye43h05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element;contains PTR5 repetitive element;	RC0-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA	yf92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3	yf92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3	Borrelia burgdorferi (section 10 of 70) of the complete genome	Human p53 (TP53) gene, complete cds	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds	yb42b11.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:73821 3' similar to similar to gb:A06977 SERUM ALBUMIN PRECURSOR (HUMAN)	Mus musculus developmental control protein mRNA, partial cds	ah37b01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1291657 3' similar to TR:Q15288 Q15288 NO Programme poortein Mortice.	USUINCTIVE TROLLER WOLL S	ONO Sabletis IIINIYA LO NIVATITA DI COMPANIA A COMPANIA C	Dano reno bone morphogenetic protein 4 precursor (biwir 4) gene, continued cus	3900/XI Soales Not'r Fe aw College Source Color College Source Color College Source Color College Source Color College Source Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color	MR3-010007-080300-104-buZ 010007 Homo sapiens culvA	Neisseria meningitidis serogroup B strain MC38 section 30 of 200 of the complete genome	Homo sapiens tumor endothelial marker / preculsor (EM/), mKIVA	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:388bb52 3	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE.3680602.5	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mKNA	Homo sapiens chromosome 12 open reading frame 4 (VIZORF4), finklyA	Gallus gallus mRNA for beta-carotene 15,15-dioxygenase (bCIDC) gene)	qt46b07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997.3	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)	Mus musculus retinoblastoma 1 (Rb1), mRNA	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds	Chlamydophila psittaci partial omp1 gene for outer membrane protein 1	Human mRNA for KIAA0223 gene, partial cds
-	Top Hit Database Source	EST HUMAN AI	EST_HUMAN R	HUMAN	HUMAN	NT	N IN	T HUMAN	NT NT	EST HUMAN to			HOMAN				EST HUMAN N			HUMAN	T_HUMAN				EST HUMAN		±N	E	۲		LN LN	LN LN	
	Top Hit Acession No.		3.8E-01 BE719219.1			-	3.8E-01 U94788.1	1	3.8E-01 AF291483.1		2.7		_		2		3.7E-01 AW878037.1	3.7E-01 AE002408.1	11525843 NT	3.7E-01 BE873743.1	3.7E-01 BE873743.1	11436739 NT	11436739 NT	3.7E-01 AJ271386.1	3.7E-01 Al336411.1	3.7E-01 X05958.1	3.7E-01 AJ297357.1	3.7E-01 AJ297357.1	3.7E-01 X04122.1	TN 8677678	3.7E-01 J04982.1	3.7E-01 AJ243525.1	3.7E-01 D86976.1
	Most Similar (Top) Hit BLAST E Value	3.8E-01 T95413.1	3.8E-01	3.8E-01 R42550.1	3.8E-01 R42550.1	3.8E-01/	3.8E-01	3.8E-01	3.8E-01	3 8F-01 T54787 1	3.8E-01		3.8E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01		3.7E-01	3.7E-01							
	Expression Signal	4,11	2.82	257	257	2.38	1.34	2.21	1.84	1 27	13		1.33	9.85	9.48	6.63	1.53	3.32	2.73	4.51	4.51	2.34	234	1.46	3.93	1.81					1.87	1.94	2.41
	ORF SEQ ID NO:			29041	29042						25180			22203	23133	23812	23898	23974	26250				26922	L	27958								
	Exon SEQ (D NO:	17304	18633	18747	18747	18997	10861	19137	19638		┚	00461		12308	L	14036	14123	١.	16101	<u> </u>	L	16727	16727	<u> </u> _	1_		L		L		L	١.	18976
	Probe SEQ ID NO:	7516	8820	8939	8930	9297	0422	9530	0017	7000	9921	1000	9970	2431	3414	4136	4225	4292	6235	6392	6392	6848	6848	7307	7864	8232	8392	8397	8762	8979	9008	9176	9272

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					J. 11.	JIE EAULI FIOD	Single Extri Flobes Expressed in reali
Probe SEQ ID S NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9634	19206		2.18	3.7E-01	3.7E-01 AL121154.1	EST_HUMAN	DKFZp762K075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
9701	19251	25217	1.52	3.7E-01	3.7E-01 Y18000.1	LN	Homo sapiens NF2 gene
9964	19746		1.31	3.7E-01	3.7E-01 AJ237934.1	NT	Bos taurus partial stat5B gene, exons 2-15 and joined CDS
979	10902		71.7	3.6E-01	3.6E-01 U89241.1	TN	Human mibp gene, partial cds
1292	11199	21054	2.59	3.6E-01	3.6E-01 T80255.1	EST HUMAN	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1292	11199	21055	2.59	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares Infant brain 1NIB Homo saplens cDNA clone IMAGE:24443 5
1874	11770	21645	6.05		AW 590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1874	11770	21646	9:05		3.6E-01 AW590184.1	EST HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1908	11803	21682	6.18		3.6E-01 AF216207.1	TN	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2007	11899		1.08		3.6E-01 AF056927.1	TN	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2223	12108		1.04	3.6E-01	3.6E-01 AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2341	12221		2.39		3.6E-01 X76725.1	Ŋ	P.Irregulare (P3804) gene for actin
2437	12314	22211	1.63		3.6E-01 AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
							PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE
2589	12460	22350	2.28		3.6E-01 P24206	SWISSPROT	METHYLTKANSFEKASE)(PIMT)(PKOTEIN L-ISOASPAKTYL METHYLTKANSFEKASE)(L- ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2869	15077				35.1	닏	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
3424	13341	23145	1.85		3.6E-01 X76758.1	N	H.sapiens serotonin transporter gene, exons 9 and 10
3424	13341	23146	1.85	3.6E-01	X76758.1	LN	H.sapiens serotonin transporter gene, exons 9 and 10
4308	14205	23988	1.16	3.6E-01	1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4635	14523	24312	0.85		3.6E-01 AJ009609.1	F	Brassica napus mRNA for MAP4K alpha2 protein
4684	14570	24367	1.23		3.6E-01 AJ229237.1	F	Bacteria from anoxic bulk soil 16S rRNA gene (strain XB45)
4941	14819		2.01	3.6E-01	3.6E-01 AW339393.1	EST_HUMAN	ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5839	15805	25928	1.6		3.6E-01 Y10196.1	NT	Homo sapiens PHEX gene
6238	16104		5.49		3.6E-01 R94090.1	EST_HUMAN	yt74a06.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:275987 5'
-	Į						wt72c10.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
6317	16180				3.6E-01 AW027174.1	EST_HUMAN	O15117 FYN BINDING PROTEIN. [1];
6816	16695	26886	13.42		3.6E-01 AL161583.2	F	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
7205	17082	27269	3.37	3.6E-01	4504956 NT	TN	Homo sapiens lysocomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7205	17082	27270	3.37	3.6E-01	4504956 NT	, F	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7302	17178	27380	1.4		AL16320	LN	Homo sapiens chromosome 21 segment HS21C004
7674	17524		15.34		3.6E-01 Q53194	SWISSPROT	PROBABLE PEPTIDE ABG TRANSPORTER ATP-BINDING PROTEIN Y4TS

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Table 4
Single Exon Probes Expressed in Heart

					"		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8314	18191	28440	1.94	3.6E-01	3.6E-01 BE902390.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
8453	18326	28585	3.69		3.6E-01 AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
							Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete
8741	17890	28134	3.56	3.6E-01	3.6E-01 AE000856.1	LN	gename
9044	19761		1.81			NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
9127	18886		30.5		3.6E-01 AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
9281	18983		3.03		3.6E-01 U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
8	70707		7			MAAN LI HOU	x80e11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN at PHA.1 CHAIN (HI MAAN).
8008			0.70		AW 180229.1	NICIONIC I TO	Alle Print Court (Courterly), Male Print Courterly (Courterly)
202					66/8933	-2	wus musculus mannose receptor, c type z (wicz), mrkwa
662			0.97	3.5E-01	AL 16158	N	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
708	10640	20466	1.24		7706136 NT	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
708	10640	20467	1.24	3.5E-01	7706136 NT	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
763	10694		3.17		_	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1603	11508	21370	1.17	3.5E-01	3.5E-01 BF310688.1	EST_HUMAN	601894653F2 NIH MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1622	11526	21384	1.05		3.5E-01 U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTP as e activating protein mRNA, complete cds
2563	12725	22327	1.85		3.5E-01 AA223252.1	EST_HUMAN	zr08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapieris cDNA clone IMAGE:650872 3'
2672	12537		0.86		3.5E-01 U05897.1	IN	Fibrobacter succinogenes S85 endoglucanase E (celE) and endoglucanase ${\sf D}$ (cel ${\sf D}$) gene, complete cds
4165	14065	23839	1.92		3.5E-01 AF071253.1	IN	Danio rerio homeobox protein (hoxb5b) gene, complete cds
4379	14275		1.29		3.5E-01 BE146585.1	EST_HUMAN	RC5-HT0218-181099-011-g02 HT0218 Homo sapiens cDNA
4790	14675		0.84		3.5E-01 N81203.1	EST HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, 240498
4849	14730	24513	3.84		3.5E-01 M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
6199	15959		3.47		3.5E-01 X98505.1	TN	S.scrofa mRNA for CD31 protein (PECAM-1)
6704	16584		1.88		11448042 NT	NT.	Homo sepiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
7171	17048	27238	3.21	3.5E-01	4507610 NT	TN	Homo saplens tyrosine kinase non-receceptor 1 (TNK1), mRNA
							VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L
7612	17463	27680	1.51		3.5E-01 Q02294	SWISSPROT	TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
7688			5			NT	X laevis gene for albumin including HP1 enhancer
8116						NT	C.griseus rhodopsin gene for opsin protein
8386					3.5E-01 AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
8386	18263	28514	2.34			NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1

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Table 4
Single Exon Probes Expressed in Heart

					2.62		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1285	11193		4.82	3.3E-01	3.3E-01 BF568880.1	EST HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1588	11492	21352	1.11	3.3E-01	LN 5898529	LN	Mus musculus disintegrin 5 (Dtgn5), mRNA
1704	11605		1.05		3.3E-01 AA332734.1	EST HUMAN	EST36722 Embryo, 8 week I Homo sapiens cDNA 5' end
2355	12235		4.74	3.3E-01	4507834 NT	_ 	Homo sepiens uridine monophosphate synthetase (orotate phosphoribosy) transferase and orotidine-5-decarboxylase) (UMPS) mRNA
2919	12846	22648	2	3.3E-01	3.3E-01 AJ251805.1	LN LN	Bacteriophage phi-YeO3-12 complete genome
2982	12910		1.12	3.3E-01	002743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P36)
3016	12944	22737	1.01	3.3E-01	3.3E-01 AJ007932.2	LN	Streptomyces argillaceus mithramycin biosynthetic genes
3450	13367	23173	1.14	3.3E-01	3.3E-01 AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3738	13650	23433	2.17	3.3E-01	3.3E-01 084645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3884	13795	23582	1.59	3.3E-01	AL161498.2	TN	Arabidopsis thaliana DNA chromosome 4, config fragment No. 10
3920	13829		1.92	3.3E-01	3.3E-01 AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4271	14170		2.74	3.3E-01	3.3E-01 D31662.1	INT	Rattus norvegicus DNA for regucalcin, partial cds
4589	14477		1.48	3.3E-01	3.3E-01 A1539114.1	EST HUMAN	tp78b12.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTICEN PEPTIDE TRANSPORTER 1 (HUMAN);
5263	15185	24960	2.68	3.3E-01	3.3E-01 X89819.1	LN	R.norvegicus mRNA for 3"UTR of ubiquitin-like protein
5263	15185		2.68	3.3E-01	3.3E-01 X89819.1	LN	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5622	15537	25623	2.71	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
5622	15537		2.71	3.3E-01	3.3E-01 BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6117	16011	26148	3.64	3.3E-01	3.3E-01 AI628131.1	EST HUMAN	ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809.3' similar to contains Alu repetitive element contains element L1 repetitive element :
							ty84h01 x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu
6117	16011	26149	3.64		3.3E-01 AI628131.1	EST HUMAN	repetitive element; contains element L1 repetitive element;
6575	16433		1.5		3.3E-01 N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
6981	16858		19.46	3.3E-01	3.3E-01 BF683954.1	EST HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
7477	17337	27542	3.26		3.3E-01 N69866.1	EST_HUMAN	za67h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE.297649 3'
7507	17295		2.81	3.3E-01	3.3E-01 BF376745.1	EST_HUMAN	RC4TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
7739	17589		2.07	3.3E-01	3.3E-01 L41044.1	LN	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
8104	17994		2.71	3.3E-01	3.3E-01 X63953.1	LN	D.mauntiana Adh gene
8104	17994	28243	2.71	3.3E-01	3.3E-01 X63953.1		D.mauritiana Adh gene
8389	18265		1.82		3.3E-01 BF526499.1	EST HUMAN	602070802F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213585 5'
8561	18431	28700	12.76		3.3E-01 BE219351.1	EST_HUMAN	hv51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'

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	Top Hit Descriptor	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)	ob71g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'	Rhizobium leguminosarum sym plasmid pRL5JI nodX gene	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (217)	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds	P.vulgaris arc5-1 gene	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)	S.cerevisiae chromosome II reading frame ORF YBR172c	EST369264 MAGE resequences, MAGD Homo sapiens cDNA	EST369264 MAGE resequences, MAGD Homo sapiens cDNA	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'	Mus musculus Pbx/knotted 1 homeobox (Pknox1), mRNA	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds	Humam h NAT allele 3-2 gene for arytamine N-acetytransferase	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME I PRECURSOR	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5	Mouse renin (Ren-1-d) gene, complete cds	Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds	CM0-HT0569-060300-269-f10 HT0569 Homo sapiens cDNA	Rat ISO-atrial natriuretic factor gene, complete cds	H.sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5
	Top Hit Database Source	SWISSPROT L	EST_HUMAN o	NT						\neg	SWISSPROT 1		EST HUMAN	T HUMAN		T HUMAN		TN	INT	/ IN	Ę	TN	ISSPROT			Ę	EST_HUMAN			EST_HUMAN
Sulp	Top Hit Acession No.		21.1		8319	3.3E-01 AP000002.1	.1		3.2E-01 AF047013.1			1	3.2E-01 AW957194.1	3.2E-01 AW957194.1	3.2E-01 AL111655.1	3.2E-01 BF203817.1	TN 6200177	3.2E-01 AF060568.1	3.2E-01 D10872.1	3.2E-01 AL161546.2	3.2E-01 M18818.1	3.2E-01 AF111167.2		3 2E-01 BF693617.1		3.2E-01 AY008847.1	3.2E-01 BE173964.1	3.2E-01 M60266.1	3.2E-01 X02508.1	3.2E-01 BF311635.1
	Most Similar (Top) Hit BLAST E Value	3.3E-01 P47953	3.3E-01	3.3E-01 X07990.1	3.3E-01	3.3E-01	3.2€-01	3.2E-01	3.2E-01	3.2E-01 Z50202.1	3.2E-01 Q48624	3.2E-01 Z36041.1	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.25-01	3.2E-01	3.2E-01	3.2E-01 Q10268	3.2F-01	3.2E-01	3.2E-01	3.2E-01	3.2€-01	3.2E-01	3.2至-01
	Expression Signal	3.94	4.79	1.88	1.63	6.05	1.98	2.05	18.99	1.04	6.25	1.22	5.5	5.5	1.16	2.89	2.9	1.55	0.96	76.0	1.35	0.87	1.33	5.86	1.18	0.98	282	1.42	13.32	14.29
	ORF SEQ ID NO:	28825		19791	28789				20902	21019	21130	21506	21513	21514	21574	21901		22433			23977	24052	24077			24771			26946	
	Exon SEQ ID NO:	18541	18763	100001	18881	19323	10393	10634	11059	11168	11274	11638	11645	11645	11698	12003	12368	12542	13470	13779	14193	}		14520	15081				16751	
	Probe SEQ ID NO:	8652	8956	8972	9119	9817	449	701	1146	1261	1368	1737	1744	1744	1800	2114	2494	2677	3556	3868	4295	4375	4397	4637	4907	5133	5223	6752	6872	6875

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	Top Hit Descriptor	1:1 . 1. H DMA shemoned 4 confictionant No 70	Arabidopsis thallana Luva cili diriosonire 4, curing magnifer chromosome 1	Deinococcus radiodurans A I security of A.29 of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the 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the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the compa	Human monocyte antigen CD14 (CD14) mRNA, complete cos	Borrelia burgdorferi plasmid cp32-2, erbC and erpD genes, complete dus, and anni gened	Homo sapiens gene for AF-b, complete cds	EST04702 Fetal brain, Stratagene (catt@36206) Homo sapiens CUIVA cione nr DUZZI	Drosophila melanogaster faminin A (Lam-A) mKNA, compiete cus	ELONGATION FACTOR IU (EF-10)	Homo sapiens deoxycylluyare user linese gene, compress our	172/5480F1 NIT WOO 20 HOURS COIN STORE THE COIN WAS A COIN STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE TO STORE 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gene)	nm61h05.s1 NCI_CGAP_Br3 Homo sapiens cUNA cione IMAGE:10/2/01 3	Homo sapiens hepatocyte nuclear Tactor-3 alpha (TINF 3A) gene, exulting	Mus musculus mRNA for polycystin	Homo sapiens filamin 2 (FLNZ) gene, exorts 10 through 22	RC3-HN0001-31030U-011-004 FIN000 I HOURD September CONTROL SEARCH R.	601306121F1 NIH MGC 39 Homo sapiens curva clone IMAGE: 345839 3'	940t01;s1 Soares Intali utali into into saparas constructions and salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari salari	602/124/43F1 NIH MIGC. 30 Hollin Septens Culvin Living Living Living Living Living Living Co. 12010111 Septens Culving Living Living Living Co. 12010111 Septens Culving Living L	602124743F1 NIH MIGC 50 HOMB SEPTEMBER CONTRIBUTION SEPTEMBER 3' similar in ph S55700	gighett.xt nci_cgaP_kids homo sapiens cona divide invaci rocesco 3 similar to gelocol 50. HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);	601883592F1 NIH MGC 57 Homo sapiens cDNA clone IMAGE:4095814 5	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA	Anolis analliure isolate OS NADH dehydrocenase subunit 2 (ND2) gene, complete cds; mitochondrial gene	for mitochondrial product	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds	Homo sapiens membrane-bound aminopeptidase P (ANPEPZ) getre, curiplete cus
	Top Hit Database Source			G EN			H	T HUMAN		ISSPROT	T	EST HUMAN 6	ST_HUMAN 9			EST_HUMAN h	7	LN FN	L HUMAN		TN	Т	EST_HUMAN	$\neg \tau$	\neg	EST. HUMAN	\neg	EST HUMAN	Γ			Ā		LN LN
	Top Hit Acession No.		2	1			Ψ.					3.2E-01 BE385776.1	R18051.1	7661971	TN 17661971		3.1E-01 AB029069.1	3.1E-01 AJ251586.1		1.1			3.1E-01 AW983549.1				3.1E-01 BF696639.1	3 1E.01 A1244001 1	0.4F 04 DE04647.4	0121011		3.1E-01 AF294308.1	3.1E-01 AF304162.1	AF195953.1
-	- Jul Sa	Value	3.2E-01 A	3.2E-01 AE002015.	3.2E-01 M86511.1	3.2E-01 U44914.1	3.2E-01 AB011399	3.2E-01 T06813.1	3.2E-01 L07288.1	3.2E-01 083217	3.2E-01 L39874.1	3.2E-01	3.1E-01		3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01				3.15-01			
	Expression Signal		1.35	1.5	2.19	3	3.25	2.7	3.28	2.97	1.58	1.57	3.73	3.45	3.45	1.01	2.78	1.15	0.99	8.66	45.03	1.94	1.34	2.4	1.87	7.76	7.76	4			1.99	1.63	1.64	2.45
	ORF SEQ ID NO:			27056		27812		28199		 -		24898	79866	22419	22420			23536		25119		25510				27874					28920			
	Exon SEQ ID	 <u>-</u>	16807	16863	17124	17591	17760	17949	19662	-				1				1_	┸	1_		L	L		16900	┖	L	1	┙	\perp	18636	18087	1	1 1
	Probe SEQ ID) 2	6269	6086	7247	7741	7010	8058	9459	6996	9801	9855	9636	2030	2886	2827	3436	3832	5073	5365	5447	5527	5890	6160	7023	7791	7791		7832	8211	8823	07.00	9315	9457

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					Ď		Oligic Even Francis Expressed in Francis
Probe E SEQ ID SE NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
_							Homo sepiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,
9086	19318		3.11	3.1E-01	AF196779.1	NT	complete cds; and L-type calcium channel a>
. 99	12635	19866	1.58		6755083 NT	NT	Mus musculus protein kinase C, epsilon (Pkce), mRNA
254	102201	20037	11.12		3.0E-01 AJ271735.1	TN	Homo sapiens Xq pseudoautosomal region; segment 1/2
1204	11114	20960	1.89		3.0E-01 AW300400.1	EST_HUMAN	xs63f08.x1 NCI_CGAP_Kld11 Homo saplens cDNA clone IMAGE:2774343 3'
1491	11396	21256	6.26		3.0E-01 AJ006755.1	TN	Balaenopfera physalus gene encoding atrial natriuretic peptide
2089	11978	21873	0.86		3.0E-01 AF237778.1	TZ	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
1_	13100		96.0		3.0E-01 AB030481.1	TN	Corynebacterium sp. ALY-1 alyPG gene for polyguluronate lyase, complete cds
3789	13701	23488	1.34		3.0E-01 AW817785.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
4412	14306	24089	1.91		3.0E-01 AJ006755.1	TN	Balaenoptera physalus gene encoding atrial nafriuretic peptide
5283	15205	24981	5.34		1	EST_HUMAN	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5
5379	15298	25147	3.18		_	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5379	15298	25148	3.18		3.0E-01 BE693575.1	EST HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5401	15320	25368	3.51		3.0E-01 U01247.1	NT	Mus muşculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
9809	16031	26171	2.61		3.0E-01 D16313.1	NT NT	Mouse cytokeratin 15 gene, complete cds
6335	16198	26358	2.57		10947007 NT	. LN	Mus musculus midnolin (Midn-pending), mRNA
6429	16290	26451	1.35		3.0E-01 AF071810.1	L	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
6625	16505	26693	1.25		3.0E-01 AE001755.1	Z	Thermotoga maritima section 67 of 136 of the complete genome
6877	16756		4.67	3.0E-01	TN 1910166	Þ	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Cleost9), mRNA
L	16815	27007	1.27	<u> </u>	BE56608	EST HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5
7944	17794	28034	1.89	3.0E-01	AB030231.1	F	Aspergillus oryzae bipA gene for ER chaperone BiP, complete cds
<u>L</u>	18785	29074	2.89		3.0E-01 H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
L	18785	29075	2.89		3.0E-01 H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
9564	19647		1.43		3.0E-01 AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
9836	19690		2.76		6677766 NT	TN	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1978	11871	21762	1.6		2.9E-01 AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2201	12088	21989	0.99		2.9E-01 AF222718.1	TN	Chrysodidymus synuroideus mitochondrion, complete genome
	13072	22873	1.03		2.9E-01 AF078111.1	ĻN	Xenopus laevis transcription factor E2F mRNA, complete cds
	13137	22939			2.9E-01 AW 754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3213	13137	22940	2.29		2.9E-01 AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA

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9514 19127 25260 1.53 2.9E-01 AW005671.1 EST HUMAN MER29 repetitive element; MER29 repetitive element; 9602 19184 25248 2.74 2.9E-01 AF092453.1 NT Homo sapiens TNF-a-inducible RNA binding protein (TIRP) gene, complete cds 9644 19212 1.33 2.9E-01 BE788199.1 EST HUMAN 601482059F1 NIH MGC_68 Homo sapiens cDNA clone IMAGE:3884559 5' 9883 19367 25188 4.86 2.9E-01 Y08937.1 NT Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
19212 1.33 2.9E-01 M E78199.1 EST HUMAN 19357 25188 4.86 2.9E-01 (Y08937.1 NT 19347 7.5180 4.86 2.0E-01 (Y08937 7.5180 4.86 2.
1.10837 1.10837 4.00 4.00 4.00 1.10833/ 1

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Single Exoll Flobes Expressed in liean.	Top Hit Descriptor	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds	Guira guira cocyte maturation factor Mos (c-mos) gene, partial cds			Human mRNA for serine/threonine protein kinase, complete cds				Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65	Arabidopsis thaliana mRNA for lipoytransferase, complete cds	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds	B.taurus microsatellite (ETH121)	B.taurus microsatellite (ETH121)	Pyrococcus horikoshii ÖT3 genomic DNA, 777001-994000 nt. position (417)	Borrelia burgdorferi (section 66 of 70) of the complete genome	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element, contains element MER22 repetitive element;	Г	and Zinc finger protein 185	Г	Human mRNA for transcription factor AREB6, complete cds	Human mRNA for transcription factor AREB6, complete cds	Bovine adenovirus 3 complete genome	602042601F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180129 5'				Homo sapiens OCTN2 gene, complete cds	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds		V UI-H-BI4-aci-f-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182.3'
gie Exoli Fit	Top Hit Database Source	NT	NT	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN		EST_HUMAN	LN	TN	TN	IN	Z L	TN	LZ	NT	NT	EST HUMAN		Z Z	SWISSPROT	NT	NT	NT	EST_HUMAN		- 11	EST_HUMAN	NT	L	N N	EST_HUMAN
0.00	Top Hit Acession No.	U67136.1	2.8E-01 AF168050.1	2.8E-01 BE313442.1	2.8E-01 BE313442.1	2.8E-01 D86550.1	2.8E-01 AW860020.1	2.8E-01 AL047620.1	2.8E-01 AW511195.1	2.8E-01 AE000494.1	2.8E-01 AE000494.1	2.8E-01 AL161565.2	2.8E-01 AB020975.1	2.8E-01 AF179480.1	2.8E-01 Z14037.1	2.8E-01 Z14037.1	2.8E-01 AP000004.1	2.8E-01 AE001180.1	2.8E-01 Al090868.1		AL021127.2	2.8E-01 P13615	2.8E-01 D15050.1	2.8E-01 D15050.1	2.8E-01 AF030154.1	2.8E-01 BF528188.1		2.8E-01 AI272669.1	2.8E-01 AA349997.1	2.8E-01 AB016625.1	2.8E-01 AF003124.1	2.8E-01 AF003124.1	2.8E-01 BF511215.1
	Most Similar (Top) Hit BLAST E Value	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01		2.8E-01	2.8⊑-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01		2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01
	Expression Signal	1.84	2.47	1.1	1.1	1.01	1.55	1.77	1.47	2.94	2.94	2.47	1.37	1.49	2.48	2.48	1.1	1.75	2.24		0.98	2.2	1.03	1.03	2.8	1.54		1.7	21.36	2.33	1.44	1.44	7.67
	ORF SEQ ID NO:		20828	21013	21014	21025	21470	21750	21869	22197	22198		22388		22667	22668	23057	23604			24034	24038	24352	24353	24394	24427		24459	24948	25419	25784	25785	26073
	Exon SEQ ID NO:	10497	10983	11163	11163	11176	11598	11860	11974	12300	12300	12375	12498	12867	12868	12868	13252	13824	14003		14248	14253	14559	14559	14608	14640	Ŀ	14672	19440	15363	15677	Ì	15941
	Probe SEQ ID NO:	556	1067	1256	1256	1269	1696	1966	2084	2423	2423	2500	2630	2940	2941	2941	3332	3915	4103		4352	4357	4673	4673	4722	4755		4787	5252	5443	5770	5770	6038

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Top Hit Descriptor	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3* similar to gb:XUb52x3_cds* and toCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN).	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5	602022987F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4136323 3	Mus musculus centrin (Ceth2) gene, complete cas	Lycopersicon esculentum peroxidase (TPX1) mrtNA, complete cus	Homo sapiens hypothetical protein (LOC) 13 19), ilinkiva	601880/94F1 NIH MGC 33 Hamo sapiens CDIVA cione invitable. 4 103000 3	601880794F1 NIH MGC 55 Homo sapiens culvA cione liviAcE:4109300 3	601852148F1 NIH, MGC, 56 Homo sapiens cUNA done liviace: 4070020	Drosophila heteroneura fruitless (fru) gene, alternative splice products, 5 Ilanking region, exons 1 through 7 and complete cds	602137418F1 NIH MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5	Mus musculus DNA for prostaglandin D2 synthase, complete cds	PM4-HT0606-030400-001-807 HT0606 Homo sapiens cDNA	11.	Homo saprens objects with the sacrotter (City) of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t	Kattus norvegicus CUK 104 mikryk	zx39b10.s1 Soares_total_fetus_Nb2Hr8_9w Homo sapiens cLNA clone invAtsE:788827 3 Similar to contains Alu repetitive element;	pomoea purpurea transposable element Tip100 gene for transposase, complete cds	G.lamblia SR2 gene	zd22h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1	Feline immunodeficiency virus env gene, isolate ITTO088PIU (M88), partial	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1	repetitive element;	CM1-H10875-060900-385-e05 H10875 Homo sapens culvA	wo92e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA cione IMAGE. 2492929 3	Homo sapiens DiGeorge syndrome critical region, telomeric end	Triticum aestivum (Wcs66) gene, complete cds
Top Hit Database Source	EST_HUMAN N	EST_HUMAN N	NT TN	T_HUMAN	NT			HUMAN		EST_HUMAN		T HUMAN		HIMAN	NICIAID.		LN	EST HUMAN	NT	NT	EST_HUMAN	SWISSPROT	NT	LN		EST_HUMAN	EST_HUMAN	EST_HUMAN	LN L	LZ
Top Hit Acession No.		_		-	2.8E-01 AF080592.1		7706163 NT	-	2.8E-01 BF241062.1	3F695970.1	2 BE 04 AE051662 1	2.8E-01 AI 031002.1			ZE1/8089.1	11433629 N I	Y17324.1	2.7E-01 AA450061.1	2.7E-01 AB004906.1	2.7E-01 X79815.1	2.7E-01 W 58067.1	P03341	AF047575.1	2.7E-01 Y13868.1		2.7E-01 AI310858.1	2.7E-01 BF088284.1	2.7E-01 Al928015.1	2.7E-01 L77569.1	2.7E-01 L27516.1
Most Similar (Top) Hit BLAST E Value	2.8E-01 Al346126.1	2.8E-01 Al346126.	2.8E-01 U51688.1	2.8E-01	2.8E-01	2.8E-01 L13654.1	2.8E-01	2.8É-01	2.8E-01	2.8E-01	2 BE 04	2 RE-01	10.0	2.8E-01 D83329.1	Z.8E-01	2.8E-01	2.7E-01 Y17324.1	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01 P03341				2.7E-01	2.7E-01	2.7E-01		
Expression Signal	1.24	1.24	2.39	7.25	1.35	1.15	2.79	2.27	2.27	3.01	6	2.02	000	6.37	3.11	1.69	2.33	3.14	1.49	1.73	2.96	1.25	2.38	8.78		3.51	1.25	1.88		0.89
ORF SEQ ID NO:	26781				27388		27872	28261	28262		_	78387			25236		20230		20996	\perp	21471			22094		3 22180	3	8 23618		
Exon SEQ ID NO:	16593	16593	16657	16871	17187	17451	17639	1	18014				\perp		19219	19651	10411	<u> </u>		⅃	1_	1		\perp	1.	12283	12883		13851	14681
Probe SEQ ID NO:	6713	6713	6778	6994	7311	7600	6877	8126	8126	8153		8254	8868	9552	9657	9828	468	597	1240	1604	1698	1738	2000	22.18	72 15	2406	2956	3929	3943	4796

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Table 4
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Sligle Lyon Flores Lypressed In Team	Hit Descriptor Top Hit Descriptor	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5	Rattus norvegicus mRNA for organic anion transporter 3, complete cds			Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds, and tunknown gene	Gallus gallus mRNA for skelctal myosin heavy chain, complete cds	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds	1	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*1) mRNA, complete cds	Ophrestia radicosa maturase-like protein (matk) gene, complete cds; chloroplast gene for chloroplast product		,	Thermotoga maritima section 123 of 136 of the complete genome	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA ckine IMAGE:2227438 3' similar to SW.NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1, contains element LTR1 repetitive element;	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW.:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;	yf37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1290043' similar to qb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);		Г					Human lambda-immunoglobulin constant region complex (germline)	Mus musculus jerky (Jrk), mRNA		Homo sapiens Na/K-ATPase gamma subunit (FXYD2) gene, complete cds, alternatively spliced
JIE LAUII F	Top Hit Database Source	ΤΝ	۲	EST_HUMAN	EST_HUMAN	LN	E	FN	EST_HUMAN	TN	Ę	EST_HUMAN	SWISSPROT	NT	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST HUMAN	EST_HUMAN	SWISSPROT	NT	NT	EST_HUMAN	NT
) IIO	Top Hit Acession No.	2.6E-01 AF229118.1	2.6E-01 AB017446.1	2.6E-01 AW959510.1	2.6E-01 BE080598.1	2 6E_04 AE475903 4	2.6E-01 AB021180.1	2.6E-01 AB021180.1	2.6E-01 AA457617.1	2.6E-01 U01103.1	2.6E-01 AF142703.1	2.6E-01 H04858.1	P08503	2.6E-01 AE001811.1	2.6E-01 AI582557.1	2.6E-01 AI582557.1	2.6E-01 R10365.1	2.6E-01 R02411.1	2.6E-01 BF343588.1	Q10199	2.6E-01 BE830339.1	2.6E-01 BE830339.1	Q28295	2.6E-01 X51755.1	10190655 NT	2.6E-01 BE883491.1	2.6E-01 AF316896.1
	Most Similar (Top) Hit BLAST E Value	2.6E-01	2.6E-01	2.6E-01	2.6E-01	10 HB 0	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01 P08503	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01	2.6E-01 Q10199	2.6E-01	2.6E-01	2.6E-01 Q28295	2.6E-01	2.6E-01	2.6E-01	2.6E-01
	Expression Signal	1.7	0.9	1	13.13	20.07	48.0	0.84	1.17	1.63	1.28	3.56	0.86	2.03	1.93	1.93	1.52	1.27	3.01	2.04	4.34	4.34	1.16	93.65	1.98	1.92	2.6
	ORF SEQ ID NO:	23295	23351	23691	23742	22035	24072	24073	24134	24224	24292	24554	24696		25777	25778	26588		26925		_	27113					25309
	Exon SEQ ID NO:	13505	13565	13916	13964	14150	14289	14289	14342	14441	14504	14776	14923	19764	15670	15670	16410		16731	16779	16923	16923	17704	18625	18892	19655	19053
	Probe SEQ ID NO:	3591	3651	4010	4062	4250	4393	4393	4448	4548	4616	4896	5051	5700	5763	5763	6552	6585	6852	0069	7046	7046	7854	8812	9136	9328	9395

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	Top Hit Descriptor	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds	ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear nemodina mitochondrial protein. mRNA	in commission of the commentation of the comme	Homo sapiens ATP synthase, H+ transporting, mitocholdinal FT complex, della subunit (ATF3D), indiceal gene encoding mitochondrial protein, mRNA	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds	Ureaplasma urealyticum section 57 of 59 of the complete genome	ye11g07.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE: 117468 5	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA	Aquifex aeolicus section 7 of 109 of the complete genome	zs11a12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE.684862 5'	B.taurus mRNA for D-aspartale oxidase	EST385464 MAGE resequences, MAGM Homo sapiens cDNA	Danio rerto peptide YY precursor gene, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR	RHIB PROTEIN	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9	and 11-16	MOLT-INHIBITING HORMONE PRECURSOR (MIH)	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'
	Top Hit Database Source	TN T	SWISSPROT /				TN S	TN	NT	EST_HUMAN			EST HUMAN	EST_HUMAN	/ INT	T_HUMAN	IN	EST_HUMAN	INT	/	EST_HUMAN		SWISSPROT	SWISSPROT		NT	SWISSPROT	LN	NT	TN.	T_HUMAN
Ē	Top Hit Acession No.	2.6E-01 AF141325.2		TIM SOCCOSE	437700	4502296 NT	2.5E-01 M26501.1	2.5E-01 U09964.1	2.5E-01 AE002156.1		2.5E-01 AL115624.1	4885406 NT	2.5E-01 BE696604.1	2.5E-01 BE696604.1	2.5E-01 AE000675.1	2.5E-01 AA251987.1	2.5E-01 X95310.1	2.5E-01 AW973471.1	2.5E-01 AF233875.1	2.5E-01 AL161517.2	2.5E-01 AI741483.1	_		Q03314		2.5E-01 AF242431.1	Q27225	AF007768.1	2.5E-01 AE004416.1	2.5E-01 AJ230113.1	2.5E-01 BE896785.1
	Most Similar (Top) Hit BLAST E Value	2.6E-01	2.6E-01 Q01631	c II	7.3E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01						2.5E-01 Q03314			2.5E-01 Q27225				
	Expression Signal	6.03	1.5	C	71.7	1,86	3.24	1.32	1.86	9.5	0.85	5.43	0.88	0.88	8.29	1.35	26.0	2.87	0.86	7.93	1.15	1.15	0.83	1.2		0.98	1.14	3.78	2.19	3.16	0.79
	ORF SEQ ID NO:				cz00Z	20025		20589		20864	21266			21613			22359	L	23211				L			24193		24324	24351		24398
	Exon SEQ ID NO:	19333	19376		10209	10209			L	11021	11407	11599	12706	L	1_	_	L.,	<u>l</u>	<u></u>		13686		L	\perp	1_	14407	14531	14535	14558	l _	
	Probe SEQ ID NO:	9833	6686		241	242	255	815	1044	1105	1503	1697	1840	1840	2357	2446	2597	3366	3490	3502	3774	3774	3977	4222		4514	4643	4649	4672	4698	4726

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Single Exull Flobes Expressed III near	Top Hit Database Source	Mus musculus gene for uncoupling protein 3, 5'-flanking region and partial 5'U'R	hh75f09,y NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968649 5' similar to contains TAR1.t2 EST_HUMAN TAR1 repetitive element;	hh75f09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968649 5' similar to contains TAR1.t2 EST HUMAN TAR1 repetitive element;		Mus musculus SKD1 (Skd1) gene, complete cds	Homo sapiens chromosome 21 segment HS210082	HUMAN 7157a03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3	HUMAN 601459238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5	HUMAN yq84f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5'	Hαπο sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds	EST_HUMAN RC3-ST0186-130100-015-a07 ST0186 Homo saplens cDNA	xg40c10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive HUMAN element; contains element MSR1 repetitive element;	Mouse L1Md LINE DNA	Human mRNA for KIAA0124 gene, partial cds	Zea mays cellulose synthase-4 (CesA-4) mRNA, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41			EST_HUMAN 602132442F1 NIH_MGC_81 Hono sapiens cDNA clone IMAGE:4271578 5'	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	Homo sapiens FLI-1 gene, partial	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds		SWISSPROT IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)	Aquifex aeolicus section 12 of 109 of the complete genome
Single E.	Top Hit Acession De No. S	70.1 NT				19.1 NT	:82.2 NT	1 EST	S.1 EST	EST	Z.	NT NT	64.1 NT	64.1 NT	1.	.1 EST		F.1	528.1 NT	141.2 NT	1	.1	.1	.1	MD.1	1.1	753.1 NT	708.1 NT	68.2		380.1 NT
	Top Hit	2.5E-01 AB011070.	2.5E-01 AW663183.1	2.5E-01 AW663183.1	2.5E-01 S83390.1	2.5E-01 AF134119	2.5E-01 AL163282	2.5E-01 BF109040	2.5E-01 BF038595.	2.5E-01 H53236.1	U89651.2	2.5E-01 U89651.2	2.5E-01 AF085164.	2.5E-01 AF085164	2.5E-01 AW581997	2.5E-01 AW152246	2.5E-01 X58491.1	2.5E-01 D50914.1	2.5E-01 AF200528	2.5E-01 AL161541	2.5E-01 AF170072	2.4E-01 AA936316.	2.4E-01 BF576124	2.4E-01 AJ289880	2.4E-01 AJ289880	2.4E-01 Y17293.1	2.4E-01 AF267753	2.4E-01 AF251708.	2.4E-01 AF111168	2.4E-01 P45384	2.4E-01 AE000680
	Most Similar (Top) Hit BLAST E Value	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01		2.5E-01	2.5E-01	2,4E-01		2.4E-01	2.4E-01	2.4E-01					
	Expression Signal	0.89	0.86	0.86	11.62	1.32	3.73	2.99	2.25	3.95	16.11	16.11	2.04	2.04	1.5	1.62	1.68	2.32	2.45	4.2	1.28	1.53	2.38	17.41	17.41	1.04	24.08	1.41	0.88	1.16	2.01
	ORF SEQ ID NO:	24421	24802	24803	24962		26532	26655	26858	27087	27554	27555	27547	27548	27904	28105	28106	28556	29117		25072	20292	20608	21041	21042			21629			22005
	Exon SEQ ID NO:	14635	15035	15035	15186	16229	16359	16463	16667	16897	17351	17351	17341	17341	17664	17860	17861	18300	18851	19729	19581	10482	10757	11190	11190	11268	11705	11754	11980	12010	12101
	Probe SEQ ID (NO:	4750	5169	5169	5264	9989	6500	6583	6788	7020	7481	7481	7522	7522	7814	8010	8011	8426	9074	9100	9559	541	830	1282	1282	1362	1808	1858	2091	2122	2215

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Portion Carlo Ca								
12213 22111 0.85 2.4E-01 BF002171.1 EST HUMAN 12366 22290 1.63 2.4E-01 Z36534.1 NT 12596 222491 2.14 2.4E-01 Z36534.1 NT 13020 2281 2.14 2.4E-01 Z71783.1 NT 13035 22831 1.85 2.4E-01 Z74209.1 NT 14700 24486 0.88 2.4E-01 Z74209.1 NT 14700 24486 0.88 2.4E-01 D00944.1 NT 14700 24486 0.88 2.4E-01 D00944.1 NT 15389 25451 7.53 2.4E-01 AF091216.1 NT 15508 25583 2.15 2.4E-01 AF091216.1 NT 15518 25584 2.56 2.4E-01 AF091216.1 NT 15519 2.56 2.4E-01 AF091216.1 NT 15510 2.56 2.4E-01 AF091216.1 NT	Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12366 22260 1.63 24E-01 Z3534.1 NT 12566 22491 2.14 2.4E-01 X71783.1 NT 13020 22510 6.68 2.4E-01 AF030154.1 NT 13025 22831 1.85 2.4E-01 AF030154.1 NT 13025 22831 1.85 2.4E-01 AF0301.1 NT 14700 24486 0.88 2.4E-01 BF03021.1 NT 15389 25451 7.53 2.4E-01 AF091216.1 NT 15589 25452 50.15 2.4E-01 AF091216.1 NT 15589 25451 7.53 2.4E-01 AF091216.1 NT 15589 25452 7.53 2.4E-01 AF091216.1 NT 15589 25451 2.5 2.4E-01 AF091216.1 NT 15613 25714 2.16 2.4E-01 AF091216.1 NT 16208 2.568 1.79 2.4E-01 AF091216.1	2332	12213		0.85		BF002171.1	EST_HUMAN	7h23d04.X1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA 042586 26S PROTEASE REGULATORY SUBUNIT 6A;
12696 22491 2.14 2.4E-01 X71783.1 NT 12618 22510 6.68 2.4E-01 AF030154.1 NT 13020 22510 6.68 2.4E-01 AF030154.1 NT 13035 22831 1.86 2.4E-01 BE160080.1 EST HUMAN 14700 24836 0.88 2.4E-01 BE160080.1 EST HUMAN 15389 25452 7.53 2.4E-01 AF091216.1 NT 15389 25452 7.53 2.4E-01 AF091216.1 NT 15389 25452 7.53 2.4E-01 AF091216.1 NT 15389 25454 7.53 2.4E-01 AF091216.1 NT 15589 25568 2.53 2.4E-01 AF091216.1 NT 15589 25568 2.53 2.4E-01 AF091216.1 NT 15610 2.5538 2.4E-01 AF093238.1 NT 16208 2.4E-01 AF093538.1 NT <	2491	12366		1.63	2.4E-01		NT	D.discoideum (Ax3-K) ponA gene
12618 22510 6.68 2.4E-01 AF030154.1 NT 13020 282 2.4E-01 L72726.1 NT 13035 22831 1.86 2.4E-01 L72726.1 NT 14700 24486 0.88 2.4E-01 BE160080.1 EST_HUMAN 15389 25452 7.53 2.4E-01 AF091216.1 NT 15389 25452 7.53 2.4E-01 AF091216.1 NT 15389 25452 7.53 2.4E-01 AF091216.1 NT 15565 25648 2.66 2.4E-01 AF091216.1 NT 15565 25648 2.66 2.4E-01 AF091216.1 NT 15613 25714 2.16-01 AF091216.1 NT 16208 2568 1.79 2.4E-01 AF098089.1 RST_HUMAN 16208 2568 1.79 2.4E-01 AF088089.1 NT 16309 25751 2.4E-01 AF089089.1 NT 163	2734			2.14	2.4E-01		NT	S.pombe swi6 gene
13020 2.82 2.4E-01 U72726.1 NT 13035 22831 1.85 2.4E-01 X74209.1 NT 14700 24486 0.88 2.4E-01 D00944.1 NT 14856 24622 50.15 2.4E-01 AF091216.1 NT 15389 25451 7.53 2.4E-01 AF091216.1 NT 15508 25583 2.13 2.4E-01 AF091216.1 NT 15516 255648 2.66 2.4E-01 AF091216.1 NT 15613 25714 2.16 2.4E-01 AF091216.1 NT 15614 25714 2.16 2.4E-01 AF035546.1 NT 16208 2566 1.79 2.4E-01 AF03698.9 RT HUMAN 16208 26371 8.87 2.4E-01 AF03698.1 NT NT 16739 2751 2.4E-01 AF03698.1 NT NT 16739 28285 3.63 2.4E-01 A	2756			6.68		1	NT	Bovine adenovirus 3 complete genome
13036 22831 1.85 2.4E-01 X74209.1 INT 14700 24486 0.88 2.4E-01 BE160080.1 EST HUMAN 15389 25451 7.53 2.4E-01 AF091216.1 NT 15389 25452 50.15 2.4E-01 AF091216.1 NT 15589 25451 7.53 2.4E-01 AF091216.1 NT 15589 25583 2.13 2.4E-01 AF091216.1 NT 15565 25648 2.66 2.4E-01 AF091216.1 NT 15574 2.15 2.4E-01 AF091216.1 NT 15608 2.566 2.4E-01 AF091216.1 NT 16509 2.566 2.4E-01 AF092336.1 ST HUMAN 16730 2.651 2.4E-01 AF036989.1 NT 16730 2.651 2.4E-01 AF036989.1 NT 16730 2.65371 2.4E-01 AF036989.1 NT 17805 2.7E-01 AF036989.1 <td>3093</td> <td>13020</td> <td></td> <td>2.82</td> <td></td> <td>U72726.1</td> <td>Ę</td> <td>Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds</td>	3093	13020		2.82		U72726.1	Ę	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
14700 24486 0.88 2.4E-01 BE160080.1 EST HUMAN 14856 24622 50.15 2.4E-01 D00944.1 NT 15389 25451 7.53 2.4E-01 AF091216.1 NT 15389 25452 7.53 2.4E-01 AF091216.1 NT 15508 25583 2.13 2.4E-01 AF091216.1 NT 1551 25648 2.66 2.4E-01 AF091216.1 NT 15613 25714 2.16 2.4E-01 AF091216.1 NT 15613 25714 2.16 2.4E-01 AF091216.1 NT 16739 2566 2.4E-01 AF091216.1 NT NT 16739 26931 1.62 2.4E-01 AF091216.1 NT 16739 26951 1.62 2.4E-01 AF09898.1 NT 16739 2751 2.4E-01 AF09998.1 NT 18037 28285 3.63 2.4E-01 AF09999.1 NT <td>3109</td> <td>L</td> <td></td> <td>1.85</td> <td></td> <td>X74209.1</td> <td>N</td> <td>H.sapiens AGT gene, Pstl fragment of intron 4</td>	3109	L		1.85		X74209.1	N	H.sapiens AGT gene, Pstl fragment of intron 4
14856 24622 50.15 2.4E-01 D00944.1 NT 15389 25451 7.53 2.4E-01 AF091216.1 NT 15589 25452 7.53 2.4E-01 AF091216.1 NT 15508 25563 2.13 2.4E-01 AF09536.1 EST_HUMAN 15518 25648 2.66 2.4E-01 AF09546.1 NT 15519 25648 2.66 2.4E-01 AF095546.1 NT 15613 25714 2.16 2.4E-01 AF095546.1 NT 16208 2.5714 2.16 2.4E-01 AF095546.1 NT 16208 2.5714 2.16 2.4E-01 AF095546.1 NT 16208 2.5714 2.16 2.4E-01 AF09889.1 EST_HUMAN 16739 2.6931 1.62 2.4E-01 AJ012586.1 NT 17306 2.7511 5.72 2.4E-01 AJ03692.1 NT 18037 2.8285 3.63 2.4E-01	4817	14700				1	EST_HUMAN	QV1-HT0412-020400-136-b10 HT0412 Homo sapiens cDNA
15389 25451 7.53 2.4E-01 AF091216.1 NT 15389 25452 7.53 2.4E-01 AF091216.1 NT 15508 25583 2.13 2.4E-01 AF091216.1 NT 15515 25648 2.66 2.4E-01 AF035546.1 NT 15613 25714 2.16 2.4E-01 AF035546.1 NT 16208 2566 1.79 2.4E-01 AF035546.1 NT 16739 26931 1.62 2.4E-01 AF035546.1 NT 16739 26931 1.62 2.4E-01 AF03554.1 NT 17305 27511 2.4E-01 AF0361.1 NT 17306 2751 2.4E-01 AF036351.1 NT 18037 28285 3.63 2.4E-01 AL161494.2 NT 18037 28285 3.63 2.4E-01 AL161494.2 NT 18037 28285 3.63 2.4E-01 AL161494.2 NT 18046 2.36 2.4E-01 AL161494.2 NT 18821 29109 1.55 2.4E-01 AL161494.2	4981	14856		50.15		D00944.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
15508 25452 7.53 2.4E-01 AF091216.1 NT 15508 25583 2.13 2.4E-01 BF592336.1 EST HUMAN 15613 25714 2.16 2.4E-01 AF035546.1 NT 15613 25714 2.16 2.4E-01 AF035546.1 NT 16208 2.66 2.4E-01 AF035546.1 NT 16739 2.6937 8.87 2.4E-01 AF03001.1 NT 16739 2.6931 1.62 2.4E-01 AJ012586.1 NT 17305 2.7511 5.72 2.4E-01 AJ012586.1 NT 18037 2.8285 3.63 2.4E-01 AL012586.1 NT 18040 2.2885 3.63 2.4E-01 AL012586.1 NT 18053 2.8285 3.63 2.4E-01 AL01268.2 NT 18040 2.24E-01 AL012049.2 NT NT 18051 2.36 2.4E-01 AL012041.1 NT 19	5469	15389		7.53		-	NT	Mus musculus Wrn protein (Wrn) gene, complete cds
15508 25583 2.13 2.4E-01 BF592336.1 EST_HUMAN 15556 25648 2.66 2.4E-01 AF035546.1 NT 15613 25714 2.16 2.4E-01 AF035546.1 NT 15842 25966 1.79 2.4E-01 Af698989.1 EST_HUMAN 16739 26931 1.62 2.4E-01 AJ012586.1 NT 17305 27511 5.72 2.4E-01 AJ012586.1 NT 17305 27511 5.72 2.4E-01 AJ012586.1 NT 18037 28285 3.63 2.4E-01 AL012586.1 NT 18037 28285 3.63 2.4E-01 AL03699.1 NT 180406 2.36 2.4E-01 AL03699.1 NT 18821 29109 1.55 2.4E-01 AF004213.1 NT 19509 1.55 2.4E-01 AF004213.1 NT 19509 1.56 2.4E-01 AF004213.1 NT <td< td=""><td>5469</td><td>15389</td><td></td><td>7.53</td><td></td><td>1</td><td>TN</td><td>Mus musculus Wnn protein (Wrn) gene, complete cds</td></td<>	5469	15389		7.53		1	TN	Mus musculus Wnn protein (Wrn) gene, complete cds
15508 25583 2.13 2.4E-01 BF592336.1 EST HUMAN 15613 25714 2.16 2.4E-01 AF035546.1 NT 15613 25714 2.16 2.4E-01 AF035546.1 NT 15614 2.566 1.79 2.4E-01 AF035546.1 NT 16208 2.6371 8.87 2.4E-01 A3001.1 NT 16739 2.6931 1.62 2.4E-01 A3012565.1 NT 17305 2.7511 6.72 2.4E-01 A16935615.1 EST_HUMAN 17306 2.7511 6.72 2.4E-01 A16935615.1 EST_HUMAN 17305 2.7611 6.72 2.4E-01 A16935615.1 EST_HUMAN 18037 2.8285 3.63 2.4E-01 A16935615.1 NT 18046 2.24E-01 A16935615.1 NT NT 1805 2.39 2.4E-01 A1693561.1 NT 1956 2.36 2.4E-01 A1693561.1 NT								7154d04.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503.3' similar to SW. SFR4_HUMAN Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 :contains element TAR1 TAR1 repetitive element
15555 25648 2.66 2.4E-01 AF035546.1 NT 15613 25714 2.16 2.4E-01 A698989.1 EST HUMAN 16208 26371 8.87 2.4E-01 L43001.1 NT 16739 26931 1.62 2.4E-01 L43001.1 NT 17305 27511 2.4E-01 AJ012586.1 NT 17305 27511 5.72 2.4E-01 AJ012586.1 NT 18037 28285 3.63 2.4E-01 AL161494.2 NT 18037 28285 3.63 2.4E-01 AL161494.2 NT 180406 2.36 2.4E-01 AL630199.1 NT 18821 29109 1.55 2.4E-01 AF030199.1 NT 1950 2.39 2.4E-01 AL731491.1 NT 1950 2.54 2.4E-01 AL701491.1 NT 1950 2.39 2.4E-01 AL701491.1 NT 1950 2.54E-01 AL701491.	5593	15508				BF592336.1	EST_HUMAN	
15842 25966 1.79 2.4E-01 Al698989.1 EST_HUMAN 16208 25371 8.87 2.4E-01 L43001.1 NT 16739 26931 1.62 2.4E-01 L43001.1 NT 17305 27511 5.72 2.4E-01 AJ012585.1 NT 17815 28056 1.93 2.4E-01 AJ03692 SWISSPROT 18037 28285 3.63 2.4E-01 AL161494.2 NT 18066 2.24E-01 AL161494.2 NT NT 18070 2.8285 3.63 2.4E-01 AL161494.2 NT 18071 2.4E-01 AL161494.2 NT NT 18821 29109 1.59 2.4E-01 AL6030199.1 NT 18821 29109 1.55 2.4E-01 AL7617491.1 NT 19509 1.56 2.4E-01 AL7617491.1 NT 19509 1.56 2.4E-01 AL7604213.1 NT 19509 1.5	5642	15555					NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
15842 25966 1 79 2.4E-01 Al698989.1 EST_HUMAN 16208 26371 8.87 2.4E-01 L43001.1 NT 16739 26931 1.62 2.4E-01 AJ012585.1 NT 17305 27511 5.72 2.4E-01 AJ012585.1 EST_HUMAN 17815 28056 1.93 2.4E-01 AJ03692 SWISSPROT 18037 28285 3.63 2.4E-01 AL161494.2 NT 18038 28347 1.99 2.4E-01 AL161494.2 NT 18821 29109 1.56 2.4E-01 AL6030199.1 NT 18821 29109 1.55 2.4E-01 AL7630199.1 NT 19509 2.54 2.4E-01 AL76311.1 NT 19509 1.55 2.4E-01 AL76319.1 NT 19509 1.56 2.4E-01 AL76319.1 NT 19509 1.56 2.4E-01 AL76013.1 NT 19509 <t< td=""><td>5705</td><td>15613</td><td></td><td></td><td></td><td></td><td>N</td><td>Homo sapiens HSPC142 protein (HSPC142), mRNA</td></t<>	5705	15613					N	Homo sapiens HSPC142 protein (HSPC142), mRNA
16208 26371 8.87 2.4E-01 L43001.1 NT 17305 27511 5.72 2.4E-01 AJ012585.1 NT 17305 27511 5.72 2.4E-01 AI693515.1 EST HUMAN 17815 28056 1.93 2.4E-01 Q03692 SWISSPROT 18037 28285 3.63 2.4E-01 AL161494.2 NT 18053 28347 1.99 2.4E-01 AL603199.1 NT 18050 28347 1.99 2.4E-01 AF030199.1 NT 18821 29109 1.55 2.4E-01 AF030199.1 NT 19526 2.39 2.4E-01 AF04213.1 NT 1956 2.4E-01 AF04213.1 NT 1950 2.54 2.4E-01 AV01507.1 NT 1950 2.4E-01 AV01507.1 NT 1950 2.4E-01 AV01607.1 NT 1935 2.4E-01 AL63289.2 NT 1935	5937	15842				A1698989.1	EST HUMAN	wc62c11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464 PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN):
17305 27511 5.72 2.4E-01 AJ012585.1 NT 17815 28056 1.93 2.4E-01 Q03692 SWISSPROT 18037 28285 3.63 2.4E-01 AL161494.2 NT 18063 28347 1.99 2.4E-01 AL161494.2 NT 18070 2.82 2.4E-01 AL161494.2 NT 18071 2.4E-01 AL6030199.1 NT 18821 29109 1.55 2.4E-01 AE030199.1 NT 19526 2.39 2.4E-01 AE04213.1 NT 19545 2.4E-01 AE04213.1 NT 19509 1.59 2.4E-01 AU278191.1 NT 19509 1.59 2.4E-01 AU5011.1 NT 19509 1.59 2.4E-01 AU5011.1 NT 19509 1.26 2.4E-01 AU5051.1 NT 19509 2.05 2.4E-01 AU5051.1 NT	6345	16208				L43001.1	NT	Bos taurus guanyly cyclase-activating protein 2 (guca2) mRNA, complete cds
17306 27511 5.72 2.4E-01 Al693515.1 EST HUMAN 17815 228056 1.93 2.4E-01 Q03692 SWISSPROT 18037 28285 3.63 2.4E-01 AL161494.2 NT 18093 28347 1.99 2.4E-01 AL161494.2 NT 18406 2.42 2.4E-01 AL60199.1 NT 19526 2.4E-01 AZ17491.1 NT 19526 2.39 2.4E-01 AZ17491.1 NT 19545 2.4E-01 AZ17491.1 NT 19509 1.55 2.4E-01 AZ17491.1 NT 19509 1.59 2.4E-01 AZ17491.1 NT 19509 1.56 2.4E-01 AZ17491.1 NT 19509 1.26 2.4E-01 <td>0989</td> <td>16739</td> <td></td> <td>1.62</td> <td></td> <td>AJ012585.1</td> <td>L</td> <td>Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2</td>	0989	16739		1.62		AJ012585.1	L	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
17805 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 2781 <t< td=""><td>7647</td><td>1720E</td><td></td><td>C 70</td><td></td><td>A1602645 4</td><td>FOR LANGE</td><td>wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains MER22 h1 TAR1 renetiting element :</td></t<>	7647	1720E		C 70		A1602645 4	FOR LANGE	wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains MER22 h1 TAR1 renetiting element :
18037 28285 3.63 2.4E-01 AL161494.2 NT 18093 28347 1.99 2.4E-01 AF030199.1 NT 16406 2.42 2.4E-01 Z21647.1 NT 19821 29109 1.55 2.4E-01 AF217491.1 NT 19526 2.39 2.4E-01 AF004213.1 NT 18945 2.54 2.4E-01 AZ78191.1 NT 19509 1.59 2.4E-01 V01507.1 NT 19716 1.26 2.4E-01 BF229975.1 EST HUMAN 19355 3.35 2.4E-01 AL63281.2 NT 10330 20153 0.9 2.3E-01 S75898.1 NT	7962	17815				Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
18093 28347 1.99 2.4E-01 AF030199.1 NT 18406 2.42 2.4E-01 Z21647.1 NT 18821 23109 1.55 2.4E-01 AF217491.1 NT 19526 2.39 2.4E-01 AF004213.1 NT 19509 1.59 2.4E-01 AJ278191.1 NT 19509 1.59 2.4E-01 AJ278191.1 NT 19716 1.26 2.4E-01 BF229975.1 EST_HUMAN 19355 3.36 2.4E-01 AL63281.2 NT 10330 20153 0.9 2.3E-01 S75898.1 NT	8149	18037				34.2	Į,	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
18406 2.42 2.4E-01 Z21647.1 NT 18821 29109 1.55 2.4E-01 AF217491.1 NT 19526 2.39 2.4E-01 AF004213.1 NT 19509 1.59 2.4E-01 AJ278191.1 NT 19509 1.59 2.4E-01 V01507.1 NT 19716 1.26 2.4E-01 BF229975.1 EST_HUMAN 19355 3.35 2.4E-01 AL63281.2 NT 10330 2.0153 0.9 2.3E-01 S75898.1 NT	8209	18093				+	Ę	Mus musculus type 1 sigma receptor gene, complete cds
18821 29109 1.55 2.4E-01 AF217491.1 NT 19526 2.39 2.4E-01 AF004213.1 NT 18945 2.54 2.4E-01 AJ278191.1 NT 19509 1.59 2.4E-01 V01507.1 NT 19716 1.26 2.4E-01 BF229975.1 EST_HUMAN 19355 3.35 2.4E-01 AL63281.2 NT 10330 20153 0.9 2.3E-01 S75898.1 NT	8534	18406				221647.1	Z	P. asiatica mosaic virus genomic RNA
19526 2.39 2.4E-01 AF004213.1 NT 18945 2.64 2.4E-01 AIZ78191.1 NT 19509 1.59 2.4E-01 V01507.1 NT 19716 1.26 2.4E-01 BF229975.1 EST_HUMAN 19355 3.35 2.4E-01 AL63281.2 NT 10330 2.0153 0.9 2.3E-01 S75898.1 NT	9030	18821	29109			AF217491.1	N	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
18945 2.64 2.4E-01 AJZ78191.1 NT 19509 1.59 2.4E-01 V01507.1 NT 19716 1.26 2.4E-01 BF229975.1 EST_HUMAN 19355 3.35 2.4E-01 AL163281.2 NT 10330 20153 0.9 2.3E-01 S75898.1 NT	9162	19526		2.39		AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
19509 1.59 2.4E-01 V01507.1 NT 19716 1.26 2.4E-01 BF229975.1 EST_HUMAN 19355 3.35 2.4E-01 AL163281.2 NT 10330 20153 0.9 2.3E-01 S75898.1 NT	9222	18945		2.54		AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
19716 1.26 2.4E-01 BF229975.1 EST_HUMAN 19355 3.36 2.4E-01 AL163281.2 NT 10330 2.0153 0.9 2.3E-01 S75898.1 NT	9439	19509		1.59	2.4E-01	V01507.1	N	Gallus gallus gene coding for a-actin
19355 3.35 2.4E-01 AL163281.2 NT 10330 20153 0.9 2.3E-01 S75898.1 NT	9650	19716		1.26		BF229975.1		RC3-CT0413-100800-023-b06 CT0413 Homo saplens cDNA
10330 20153 0.9 2.3E-01 S75898.1 NT	9865	19355		3.35		AL163281.2	LN	Homo sapiens chromosome 21 segment HS21C081
	383	10330		6.0		S75898.1	NT	aromatase [Poephila guttata≂zebra finches, ovary, mRNA, 3188 nt]

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Single Exol Plobes Explessed in hear	. Top Hit Descriptor	Mycoplasma genitalium section 35 of 51 of the complete genome	Methanococcus jannaschii section 138 of 150 of the complete genome	601142073F1 NIH_MGC_14 Homo saplens cDNA clone IMAGE:3505818 5'	Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA	Yersinia pestis HmsH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds	Brassica napus sig gene for S-locus glycoprotein, cultivar T2	Mus musculus cdh5 gene, exon 1, partial	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'	Human crythropoletin gene, complete cds	Marinilabilia agarovorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957	no16d06.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu	Tepeuve dement, contains element i rin Tepeuve element, i Vir21b07.s1 Soares placenta Nb2HP Homo saniens cDNA clone IMAGE-130357.3*	INDICATOR OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STA	M9/10/11 Soares fetal liver speen TNFLS Homo sapiens cUNA clone IMAGE 213283 &	GSTA5=glutathione S-transferase Yc2 subunit {5' region, intron 1} [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3}	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA	y17f01.r1 Scares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'	Mus musculus renin (Ren-1c) gene, promoter region	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA	Human phenylethanolamine N-methyltransferase gene, complete cds	601896136F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125368 5'	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genomo	Homo sapiens mRNA for KIAA1512 protein, partial cds	7k30b06x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10];
ie Exull Flon	Top Hit Dafabase Source	NT	N	EST HUMAN	ト	TN.	LN	NT	NT	EST_HUMAN	NT	IN	TO HOU	EST HIMAN	TOTAL TOTAL	EST HOMAN	뉟	 - - -	EST_HUMAN	NT	N F	NT	בן.	NT	EST_HUMAN	۲.	Ę	F	EST_HUMAN
Billo	Top Hit Acession No.			2.3E-01 BE311893.1	6677980 NT	U22837.2	2.3E-01 AJ245480.1		1	2.3E-01 BE297718.1		2.3E-01 AB015033.1	,	2.3E-01 AA6013/9.1		2.3E-01 H69836.1	S82821.1	7662133 NT	R82252.1		2.3E-01 D90899.1	2.3E-01 AF092535.1	5031984 NT		2.3E-01 BF316135.1	2.3E-01 U91328.1	1.0	_	2.3E-01 BF058381.1
	Most Similar (Top) Hit BLAST E Value	2.3E-01 U39713.1	2.3E-01 U67598.1	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01 Y10887.2	2.3E-01	2.3E-01	2.3E-01 M11319.1	2.3E-01	1000	2.3E-01 /	70.0	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01 L78789.1	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01
	Expression Signal	4.42	19.84	3.35	1.5	0.88	1.38	2.75	1.3	1.56	1.02	0.88		1.28	27.5	1.09	1.1	3.72	0.85	3.35	1.02	2.08	5.1	0.82	0.95	0.98	26.95	2.6	1.71
	ORF SEQ ID NO:		20403	20687	21258		21351	21378		22169	22372	21127	70000	725661	73000	23051	23461		23926		24031	24061	24140	24455	24641	24745	24783	24942	25074
	Exon SEQ ID NO:	10558	10587	10842	11398	11451	11490	11518	11892	12274	12483	11271	7,000	12861	7167	13244	13679	13767	14152	14198	14245	14282	14348	14668	14877	14969	15013	15169	15252
	Probe SEQ ID NO:	621	651	918	1494	1546	1586	1614	1999	2396	2615	2794	, 600	2934	CT COS	3324	3766	3856	4253	4300	4349	4386	4424	4956	5002	5101	5146	5246	5332

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	Top Hit Descriptor	C.familiaris rom1 gene	as27e12.x1 Barstead aorta HPLRB6 Homo saplens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME G OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element;	Glycine max resistance protein LM17 precursor RNA, partial cds	Mus musculus myosin XV (Myo15), mRNA	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'	za12e08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE: 292358 5'	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene,	Hammohilus influenzas genes for Hinel Testriction modification exetam (Hinell mathythansferses (F)	2.1.1.72) and Hindl endonuclease (EC 3.1.21.4))	MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes	601646155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)	Chlamydophila pneumoniae AR39, section 4 of 94 of the complete genome	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds	HCOEST44 HT29M6 Homo sapiens cDNA clone HCoE44 5'	chn1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'	PM4-SN0012-030400-001-b06 SN0012 Homo sapiens cDNA	xv21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175 C92175 C92175 VSY1 OXIDASE-RFI ATED PROTEIN 2 remains PTR5 by TAR1 remains element	R01507202E1 NIH MGC 71 Homo carians ADMA clans MACE ranges of the control of the control of the control of the control of the control of the control of the control of the control of the control of the 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an i liova digino	Top Hit Database Source	NT	EST_HUMAN	EST HUMAN	EST HUMAN	N FN	占	EST_HUMAN	EST_HUMAN	ŀ		Z L	EST_HUMAN	N	EST_HUMAN	N	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	FST HIMAN	EST HIMAN	ECT LITTAN	NICHOLD IN IN	N-1	LN	EST_HUMAN	
	Top Hit Acession No.	2.3E-01 X96587.1	2.3E-01 AI708840.1	2.3E-01 AI708840.1	2.3E-01 AI718148.1	2.3E-01 AF175389.1	6754779 NT	2.3E-01 BE888071.1	2.3E-01 N80983.1	2 3E.01 M68031 1	1.10000	2.3E-01 X52124.1	2.3E-01 BE173060.1	2.3E-01 AJ293261.1	2.3E-01 BF133577.1	2.3E-01 AJ250189.1	2.3E-01 AJ250189.1	AE002167.2	2.3E-01 U45426.1	2.3E-01 T27231.1	2.3E-01 AA089819.1	2.3E-01 AW863940.1	2 3F-01 AW303623 1	2 3E-01 BE882464 1	2.3E 04 DE62240 4	5.003519.1	2.3E-01 AJ006519.1	AJ006519.1	2.3E-01 BF475611.1	
	Most Similar (Top) Hit BLAST E Value	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2 3E_04	7.01	2.3E-01			2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01			2 20 04	2.35-01	2.3E-01	2.3E-01	2.3E-01	
	Expression Signal	4.83	1.87	1.87	3.93	2.62	3.19	1.59	2.9	80.0	27-7	1.37	2.54	2.26	4.95	2.84	2.84	2.39	2.53	20.46	1.65	2.07	2.05	88 7	1 03	0.00	2.09	4.54	2.67	
	ORF SEQ ID NO:	25361	25617	25618		26408		26519		78741	100	27732		27811		28663	28664						24990							
	Exon SEQ ID NO:	15314	15533	15533	16005	16246	16345	16349	16418	16544	1	17507	17562	17590	17824	18397	18397	18547	18898	18951	19477	18970	19665	4070k	10060	1		19088	19310	
	Probe SEQ ID NO:	5395	5618	5618	6111	6384	6487	6491	929	6664	1000	7657	7712	7740	7974	8525	8525	8658	9144	9232	9258	9266	9224	0358	0407	1016	9456	9549	9793	

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Single Exon Probes Expressed in Heart

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Table 4
Single Exon Probes Expressed in Heart

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oliigia Lauti riodas Eaptassau III neatt	Top Hit Descriptor	Saccharomyces cerevisiae tau 138 (TFC3) gene, complete cds	602152001F1 NIH MGC 81 Homo sapiens cDNA clone IMAGE:4293001 5	Human olfactory receptor (OR17-2) gene, partial cds	Archaeoglobus fulgidus section 135 of 172 of the complete genome	Canis familiaris keratin (KRT9) gene, complete cds	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, parrial cds	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein partial cds	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4 113), mRNA	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcD), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcl) genes, complete ods	S.cerevislae chromosome II reading frame ORF YBL025w	A.thaliana mRNA for AtRanBP1b protein	Homo saplens p53R2 gene for ribonucleotide reductase, exon 6	Beta vulgaris mRNA for elongation factor 1-beta	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) (80 KD DIACYLGLYCEROL KINASE)	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA	RC3-HT0622-040500-013-b11 HT0622 Homo sapiens cDNA	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds	Human granulin gene	7a59e02x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3223034 3'	Salvelinus alpinus mitochondrion, complete genome	Gallus gallus mRNA for avena, complete cds	Homo sapiens CGI-18 protein (LOC51008), mRNA	O.cunniculus germline IgH heavy chain V-H pseudogene, allotype VHa2	Mus musculus Major Histocompatibility Locus class II region	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915	Homo sapiens chromosome 21 segment HS21C013	Homo saplens rac1 gene	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
lie LAUII FIU	Top Hit Databaso Source	N F	EST_HUMAN	NT	N-	NT	NT	L L	F	Z	N	F	Z.	NT	SWISSPROT	Z	EST_HUMAN	N	NT	EST HUMAN	ᄓ	NT	卢	NT	NT	LN	L	NT	EST_HUMAN	누
3,110	Top Hit Acession No.	2.1E-01 M98261.1		2.1E-01 U04642.1			2.1E-01 AF068687.1	2.1E-01 AF068687.1	7305030 NT				9.1	2.1E-01 Z97067.1	P52824	11036647	+	2.1E-01 AF217490.1		2.1E-01 BE672330.1	5835904 NT	AB017437.1	7705601		1.1		2	5	2.0E-01 AW384937.1 EST	4503408
	Most Similar (Top) Hit BLAST E Value	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01	2.1E-01			2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01/	2.0E-01
	Expression Signal	0.99	5.99	1.86	1.97	1.74	1.35	1.35	1.21	4.78	5.88	2.36	1.19	2.49	1.49	2.31	2.15	1.6	1.4	1.29	1.29	1.72	2.39	1.19	1.81	1.03	2.57	1.42	1.29	13.51
-	ORF SEQ ID NO:	24772	24938	26106		26572	26596	26597		27022	27289	27553	27611	28006	28018		28964			25174		19983		20440	20563	20759	20866	20993	21047	21241
	Exon SEQ ID NO:	15001	15167	15970	16247	16393	16417	16417	16585	16829	17101	17349	17398	17767	17779	18661	18674	19132	19634	19382	19436	10165	10465	10617	10722	10915	11024	11141	11194	11376
	Probe SEQ ID NO:	5134	5243	6123	6385	6535	6559	6559	6705	6951	7224	7479	7547	7917	7929	8849	8862	9522	9730	9905	9979	193	523	684	793	395	1109	1234	1286	1471

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Single Exon Probes Expressed in Heart

Oligie Lyull Tobes Lypressed III near	Top Hit Database Source	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505	Homo sapiens sodium/fodide symporter mRNA, partial cds	Homo sapiens 14q32 Jagged2 gene, complete cds, and unknown gene	Methanococcus jannaschii section 67 of 150 of the complete genome	Г	Γ		Homo sapiens full length insert cDNA YH85A11	SWISSPROT PROTEIN ATHB-10) (HD-ZIP SWISSPROT PROTEIN ATHB-10) (HD-ZIP SWISSPROT PROTEIN ATHB-10)	xp15b02.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element	T	Τ	EST HUMAN QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA	Г	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA	Homo sapiens putative psihHbD pseudogene for hair keratin, exons 1 to 9	Rat SOD-2 gene for manganese-containing superoxide dismutase	Homo saplens dual oxidase-like domains 2 (DUOX2), mRNA	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds	M.auratus mu class glutathione transferase gene	HUMAN PM1-CT0247-141099-001-g06 CT0247 Homo sapiens cDNA	Andes virus strain Ol23133 glycoprotein G1 and G2 precursor, gene, partial cds	M.musculus scp2 gene exon 14	Chlamydia trachomatis section 5 of 87 of the complete genome	Homo sapiens filamin 2 (FLN2) mRNA, complete cds	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds	Salvelinus pluvius mRNA for transferrin, complete cds	Salvelinus pluvius mRNA for transferrin, complete cds		EST_HUMAN ov80a10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643610.3	
Diligio I	Top Hit Acession L	2.0E-01 AB007974.1 NT	2.0E-01 AF260700.1 NT	6		1	2.0E-01 BE871330.1 EST		2.0E-01 AF074990.1 NT		AW238005 1		1	5.1	2.0E-01 AF147083.1 NT	8922080 NT	/19216.1 NT	i	11432540 NT	J15300.1 NT		5.1	2.0E-01 AF028026.1 NT		2.0E-01 AE001278.1 NT	NF146692.1 NT	.1	.1	NT NT NT	389088.1 NT	2		2
	Most Similar (Top) Hit BLAST E Value	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01 X82877.1	2.0E-01	2.0E-01 P46607	2 OF-01	2.0E-01		2.0E-01	2.0E-01	2.0E-01	2.0E-01 Y19216.1	2.0E-01 X56600.1	2.0E-01	2.0E-01 U15300.1	2.0E-01)	2.0E-01 /	2.0E-01 /	2.0E-01 X91151.1	2.0E-01 /	2.0E-01 AF146692	2.0E-01 AF086907	2.0E-01 AF086907	2.0E-01 D89088.1	2.0E-01 D89088.1	2.0E-01	2.0E-01 /	2.0E-01 AF078164.
	Expression Signal	2.51	1.59	1.82	1.64	1.33	1.33	1.67	0.95	0.8	68 0	0.81	0.8	8.47	1.07	6.07	1.1	2.55	2.13	5.29	4.31	3.54	6.95	4.18	4.39	2.07	1.95	1.95	2.7	2.7	1.37	3.22	6.61
	ORF SEQ ID NO:	21295	21300				21619			23166		23346	23628		24519	24618	24687	25089	25491	25705	25900	25962		26839			27857	27858	28350	28351		25202	
	Exan SEQ ID NO:	11438	11442	11590	L	11743	11743	12181	12789	13359	13436	13560	13853	14358	14739	14847	14913	15263	15428	15603	15780	15839	16517	16651	17299	17542	17624	17624	18098	18098	19118	19308	19288
	Probe SEQ ID NO:	1534	1538	1688	1723	1847	1847	2299	2861	3442	3520	3646	3945	4484	4859	4972	5041	5342	5510	5694	5874	5934	6637	6772	7511	7692	7774	7774	8214	8214	9503	9747	9769

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Single Exon Probes Expressed in Heart

	Top Hit Descriptor	Mus musculus fructosamine 3 kinase (Fn3k), mRNA	Rattus norvegicus Ary hydrocarbon receptor nuclear translocator 1 (Arnt1), mRNA	Mus musculus bale ear (ep) gene, wild type allele, 3' region, partial cds	Homo saniens lambda/lota protein kinase C-interacting protein mRNA, complete cds	Homo saniens lambda/lota protein kinase C-interacting protein mRNA, complete cds	Trong experience processing Arman States CDNA	NCS-B 1030Z-23 133-21 - 401 B 1050Z 1330Z 1320Z	NC3-B 10302-23 1139-3 1-40 1 D 0002 1300 0 mRNA	MUS INSTANCE IN TRANSPORT TO THE TRANSPORT THE CONTRACTOR TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE TRANSPORT TO THE 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count injuried. Leading	Rattus norvegicus arylacetamide deacetylase gene, comprere cus	PAIR-RULE PROTEIN OUD-PAIRED	Schizosaccharomyces pombe UNA for Gypplasmic dynein neuvy crian, complete cas	CM3-C10315-271199-045-011 C10319 Homo sapiens CDNA	MR1-FN0010-290700-007-004 FINOU ID TIGITIO SQUIGITS COLVA	Arabidopsis mailana DINA Cili di lusuma 4, comug ingamon voc. c	Fugur Dinpes genes encounting carbanasy prosperate of missions of missions of missions of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the co	ILS-CIUZIP-IOZOV-ODI-ZOZ O 1 0 2 10 1 10 10 0 0 0 0 0 0 0 0 0 0 0	attus norvegicus chenidalite receptus Cacino mara, Campaca caci	KINESIN-LIKE PROTEIN NIP4	Phoca vitulina partial darzib gene for alpha adrenergic reception zu	S.mansoni elastase HP1 gene	ts93912.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2238886 3' similar to gb:M21574 ALPHA	PLATELET-DERIVED GROW I H FACTOR RECEPTOR PRECONSON (TIGHTAN)	Mus musculus Notich gene nomotog 3, (Diosophilia) (Noticino), mixing	xf29a07.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2619444 3: similar to gp:///1/1/9 NETINGUE. ACID RECEPTOR ALPHA-1 (HUMAN);	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a	
	Top Hit Database Source							LOMAN	TOMAN		EST HUMAN E				NT	NT		T HUMAN	一	SWISSPROT	\neg	HUMAN	1 HUMAN			HOMAN	T	ISSPROT	NT	N		T_HUMAN		T_HUMAN		
	Top Hit Acession No.	11528495 NT		243743	_			_	3E070801.1 EST	7305180			1.9E-01 AF184623.1	8922533 NT			1.9E-01 D13197.1		17.1		84.1	1.9E-01 AW754106.1	1.9E-01 BE834943.1	1.9E-01 AL161493.2	1.9E-01 Z93780.1	1.9E-01 AW849203.1	1.9E-01 AF223642.1	1.9E-01 095239	1.9E-01 AJ251178.1	1.9E-01 Z70296.1		AI631199	TN 580829 NT	1.9E-01 AW130149.1	1 0E-01 AE127937 1	
	Most Similar (Top) Hit BLAST E Value	2 OF 01	2.02.0	1.95-01	1.9E-01 AF004333	1.9E-01 U32581.2	1.9E-01	1.9E-01 BE070801	1.9E-01 BE070801	1.9E-01	1.9E-01	1.9E-01 /	1.9E-01	1.9E-01	1.9E-01 U66066.1	1.9E-01 J00922.1	1.9E-01	1.9E-01	1.9E-01	1.9E-01 P39768	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01		1.9E-01				,
	Expression Signal	7	0.	10.35	9	1.31	1.31	5.37	7.32	1.61	6.3	2.3	3.91	3.31	3.91	5.55	3.4	4.63	0.93	96.0	3.02	1.89	1.06	0.89	0.84	0.86	1.04	1.11	1.03			1.19	0.99			
	ORF SEQ ID NO:	00710	25193		20126	20392	20393	20400	20400		20846	21110		22109			23072								24338	24566		24605					24789			22440
-	Exon SEQ ID NO:		19374	10086	10308	10577	10577	10584	10584	10893	11004	11254	11322	12211	12819					1_	_	L	1_	14265	14548	14791	14821	14837	L	\perp		14991	1_		1	15380
	Probe SEQ ID NO:	1	9897	105	349	640	640	647	648	970	1088	1348	1416	2330	2892	2008	3349	3434	3735	3762	3910	3992	4138	4369	4662	4912	4943	4962	5034	5443	2 0	5123	5153	5444	1440	5466

Page 68 of 413 Table 4 Single Exon Probes Expressed in Heart

Single Extra Propes Expressed In Tear	Most Similar Expression (Top) Hit Top Hit Acession Database Signal BLAST E No. Source	2.26 1.9E-01 AU133116.1 EST_HUMAN AU133116 NT2RP4 Homo sapiens dDNA clone NT2RP4001328 5'	T HUMAN	26446 1.43 1.9E-01 U80922.1 NT Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPPR) gene, complete cds		1.62 1.9E-01 AL161557.2 NT	NT	2.16 1.9E-01 AL161503.2 NT	2.16 1.9E-01 AL161503.2 NT		1.9E-01 AF223391.1 NT	29060 2.61 1.9E-01] AJ243213.1 NT Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5		1.26 1.9E-01 AF001168.1 NT Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds	19811 2.26 1.8E-01 U73200.1 INT Mus musculus p116Rip mRNA, complete cds	20041 1.22 1.8E-01 AB022090.1 NT Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated	2 45 4 BE 04 AB024400 2	0.85 1.8E-01/AI912212.1 EST HUMAN	1.21	5.28 1.8E-01 AL117189.1 NT	1.29 1.8E-01 6753947 NT	21253 1.29 1.8E-01 6753947 NT Mus musculus guanylate nucleotide binding protein 1 (Cbp1), mRNA	0.92 1.8E-01 4505036 NT	1.93 1.8E-01 A1733708.1 EST_HUMAN GAMMA BUTYROBETAINE HYDROXYLASE;	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A5 precursor, complete cds	2 00 C T RE-01 AW035728 1 FST HIMAN	1 BE-01 AF184589.1	1.09 1.8E-01 AW182300.1 EST_HUMAN	1.8E-01 AW995178.1
	ORF SEQ EXPI		24863	26446	26476	26735	27109	28176	28177		28271	29060			19811	20041	2014	20,00	20735	20832	21024	21252	21253			71644	17017		22595	22803
	Exon O SEQ ID NO:	15503	15119	16284	16310	16538	16918	17930	17930		18025	18768	19146	19546	1001	12663			10889		<u> </u>	11392	11392	11700	11720	11760	\perp	1	1	
		5588		6423	6449	6658	7041	8038	8038	_	8137	8961	9546	9880	g	260	996		996	1075	1267	1487	1487	1803	1823	4073	2680	2007	1 im	3085

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Table 4
Single Exon Probes Expressed in Heart

Probe Exon SEQ ID SEQ ID NO: NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3570 13484	23275	1.07	1.8E-01	1.8E-01 H03369.1	EST_HUMAN	1/45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
3570 13484	23276	1.07	1.8E-01	1.8E-01 H03369.1	EST_HUMAN	145e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
4154 14054	4 23828	8.0	1.8E-01	1.8E-01 AJ271735.1	Z-L	Homo sapiens Xq pseudoautosomal region; segment 1/2
4238 14137	/	1.13	1.8E-01	1.8E-01 D37954.1	Z	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4456 14350	24141	5.12	1.8E-01	1.8E-01 AL161556.2	TN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4663 14549	24339	2.36		1.8E-01 AB051897.1	<u> </u>	Mus musculus Soya6, Soya16-ps, Soya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A5 precursor, small inducible cytokine A5 precursor, small inducible cytokine A5 precursor.
4700 14586				1.8E-01 X92179.1	N	S. tuberosum mRNA for alcohol dehydrogenase
4977 14852	2 24618		1.8E-01	1.8E-01 AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-908 ST0203 Homo sapiens cDNA
5027 14900	24670	4.17	1.8E-01	1.8E-01 AF181258.1	Z F	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5053 14925	5 24697	1.28	1.8E-01	1.8E-01 AI439881.1	EST_HUMAN	t57e04x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5117 14985		1.03	1.8E-01	1.8E-01 AJ000742.1	NT	Homo Saplens hist11 gene, 5' UTR
5549 15465	5 25535	1.41	1.8E-01	1.8E-01 AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
		1.29	1.8E-01	1.8E-01 Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
5948 15853	3	2.5	1.8E-01	1.8E-01 N94853.1	EST_HUMAN	yy62h02.r1 Soares_multiple_scierosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278163 5'
			1.8E-01	1.8E-01 AB018561.1	L'A	Citrullus lanatus mRNA for wsus, complete cds
6179 16065			1.8E-01	1.8E-01 AB018561.1	NT	Citrullus lanatus mRNA for wsus, complete cds
		1.72	1.8E-01	1.8E-01 M73258.1	LN	Human cellular DNA/Human papillomavirus proviral DNA
7396 17314		1.22	1.8E-01	9626232 NT	NT	Bacteriophage Ike, complete genome
7933 17783				1.8E-01 X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
8033 17925	5 28172	3.19		1.8E-01 X77336.1	N _T	A.thaliana mRNA for ribonucleotide reductase R2
8065 17956	3 28205	6.65	1.8E-01	1.8E-01 U38906.1	Ŋ	Bacteriophage r11 integrase, repressor protein (rro), dUTPase, holin and lysin genes, complete cds
8118 16065		2.9	1.8E-01	1.8E-01 AB018561.1	LN TN	Citrullus lanatus mRNA for wsus, complete cds
8118 16065	5 26215	2.9	1.8E-01	1.8E-01 AB018561.1	N	Cltrullus lanatus mRNA for wsus, complete cds
8119 18007	7 28254	3.88	1.8E-01	1.8E-01 AF019107.1	NT	Dictyostelium discoideum unknown (DG1041) gene, complete cds
8381 18258	3 28507	2.64	1.8E-01	1.8E-01 M59257.1	N	Human carcinoembryonic antigen (CEA) gene, exon 4
8758 17907		3.98	1.8E-01	1.8E-01 X57033.1	NT	B.taurus mRNA for potassium channel
		2.83	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbxa2r), mRNA
	2 25344		1.8E-01	1.8E-01 BF348623.1	EST_HUMAN .	602019928F1 NCL CGAP Brn67 Hamo sapiens cDNA clone IMAGE:4155318 5'
9625 19200	0	2.05	1.8E-01	1.8E-01 Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)

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Table 4
Single Exon Probes Expressed in Heart

Top Hit Describtor Top Hit Describtor Dathhase Source EST HUMAN EST HUMAN MIT Heliange mRN4 for hexokinsee (hwk1) EST HUMAN EST HOMAN WARR1021 Source placenta Nb2-PF Homo septens cDNA clone INAGE-133027 57 EST HUMAN EST HOMAN WARR1021 NBLENOFILLARENT TRIFFLET PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L). Lymantia dispar nucleopolyhedrovirus, complete genome NIT Homo septens BNIP3-H (RNIP3-H) gene, complete genome Lymantia dispar nucleopolyhedrovirus, complete genome NIT Homo septens BNIP3-H (RNIP3-H) gene, complete ods, and YRAL VIBCO gene, partial cds, hemagglutinin/protease NIT Nipho choleree hypoxanthine phosphoribosyltransferase (hyb) gene, partial cds, hemagglutinin/protease NIT Nipho sholeree hypoxanthine phosphoribosyltransferase (hyb) gene, partial cds, hemagglutinin/protease NIT NIPHON SEPTED STATES (RNIP3-H) gene, complete cds, and YRAL VIBCO gene, partial cds, hemagglutinin/protease NIT Nipho sholeree hypoxanthine phosphoribosyltransferase (hyb) gene, partial cds, hemagglutinin/protease NIT Nipho sholeree hypoxanthine phosphoribosyltransferase (hyb) gene, partial cds, hemagglutinin/protease NIT Nipho sholeres hypoxanthine phosphoribosyltransferase (hyb) gene, partial cds, hemagglutinin/protease NIT Nipho sholeres hypoxanthine phosphoribosyltransferase (hyb) gene, partial cds, hemagglutinin/protease NIT Nipho sholeres hypoxanthine phosphoribosyltransferase (hyb) gene, partial cds, hemagglutinin/protease NIT Nipho sholeres hypoxanthine phosphoribosyltransferase (hyb) gene, partial cds, hemagglutinin/protease NIT Nipho sholeres generalyderenty of the ALL-1MALLI-HXX gene fused to the AE-4/FEL gene NIT Homo septens derivative protein frament, partial intron 10 of the ALL-1MALLI-HXX gene fused to manting excensional partial larger septems has complete cds. NIT Homo septems derivative and partial protein file gene. complete cds NIT Rea mays calculant-dependent protein file gene. complete cds NIT Rea mays calculant-dependent protein file gene. complete cds	Top Hit Database Source Source Source Source Source Source Source Source Source NT NT LI NT NT NT NT NT NT NT NT NT NT NT NT NT	Sing t Similar 4ST E	Most (To)	Signs	RO	m % - 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Probe SEQ ID NO: 9738 9779 9453 1042 1042 1042 1042 1042 1042 1042 1042
							5820
				7007	00000	COPLY	5820
NUMBOSOWAL TROTLEM 1 (1 COUNTY),	Т	AA4/UDSD. I				- 1	5321
CITIC PIROSONAL PROTEIN P1 (HIMAN)		A A 470 EQE 4					7007
e13a02.s1 NCI CGAP Co3 Horno sapiens cDNA clone IMAGE:881066 3' similar to gb.M17886 60S					L	L	Γ
CIDIC RIBOSOMAL PROTEIN P1 (HUMAN);		AA470686.1					5321
e13a02.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S							
ea mays starch branching enzyme IIb (ae) gene, complete cds		AF072725.1		1.18			5067
ea mays calcium-dependent protein kinase (MZECDPK2) mRNA, complete cds		U28376.1		1.16			986
ontains OFR.b1 OFR repetitive element;	HUMAN	AI247635.1					1732
h57e09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to							
chistocerca gregaria alpha repetitive DNA		X52936.1		1.88			459
of the AF-4/FEL gene		AJ235377.1					859
omo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron							
omo sapiens nap1 gene, complete CUS		AJ224877.1	1.7E-01				222
		17700000. I				\perp	£
The bank and and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and a few and		A IDEDENE 4					Ş
nabaens sp. ORF4 (partial), ORF3, ORF2, ORF1, adbA gene, adbB gene, adbC gene, adbE							T
axus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds		AF081514.1				_	790
aja naja atra ctx≺1 gene, exons 1-3		AJ238736.1				L	296
aja naja atra cbr-1 gene, exons 1-3		AJ238736.1		1.35			296
ST41661 Endometrial turner Hemo sapiens cDNA 5' end	HUMAN	AA336909.1					896
gulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds		AF000716.1			,	-	829
ibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease							
guiatory protein (napry) gene, comprete cus, and man, vioco gene, partar cus		AF000716.1	-				339
ibrio cholerae hypoxanthine phosphoribosytransferase (hpt) gene, partial cds, hemagglutinin/protoase							
omo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product				3.8			338
mantria dispar nucleopolyhedrovirus, complete genome				1.6			242
mantria dispar nucleopolyhedrovirus, complete genome				1.6			042
EUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)	ISSPROT		1.7E-01	1.89			345
dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4			1.7E-01	2.04	20559		887
31274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5	HUMAN		1.7E-01				563
dispar mRNA for hexokinase (hxk1)			1.8E-01				67.
I DINIA for bearing the day				F .		_[2
48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'	HUMAN		1.8E-01	7.94			738
	Source	oʻ.	BLAS1 E Value	Signal	 O O O	Ö	
Top Hit Descriptor	Top Hit Database	Top Hit Acession	Most Similar (Top) Hit	Expression	ORF SEQ	Exon SEQ ID	
Expressed in heard	jie Exon Probe	Sing					

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Table 4
Single Exon Probes Expressed in Heart

	Top Hit Descriptor	601569022F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA	Rat (SHR strain) SX1 gene	Bacillus halodurans genomic DNA, section 2/14	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3	Homo sapiens chromosome 21 segment HS210084	Homo saplens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2),	mRNA	Ind60e07.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1148292.3' similar to gp:L25031 TPANSFORMING PROTFIN RHOC (HTIMAN)	INVINCE CHARGE AND AND AND AND ADDRESS OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE CHARGE STATE OF THE	60128654/F1 NIH, MGC 44 Homo sapiens GUNA digner INIAGE, 501520 0	of43a03.s1 NCL_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:14269243	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA	AMP NUCLEOSIDASE	Horno sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA1), mKNA	Homo sapiens chromosome 21 segment HS21C078	bx69g05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2274872.3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);	Human bela globin region on chromosome 11	Homo sapiens mevalonate kinase gene, exon 6 and 7		Homo sapiens homeobox protein OTX2 gene, complete cds		Crassostrea gigas RNA polymerase II largest subunit mRNA, parital cds	H.sapiens mRNA for novel T-cell activation protein	Homo sapiens mRNA for KIAA1308 protein, partial cds	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region	Populus frichocarpa cv. Trichobel ABI3 gene	Populus trichocarpa cv. Trichobel ABI3 gene	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
	Top Hit Database Source	EST HUMAN	LN	NT	N FN	LN	NT	NT	NT		NT	HOL	EST TOWNAIN	EST_HUMAN	EST HUMAN	NT	NT	SWISSPROT	LZ	N	EST HUMAN	NT	N.	EST_HUMAN	LN L	SWISSPROT	٦	Z	Į.	NT TN	INT	NT	NT	LN
)	Top Hit Acession No.	1.7E-01 BE734179.1	_	7706426 NT	7706426 NT		2.1		1.7E-01 AL163284.2		11427203 NT	7 020100	1./E-01 AA62/9/2.1	1.7E-01 BE390835.1	1.7E-01 AA814617.1	7106300 NT	7106300 NT	P15272	11418157 NT	1.7E-01 AL163278.2	1 7F-01 AI824404 1	1.7E-01 U01317.1	1.6E-01 AF217532.1	1.6E-01 R31497.1	1.6E-01 AF298117.1		1.6E-01 U10334.1	1.6E-01 X94232.1	1.6E-01 AB037729.1	1.6E-01 AF185589.1	1.6E-01 AF185589.1	1.6E-01 AJ003165.1	1.6E-01 AJ003165.1	1.6E-01 AE004413.1
-	Most Similar (Top) Hit BLAST E Value	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01 D00384.1	1.7E-01	1.7E-01 U16288.1	1.7E-01		1.7E-01	1	1./E-01/	1.7E-01	1.7E-01	1.7E-01	1.7E-01		1.7E-01	1.7E-01	1 7F-01	1.7E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01 P22063	1.6E-01	İ					1.6E-01	1.6E-01
	Expression Signal	7.96	12	7.03	7.03	2.46	7.38	2.06	2.42		1.48		1.57	9.13	2.47	7.88	7.88	1,92	4.38	1.5	1 28	5 79	1.88	1.53	4.05	2.4	1	96.0		8.9	8.9		1.31	2.61
-	ORF SEQ ID NO:	26344			26883						28032		28033	28208		L	28590		29107	L		25218		1_				22115						
	Exon SEQ ID NO:	16183		16693	16693	16943	17382	17452	1]	17792		17793	17958	18068					1_		_	1_	_	L	1_		_	1	_			1_	
	Probe SEQ ID NO:	6320	8588	6814	6814	7066	7531	7604	7875		7942	·	7943	8067	8182	8456	8456	8949	9012	9130	6,000	0705	120	664	1505	1882	1941	2335	2443	2863	2863	3581	3581	3919

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Table 4
Single Exon Probes Expressed in Heart

1		_	_	τ-	Τ-	T-	T.c	_	т-		т —		_	_	т-	т-	_	_	Τ-	_	_	_	_	_	$\overline{}$	_		_			
Oilgic Expirations Expirate III Tealt	Тор Hit Descriptor	Homo sapiens apelin gene, complete cds	EST380677 MAGE resequences, MAGJ Homo sapiens cDNA	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA	S.cerevisiae chromosome XI reading frame ORF YKR105c	S.cerevisiae chromosome XI reading frame ORF YKR105c	2/84h09.s1 Strategene colon (#93/204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955 E221955 38,855 BP SEGMENT OF CHROMOSOME XIV.;	Lycopersicon esculentum Rsal fragment 2, satellite region	Lycopersicon esculentum Rsal fragment 2, satellite region	bb83h08.yf NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049023 5' similar to gb:M61715 TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:X69657 M.musculus (MOUSE);	xm43f01.x1 NGL CGAP_GC6 Horno sapiens cDNA clone IMAGE:2686969 3' similar to TR:075984 075984 HYPOTHETICAL 127.6 KD PROTEIN ;	xm43f01.x1 NCI_CGAP_GC6 Home sapiens cDNA clone IMAGE:2888969 3' similar to TR:075984 075984 HYPOTHETICAL 127.6 KD PROTEIN ;	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84	UI-H-BI2-agi-b-06-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'	Gorilla gorilla androgen receptor gene, partial exon	S.cerevisiae chromosome X reading frame ORF YJR001w	RC3-ST0200-041199-011-h01 ST0200 Homo sapiens cDNA	S.cerevisiae chromosome X reading frame ORF YJR001w	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA	QV2-PT0010-160400-133-a08 PT0010 Homo sapiens cDNA	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), niRNA	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds	Homo sapiens mRNA for FLJ00104 protein, partial cds
פום בעמיי י ימר	Top Hit Database Source	NT	EST_HUMAN	NT	Z L	FZ	EST_HUMAN	N	LN LN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	N	NT		EST_HUMAN	NT	NT	EST_HUMAN	NT	EST_HUMAN	SWISSPROT	SWISSPROT	NT	NT	EST_HUMAN	IN	EST_HUMAN	LN	NT
	Top Hit Acession No.	1.6E-01 AF179680.1	1.6E-01 AW968601.1	6753319 NT	1.6E-01 Z28330.1	1.6E-01 Z28330.1	1.6E-01 AA088343.1	1.6E-01 AJ006356.1	1.6E-01 AJ006356.1	1.6E-01 BE018707.1	1.6E-01 AW197496.1	1.6E-01 AW 197496.1	1.6E-01 AF034716.1	AL161588.2	1.6E-01 AL161588.2	AW291215.1	1.6E-01 AW246359.1	49349.1	Z49501.1	1.6E-01 BF375171.1	Z49501.1	AW850853.1	014647	014647	1.6E-01 AF106064.1	6671552 NT	AW877127.1	6679466 NT	1	_	1.6E-01 AK024496.1
	Most Similar (Top) Hit BLAST E Value	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01 L49349.1	1.6E-01 Z49501.1	1.6E-01	1.6E-01	1.6E-01	1.6E-01 014647	1.6E-01 014647	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01	1.6E-01
	Expression Signal	7.92	2.44	4.01	0.86	0.80	1.14	1.92	1.92	1.09	3.12	3.12	2.07	2.24	2.24	3.7	1.84	1.42	1.89	1.7	1.91	2.71	1.78	1.78	7.6	10.07	2.69	2.17	2.33	6.33	2.84
	ORF SEQ ID NO:	23908			24451	24452	24524	24546	24547	24601	25162	25183	25364	25898	25899	24858	26612	26662	27254		27631	28190	28490	28491		28814	29097		28795		1
	Exon SEQ ID NO:	14132	14249	14257	14665	14665	14745	14769	14769	14833	15309	15309	15317	15779	15779	15115	16429	16472	17064	17415	17416	17940	18241	18241		18530	18804	19678	18896		19265
	Probe SEQ ID NO:	4234	4353	4361	4781	4781	4865	4889	4889	4958	5390	5390	5398	5873	5873	6157	6571	6592	7187	7564	7565	8049	8364	8364	8459	8713	9001	9025	9141	9565	9727

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		1.82 1.36 2.81 2.81 1.49 1.149 1.154 0.89 0.89 0.87 0.87 0.87 0.87 0.87 0.86 0.86 0.86 0.89	10214 20030 187 10214 20031 187 12640 2.28 1.4 10697 20534 0.88 10992 20834 0.88 10997 20838 1.87 11013 20953 1.36 11161 2.1010 2.81 11162 2.1038 1.49 11762 2.1636 1.54 13771 2.2435 1.12 13242 2.2435 1.12 13242 2.3034 4.22 13242 2.3049 0.87 13242 2.3049 0.96 13610 2.3394 1.34 13703 2.3506 0.96 13718 2.3506 0.96 13718 2.3509 0.96 13718 2.3509 0.96 13718 2.3509 0.96 13718 2.3509 0.96 1371 2.3649 0.96 13871
AL163284.2 RE687665		0.97	13912 23687 0.97 13991 23768 8.36
		1.82 1.36 2.81 2.81 1.49 1.149 0.87 0.87 0.87 0.96 0.96 0.96 0.96 0.96 0.96 0.96 0.97 0.97 0.97	10992 20834 0.88 10997 20838 1.87 11013 20953 1.36 11161 21010 2.81 11762 21636 1.49 11762 21636 1.54 12927 22719 0.89 13242 23048 0.87 13242 23049 0.87 13242 23394 1.34 13610 23340 2.35 13703 23403 185.26 13718 23506 0.96 13718 23507 0.96 13871 23649 0.96 13912 23687 0.97 13911 23788 8.36 14511 24301 1.34

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					ונים ו	יייי ווייארן טונ	Origin Lyon Lybrasia II Toda
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4645	12544	22435	2.18	1.5E-01	1.5E-01 BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5
4680	14566	24361	1.08		1.5E-01 BE173796.1	EST HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4680			1.08		1.5E-01 BE173796.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4929	14808	24576	1.3	1.5E-01	1.5E-01 AL161560.2	NT	Arabidopsis thaliana DNA chromoscme 4, contig fragment No. 60
5072	14942	24716	0.94	1.5E-01	1.5E-01 AF003105.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds
5216	ļ	24833	2.02		1.5E-01 P07996	TORISSIMS	THROMBOSPONDIN 1 PRECURSOR
5266	15188		5.67	1.5E-01	1.5E-01 P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN)
5400	1	25367			1.5E-01 AW850754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo saplens cDNA
5424		25398	6.77	1.5E-01	1.5E-01 U65016.1	LN LN	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5424] _		6.77	1.5E-01	1.5E-01 U65016.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5652	15564	25660	1.9	1.5E-01	6753659 NT	LN	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5652	15564	25661	1.9		6753659 NT	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5684	15593	25694	1.87	1.5E-01	1.5E-01 AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
5760	15668	25774	2.44		1.5E-01 BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:383398° 5'
5785	15691		1.66	1.5E-01	4506396 NT	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
5828	15734	25845	1.78		1.5E-01 AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
5917	19455	25948	1.96		1.5E-01 AE001039.1	LZ	Archaeoglobus fulgidus section 68 of 172 of the complete genome
5935	15840	25963	5.13	1.5E-01	11417236 NT	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
	1						GLUTAMATECYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYLCYSTEINE
5942					1.5E-01 P48508	SWISSPROL	STN THE FACE) (GAMMA-ECS) (GCS LIGHT CHAIN)
5972			7		1.5E-01 Q28462	SWISSPRO	AMBELOGENIN
6031					1.5E-01 P30143	SWISSPRO	HYPOTHETICAL 31.7 KD PROTEIN IN THRC-TALB IN TERGENIC REGION (URTR)
6166		3 24866			1.5E-01 AW970295.1	EST HUMAN	ES I 382376 MAGE resequences, MAGK Homo sapiens cUNA
6284	16148		1.77	1.5E-01	1.5E-01 AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
6374	16236		1.88		1.5E-01 AI973157.1	EST HUMAN	wr52c08.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2491310 3'
6481	16340		1.68		1.5E-01 AW500611.1	EST HUMAN	UI-HF-BN0-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6481	16340	26508	1.68		1.5E-01 AW 500611.1	EST_HUMAN	UI-HF-BN0-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6786	16665	26856	1.22		1.5E-01 AA970317.1	EST_HUMAN	0085g12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
6895	16774		11.77		1.5E-01 C16800.1	EST_HUMAN	C16800 Ciontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA cione GEN-529H09 5
6912]]				1.5E-01 L27835.1	LN	Pangasianodon gigas growth hormone (GH) mRNA, complete cds
9669	16873	3 27064	1.44		1.5E-01 D84476.1	LN	Homo sapiens mRNA for ASK1, complete cds

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olligie Lyona Lypresseu III lean	Top Hit Descriptor	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA	za59e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE.296866 3' similar to PIR:S44443 S44443 RAD23 protein homoloo2 - human :	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'	Aclpenser transmontano vitellogenin mRNA, partial cds	Aplysia californica carboxypeptidase D mRNA, complete cds	Aplysia californica carboxypeptidase D mRNA, complete cds	P.leniusculus mRNA for Integrin beta subunit	wk53h12x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2419175 3' similær to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);	wk53h12.x1 NOL_CGAP_Pt22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);	Danio reno transcription factor Pax9b (Pax9) mRNA, complete cds	Claviceps purpurea ps1 gene	Claviceps purpurea ps1 gene	Homo sapiens chromosome 21 segment HS21C080	Homo sapiens chromosome 21 segment HS21C080	Sus scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA	wr52c08.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2491310 3'	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'	yp87e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'	AV741272 CB Homo sapiens cDNA clone CBDAGD04 5'	Campylobacter jejuni NCTC11168 complete genome; segment 1/6	Sus scrofa mRNA for sodium iodide symporter	Rattus norvegicus pyridoxal kinase mRNA, complete cds	Homo sapiens T cell receptor beta locus, TCRBV8S5P to TCRBV21S2A2 region	Xenopus laevis mRNA for DNA (cytosine-5-)-methytransferase, complete cds	yd54c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'	Mus musculus growth differentiation factor 5 (Gdf5), mRNA	Thermotoga maritima section 22 of 136 of the complete genome	UI-H-BI1-acf-a-09-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'	ny72d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
אום באטווו וטמב	Top Hit Database Source		EST HUMAN P	HUMAN		N L	NT TA	F	EST_HUMAN G	EST HUMAN G	1	N P	- L	F	F		EST_HUMAN II	EST_HUMAN w	EST HUMAN 6		EST_HUMAN A	NT	NT	NT	F	X	EST_HUMAN y		L	EST_HUMAN U		SWISSPROT
3110	Top Hit Acession No.	4501972 NT	1.5E-01 N74226.1	9.1		1.5E-01 AF007570.1		1.5E-01 X98852.1	1.5E-01 AI814046.1	1.5E-01 AI814046.1	1.5E-01 U40932.1	1.5E-01 AJ011964.1	1.5E-01 AJ011964.1	1.5E-01 AL163280.2		1.5E-01 AB042975.1	Ţ	1.5E-01 AI973157.1	1	1.5E-01 R83077.1	1.5E-01 AV741272.1	2	1		1.4E-01 AF009663.1	1.4E-01 D78638.1	1.4E-01 T91864.1	TN 0866799	1.4E-01 AE001710.1	1.4E-01 AW135741.1	1.4E-01 AA720615.1	P30706
	Most Similar (Top) Hit BLAST E Value	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5Ë-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01	1.4E-01 P30706
	Expression Signal	1.71	2.48	2.98	9.9	7.02	7.02	2.86	2.45	2.45	1.54	1.35	1.35	5.15	5.15	1.74	1.73	2.17	20.02	4.14	2.14	3.99	3.01	1.58	1.96	2.57	1.62	1.43	1.53	0.94	10.35	76.0
	ORF SEQ ID NO:	27200	27335		26641	27781	27782	27955	27998	27999	28031	28103	28104	28334	28335		28555	26396				25133	25179						21487			22199
	Exan SEQ ID NO:	17007	17142	17182	16451	17556	17556	17710	17758	17758	17789	17859	17859	18084	18084	18219	18299	16236	19547	19565	19588	19497		19432	10260	10818	11145	11615	11618	11759	11837	12303
	Probe SEQ ID NO:	7130	7265	7306	7438	27706	27706	7860	8062	7908	7939	6008	8008	8199	8199	8342	8425	9058	6606	9531	9621	9726	9932	9972	296	892	1238	1714	1717	1863	1942	2426

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Single Exon Probes Expressed in Heart

			1				
Probe SEQ ID	Exon SEO ID	ORF SEQ	Expression	Most Similar (Top) Hit	Top Hit Acession	Top Hit Database	Top Hit Descriptor
S S S	OZ	D NO:	Signa	BLAST E Value	o Z	Source	
2762	12624	22517	3.07	1.4E-01	1.4E-01 AI933496.1	EST HUMAN	wm74d01.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2441665 3'
3823	13735	23524	1	1.4E-01	1.4E-01 R59232.1	EST HUMAN	yg97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
3823	13735	23525	1	1.4E-01	1.4E-01 R59232.1	EST_HUMAN	yg97a03.r1 Soares infant brain 1NIB Homo saplens cDNA clone IMAGE:41467 5'
4083	13985	23762	8.38	1.4E-01		EST_HUMAN	tx56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4083	13985	23763	8.38	1.4E-01	1.4E-01 AI699094.1	EST_HUMAN	tx56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE.2273570 3
4144	14044		3.16	1.4E-01	1.4E-01 AE001710.1	LN	Thermotoga maritima section 22 of 136 of the complete genome
							zj50b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to
				_			gb:X01057_ma1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);contains Alu
4313	14210		0.8	1.4E-01	1.4E-01 AA776287.1	EST_HUMAN	repetitive element;
5032	14904		0.91	1.4E-01	1.4E-01 AW866022.1	EST HUMAN	QV3-SN0022-100500-186-h09 SN0022 Homo sapiens cDNA
5116	14984	24759	1	1.4E-01	1.4E-01 AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2147	15014	24784	0.81	1.4E-01	1.4E-01 AJ005180.1	NT	Lycopersicon esculentum genomic RAPD band 26
5248	15171	24944	4.5	1.4E-01	1.4E-01 T90677.1	EST_HUMAN	ye15c11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5267	15189	24963	4.29	1.4E-01	1.4E-01 AB004556.1	N	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5267	15189		4.29	1.4E-01	1.4E-01 AB004556.1	Z	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate detrydrogenase, complete cds
5805	15710	25823	2.72	1.4E-01	1.4E-01 BE326891.1	EST_HUMAN	hr67c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
2903	15809	25934	5.64	1.4E-01	1.4E-01 AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sepiens cDNA clone HEMBA1000769 5'
5903	l'	25935	5.64	1.4E-01	1.4E-01 AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
2958	15863	25985	3.07	1.4E-01	1.4E-01 AW082796.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3
2969	15874		1.56	1.4E-01	1.4E-01 BE266536.1	EST HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
2885	15887	26009	1.89	1.4E-01	1.4E-01 BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-d09 UM0036 Homo sapiens cDNA
6371	16233		1.62	1.4E-01	1.4E-01 AW015373.1	EST_HUMAN	UI-H-BI0-eat-c-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
9869	16814		1.33	1.4E-01	1.4E-01 AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3'
7167	17044	27236	4.48	1.4E-01	1.4E-01 AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Hono sapiens cDNA 5' end
7300	17176	27377	8.05	1.4E-01	1.4E-01 BF310959.1	EST_HUMAN	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
							zd94a04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102.5' similar to contains
7343	17211	27410	1.36	1.4E-01	1.4E-01 W93411.1	EST_HUMAN	element KER repetitive element;
7387	17256	27461	1.56	1.4E-01	1.4E-01 Y10196.1	INT	Homo saplens PHEX gene
7387	17256	27462	1.56	1.4E-01	1.4E-01 Y10196.1	Z	Homo sapiens PHEX gene
							Drosophila melanogaster signal transducting adaptor protein (STAM), serine threonine kinase lal (IAL), and
7436	16449	26639		1.4E-01	1.4E-01 AF121361.1	NT	zinc finger protein (DNZ1) genes, complete cds
8091	17982		2.02	1.4E-01	1.4E-01 AA811480.1		oa99a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
8216	18100	28352	3.28	1.4E-01	1.4E-01 R53400.1	EST HUMAN	y/70c05.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154088 5'
8613	18480	28751	1.89	1.4E-01	1.4E-01 X66092.1	TN	C.perfringens ORF for putative membrane transport protein

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Tcp Hit Database Source	 Top Hit Doscriptor
8764	17913	28158	2.23		1.4E-01 U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
8813	18626		3.02		1.4E-01 X52102.1	NT	M.musculus p16K gene for 16 kDa protein
9365	19517	25138	1.48		1.4E-01 AB000890.1	IN	Ephydatia fluviatilis mRNA for aldolase, partial cds
9413	19065	25277			1.4E-01 X74773.1	TN	P.salina plastid gene secY
9427	19073		1.89		11968117 NT	IN	Rattus norvegicus desmin (Des), mRNA
9470	19734		1.82		1.4E-01 BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
							Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycinamide ribonucleotide
9560	19156		3.01	1.4E-01	1.4E-01 AF083221.1	NT	transformylase (GART) genes, complete cds
9573	19163		2.29		1.4E-01 D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
9646	19754		3.28	1.4E-01 P10447	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
9762	19282		1.41		1.4E-01 BE782738.1	EST_HUMAN	601465575F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868795 5'
9831	19332		1.42	1.4E-01	11425031 NT	Z	Homo sapiens ephrin-B3 (EFNB3), mRNA
9850	19566		3.41	1.4E-01	D82983.1	N	Mus musculus mRNA for prolidase, complete cds
9356	19398		1.77	1.4E-01	AW377998	EST_HUMAN	MR0-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
319	10281	20098	2.69	1.3E-01	4758467 NT	Ę	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
319	10281		2.69		4758467 NT	뉟	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
518	10460	20271	1.86		1.3E-01 AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
620	10557	20369	08.0		1.3E-01 AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
	L						
620					1.3E-01 AJ277606.1	Z	Human calictvirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
820					1.3E-01 X53330.1	Z	r. aumerilli ristane gene cluster for care nistanes HZA, HZB, H3 and H4
876		20852			1.3E-01 AF139518.1	L _N	Kattus norvegicus A-kinase anchor protein mRNA, complete cds
1010	10928				1.3E-01 AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1111	11026		2.23		1.3E-01 AL115265.1	ΝŢ	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1197	11107	20952	1.07		1.3E-01 AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'
1426	11331				1.3E-01 AF146277.1	NT -	Homo sapiens adapter protein CMS mRNA, complete cds
1916	11811	21689	2.56		1.3È-01 AL117078.1	۲	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2124	12012		1.29		1.3E-01 AJ243578.1	LN	Rhodopseudomonas acidophila pucB5, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151
2245	12129		1.17		1.3E-01 AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2329	L.		2.99		1.3E-01 AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2542	12416	22306	3.49		1.3E-01 M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds

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Single Exon Probes Expressed in Heart	Most Similar Top Hit Acession Top Hit Descriptor Top Hit Descriptor Source		1.3E-01 AP000001.1 NT	1.3E-01 AP000001.1 NT	1.3E-01 AB032159.1 NT	1.3E-01 AP000001.1 NT Pyrococus horikoshii OT3 genomic DNA, 1-287000 nt position (1/7)	1.3E-01 AP000001,1 NT	1.3E-01 6978840 NT	1.3E-01 AL161581.2 NT	1.3E-01 AF020713.1 NT	1.3E-01 AW364341.1 EST HUMAN	1.3E-01 AF026805.1 NT	1.3E-01 AW273741.1 EST HUMAN	1.3E-01 AV752279.1 EST_HUMAN	1.3E-01 AV752279.1 EST_HUMAN	1.3E-01 AL163280.2 NT	1.3E-01 BE272339.1 EST_HUMAN	1.3E-01 BF679654.1 EST_HUMAN	1.3E-01 BE884017.1 EST HUMAN	1.3E-01 AU136619.1 EST_HUMAN	1.3E-01 AL163284.2 NT	1.3E-01 AL163284.2 NT	1.3E-01 BF679819.1 EST_HUMAN	1.3E-01 BF679819.1 EST_HUMAN	1.3E-01 AW804417.1 EST HUMAN	1.3E-01 AF056880.1 NT	1.3E-01 AB031326.1 NT	1.3E-01 X88891.1 NT	H48664.1 EST_HUMAN	1.3E-01 11423294 NT	1.3E-01 BF690522.1 EST_HUMAN	1.3E-01 Z74102.1 NT	1.3E-01 8923919 NT	1.3E-01 BF690522.1 EST_HUMAN	1.3E-01 AF023129.1 NT
		1.3E-01 M2157	1.3E-01 AP000	1.3E-01 AP000	1.3E-01 AB032	1.3E-01 AP000	1.3E-01 AP000	1.3E-01	1.3E-01 AL161	1.3E-01 AF020	1.3E-01 AW36	1.3E-01 AF026	1.3E-01 AW27;	1.3E-01 AV752	1.3E-01 AV752	1.3E-01 AL163;	1.3E-01 BE272	1.3E-01 BF679	1.3E-01 BE884	1.3E-01 AU136	1.3E-01 AL163;	1.3E-01 AL163;	1.3E-01 BF679	1.3E-01 BF679	1.3E-01 AW804	1.3E-01 AF056	1.3E-01 AB031	1.3E-01 X88891	1.3E-01 H4866	1.3E-01	1.3E-01 BF690	1.3E-01 Z74102	1.3E-01	1.3E-01 BF690	1.3E-01 AF0231
	Expression Signal	0.95	1.18	1.18	0.78	0.86	0.86	0.85	1.7	1.15	3.44	1.89	16.36	0.85	0.85	1.65	2.16	0.81	3.17	0.86	1.21	1.21	6.0	0.0	2.51	1.79	13.21	2.04	2	1.34	1.28	4.54	4.14	1.27	4.45
	ORF SEQ ID NO:							23431										24202						24806	25013	1	25936	25983		26723	26744			27031	27467
	Exon SEQ ID NO:	13321	13575	13575	13581	13575	13575	13646	13816	13948	13968	13977	13993	14092	14092	14116	14328	14418	15075	14783	14944	14944	15039	15039	15213	15348	15810	15861	16169	16529	16548	16737	16765	16838	17261
	Probe SEQ ID NO:	3404	3661	3661	3667	3714	3714	3734	3906	4046	4066	4075	4093	4192	4192	4218	4433	4525	4771	4903	5074	5074	5173	5173	5292	5428	5904	5956	6305	6649	8999	6858	9889	0969	7452

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Single Exon Probes Expressed in Realt	Top Hit Descriptor	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)	QV1-BT0259-261099-021-d05 BT0259 Homo saplens cDNA	Methanococcus jannaschii section 142 of 150 of the complete genome	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053668 3'	P.clarkii mRNA; repeat region (ID 2MRT7)	P.clarkii mRNA; repeat region (ID 2MRT7)	HEMOLYSIN PRECURSOR	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME I	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME I	UI-HF-BK0-aah-d-01-0-UI.r1 NIH_MGC_36 Horno sapiens cDNA clone IMAGE:3053617 5'	zc08d02.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'	Homo sapiens gene encoding plakophilin (exons 1-13)	601493518F1 NIH_MGC_70 Home sapiens cDNA clone IMAGE:3895613 5'	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA	Mouse galactosyltransferase mRNA, complete cds	PM3-BN0137-290300-002-f09 BN0137 Homo sapiens cDNA	wc99g03.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN Q99735 MICROSOMAL CLUTATHIONE S-ȚRANSFERASE II;	xc49d07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A	(HUMAN);	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds, and transcriptional	regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds	Haemophilus influenzae Rd section 29 of 163 of the complete genome	S.cerevisiae HXT5 gene	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5'	Yeast MPT5 gene for suppressor protein, complete cds	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'	Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17
e Exon Propes	Top Hit Database Scurce	NT	EST_HUMAN OV	NT	NT Bac	NT Wh	NT Wh	NT Bac	T_HUMAN_	NT P.c	NT P.c	SWISSPROT HE	SWISSPROT HY	SPROT	HUMAN	EST_HUMAN zco	NT	HUMAN	EST_HUMAN 1L0	NT	EST_HUMAN PM	WCST_HUMAN Q9		EST HUMAN (HI	Sta	NT reg	NT	NT S.c	EST_HUMAN AV	NT Ye	EST HUMAN 60	T_HUMAN	NT
Buic	Top Hit Acession No.	1.2E-01 X56882.1	1.2E-01 AW370668.1	1.2E-01 U67600.1			1.2E-01 X56882.1		1.1						1.2E-01 AW 401836.1		1.2E-01 Z98266.1		1.2E-01 AW845275.1	1.2E-01 M26925.1	1.2E-01 BE007072.1	1.2E-01 Al913753.1		1.2E-01 AW083652.1		1.2E-01 AF053772.1	1.2E-01 U32714.1	1.2E-01 X77961.1	7.1	1.2E-01 D26184.1			1.2E-01 AF190493.1
	Most Similar (Top) Hit BLAST E Value	1.2E-01	1.2E-01	1.2E-01	1.2E-01 Z99118.1	1.2E-01	1.2E-01	1.2E-01 Z99118.1	1.2E-01	1.2E-01 Z54255.1	1.2E-01 Z54255.1	1.2E-01 P16466	1.2E-01 Q10441	1.2E-01 Q10441	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01		1.2E-01		1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01
	Expression Signal	86.0	2	76.0	0.79	1.14	1.14	1.2	0.88	2.2	2.2	1.04	1.47	1.47	2.47	2.63	1.9	1.69	2.19	1.56	1.21	2.46		9.72		3.86	2.27	1.5	1.51	2.95	3.35	1.93	2.6
	ORF SEQ ID NO:	22700	22923			23198	23199			23766	23767		24807	24808		24947	25021	25776	25824	25858		26715						27546	27819				28715
	Exon SEQ ID NO:	12901	13117	13143	13350	13393	13393	13350	13617	13990	13990	14886	15040	15040	15062	15174	15218	15669	15711	15745	16487	16522		16772		16782	16920	17340	17597	18140	18291		18447
	Probe SEQ ID NO:	2974	3192	3219	3433	3477	3477	3554	3704	4090	4090	5012	5174	5174	5199	5251	5297	5762	5806	5839	6607	6642		6893		6904	7043	7521	7747	8260	8417	8487	8579

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Single Exon Probes Expressed in Heart

Product (2010) Exam (2010) Exam (2010) Top Hill (2014) Top Hill Acession (2014) Top Hill Acession (2014) Top Hill Acession (2014) Top Hill Acession (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descriptor (2014) Top Hill Descri	-	-					
18612 2.02 1.2E-01 AV58033.1 NT 18822 2.22 1.2E-01 AV58033.1 EST_HUMAN 19683 2.4897 2.58 1.2E-01 AV58033.1 NT 19683 2.4897 2.58 1.2E-01 AF039442.1 NT 10476 7.69 1.2E-01 AF039442.1 NT 19200 1.41 1.2E-01 AF039442.1 NT 19706 24903 2.36 1.2E-01 AF039442.1 NT 19706 24903 2.36 1.2E-01 AF03942.1 NT 19706 24903 2.36 1.2E-01 AF03942.1 NT 19706 24903 2.36 1.2E-01 AF03903.1 EST_HUMAN 19285 2.07 1.2E-01 BE061418.1 EST_HUMAN 19424 2.18 1.2E-01 BE06103.1 EST_HUMAN 10536 2.07 1.1E-01 AM997138.1 EST_HUMAN 10540 1.1E-01 AM997138.1 EST_HUMAN 11408 2.12E-01 BE067308.1 EST_HUMAN 1250 1.1E-01 AW972168.1 EST_HUMAN			Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
18822 2.22 1.2E-01 AV658033.1 EST_HUMAN 19043 2.78 1.2E-01 AJ271736.1 NT 19043 2.4897 2.58 1.2E-01 AJ271736.1 NT 190476 7.69 1.2E-01 AG59442.1 NT NT 19230 2.4897 2.58 1.2E-01 AG59442.1 NT 19230 2.4803 2.36 1.2E-01 BE061418.1 EST_HUMAN 19285 2.5231 3.68 1.2E-01 AL729043.1 EST_HUMAN 19424 2.07 1.2E-01 BE061418.1 EST_HUMAN 10455 2.0301 0.95 1.1E-01 AB61003.1 EST_HUMAN 10546 2.0303 0.95 1.1E-01 AB69006.1 EST_HUMAN 1056 2.0304 3.38 1.1E-01 AA658006.1 EST_HUMAN 1056 2.0304 1.53 1.1E-01 AA658006.1 EST_HUMAN 1056 2.0305 1.1E-01 AA972168.1 EST_HUMAN	1	3612	2.02			LN	Rabbit glycogen-essociated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
19643 2.78 1.2E-01 AJ271736.1 NT 19693 24897 2.58 1.2E-01 AG9942.1 NT 19730 1.2E-01 AG99442.1 NT NT 19230 24903 2.36 1.2E-01 AG99442.1 NT 19230 24903 2.36 1.2E-01 AG9941.1 NT 19281 25231 3.68 1.2E-01 AG9903.1 EST_HUMAN 19265 2.07 1.2E-01 L10187.1 NT 19424 2.0301 0.95 1.1E-01 AB61003.1 EST_HUMAN 10453 20304 3.38 1.1E-01 AB61003.1 EST_HUMAN 10540 20709 1.53 1.1E-01 AB61003.1 EST_HUMAN 10556 20709 1.53 1.1E-01 AB69006.1 EST_HUMAN 10556 20709 1.53 1.1E-01 AB69006.1 EST_HUMAN 1056 20500 1.72 1.1E-01 AB69006.1 EST_HUMAN		3822	2.22			I. II	AV658033 GLC Homo sapiens cDNA clone GLCFIB12 3'
19693 24897 2.58 1.2E-01 AC04912 SWISSPROT 10476 769 1.2E-01 AF033442.1 NT 19230 1.41 1.2E-01 AF033442.1 NT 19230 2.36 1.2E-01 AF03344.1 EST_HUMAN 19231 2.5231 3.68 1.2E-01 AI29903.1 EST_HUMAN 19242 2.07 1.2E-01 BF06148.1 EST_HUMAN 19424 2.07 1.2E-01 BF06148.1 EST_HUMAN 10483 2.0301 0.95 1.1E-01 AA569006.1 EST_HUMAN 10463 2.0209 1.72 1.1E-01 AA569006.1 EST_HUMAN		3043	2.78			NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
19476 7.69 1.2E-01 AF039442.1 NT 19706 24903 2.36 1.2E-01 K53981.1 NT 19706 24903 2.36 1.2E-01 BE061418.1 EST_HUMAN 19285 2.07 1.2E-01 A172 EST_HUMAN 19424 2.07 1.2E-01 BF314481.1 EST_HUMAN 10453 20301 0.95 1.1E-01 A4568008.1 EST_HUMAN 10586 20769 1.53 1.1E-01 A4568008.1 EST_HUMAN 10885 20304 3.38 1.1E-01 A4568008.1 EST_HUMAN 10886 20769 1.53 1.1E-01 A4568008.1 EST_HUMAN 1137 20890 4.06 1.1E-01 A4668008.1 EST_HUMAN 12085 20890 1.72 1.1E-01 AW972158.1 EST_HUMAN 12085 20690 1.77 1.1E-01 AW972158.1 EST_HUMAN 12085 2.254 1.1E-01 AW821609.1 EST_HUMAN <td></td> <td></td> <td></td> <td></td> <td>Q04912</td> <td>SWISSPROT</td> <td>MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)</td>					Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
19230 1.41 1.2E-01 K53981.1 INT 19706 24903 2.36 1.2E-01 BE061418.1 EST HUMAN 19281 25231 3.68 1.2E-01 L10187.1 INT 19295 2.07 1.2E-01 L10187.1 INT 19424 2.03 4.72 1.2E-01 BF814481.1 EST HUMAN 10493 2.0301 0.95 1.1E-01 BF814481.1 EST HUMAN 10535 2.0344 3.38 1.1E-01 AB568006.1 EST HUMAN 10985 2.0769 1.53 1.1E-01 AB68006.1 EST HUMAN 12086 2.0769 1.53 1.1E-01 AL161580.2 INT 1408 2.1267 2.25 1.1E-01 AW972158.1 EST HUMAN 12080 1.72 1.1E-01 AW972158.1 INT 12254 1.17 1.1E-01 AW9821909.1 EST HUMAN 12254 1.15 1.1E-01 AW821909.1 EST HUMAN					-	NT	Homo saplens colon cancer antigen NY-CO-45 mRNA, partial cds
19706 24903 2.35 1.2E-01 BE061418.1 EST HUMAN 19281 25231 3.68 1.2E-01 AI299003.1 EST HUMAN 19295 2.07 1.2E-01 L10187.1 NT 19424 2.18 1.2E-01 BF314481.1 EST HUMAN 19424 2.18 1.2E-01 BF314481.1 EST HUMAN 10536 20301 0.95 1.1E-01 AA569006.1 EST HUMAN 10586 20799 1.53 1.1E-01 AA569006.1 EST HUMAN 10586 20799 1.53 1.1E-01 AW972158.1 EST HUMAN 11137 20890 1.72 1.1E-01 AW972158.1 EST HUMAN 1250 2.25 1.1E-01 AW972158.1 EST HUMAN 12750 2.25 1.1E-01 AW972158.1 EST HUMAN 12751 2.25 1.1E-01 AW821509.1 EST HUMAN 12754 2.25 1.1E-01 AW821509.1 EST HUMAN 12754 1.34 1.1E-01 AW821509.1 EST HUMAN 12754 2.25 1.1E-01 AW821909.1 EST HUMAN		9230	1.41	1.2E-01		LN LN	R.norvegicus NF68 gene for 68kDa neurofilament
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19636 4.72 1.2E-01 O96433 SWISSPROT 19424 2.18 1.2E-01 BF314481.1 EST_HUMAN 10493 20301 0.95 1.1E-01 AA569006.1 EST_HUMAN 10586 20799 1.53 1.1E-01 BF697308.1 EST_HUMAN 10986 20799 1.53 1.1E-01 AA569006.1 EST_HUMAN 11070 20899 4.06 1.1E-01 AW972158.1 EST_HUMAN 11137 20990 1.72 1.1E-01 AW972158.1 EST_HUMAN 12150 2.247 1.1E-01 AW972158.1 EST_HUMAN 12150 2.25 1.1E-01 AW972158.1 EST_HUMAN 12754 2.25 1.1E-01 AW821509.1 EST_HUMAN 12754 2.25 1.1E-01 AW821609.1 EST_HUMAN 12294 1.17 1.1E-01 AW821609.1 EST_HUMAN 12254 1.25 1.1E-01 AW821609.1 EST_HUMAN 13221 0.8		3295	2.07		L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
19424 2.18 1.2E-01 BF314481.1 EST HUMAN 10493 20301 0.95 1.1E-01 AA569006.1 EST HUMAN 10536 20344 3.38 1.1E-01 BF697308.1 EST HUMAN 10956 20799 1.53 1.1E-01 BF697308.1 EST HUMAN 10985 20899 4.06 1.1E-01 AW972158.1 EST HUMAN 11137 20890 1.72 1.1E-01 AW972158.1 EST HUMAN 12150 2.247 1.1E-01 AW972158.1 EST HUMAN 1250 1.25 1.1E-01 AW972158.1 INT 1256 2.25 1.1E-01 AW972158.1 INT 1256 2.25 1.1E-01 AW921609.1 EST HUMAN 12754 2.25 1.1E-01 AW821609.1 INT 12754 1.34 1.1E-01 AW821609.1 INT 12754 2.25 1.1E-01 AW821609.1 INT 13221 0.8 1.1E-01 <td< td=""><td></td><td>9636</td><td>4.72</td><td></td><td>096433</td><td>SWISSPROT</td><td>CYCLIN T</td></td<>		9636	4.72		096433	SWISSPROT	CYCLIN T
10493 20301 0.95 1.1E-01 AA569006.1 EST HUMAN 10536 20344 3.38 1.1E-01 AA569006.1 EST HUMAN 10956 20799 1.53 1.1E-01 BF697308.1 EST HUMAN 10985 20899 4.06 1.1E-01 AW972158.1 EST HUMAN 11137 20890 1.72 1.1E-01 AW972158.1 EST HUMAN 12150 2.247 1.1E-01 AW972158.1 EST HUMAN 12150 2.25 1.1E-01 AW972158.1 INT 12267 2.25 1.1E-01 AW972158.1 INT 12394 1.17 1.1E-01 AW821609.1 EST HUMAN 12754 2.25 1.1E-01 AW821609.1 EST HUMAN 12754 1.39 1.1E-01 AW821609.1 EST HUMAN 13221 0.8 1.1E-01 AW821609.1 EST HUMAN 13222 2.25717 0.8 1.1E-01 AW821960.1 EST HUMAN 13223 2		3424	2.18		BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5
10535 20344 3.38 1.1E-01 AA569006.1 EST_HUMAN 10956 20799 1.53 1.1E-01 BF697308.1 EST_HUMAN 10985 1.29 1.1E-01 AL161560.2 NT 1137 20899 4.06 1.1E-01 AW972158.1 EST_HUMAN 11408 21267 2.47 1.1E-01 AW972158.1 EST_HUMAN 1250 1.72 1.1E-01 AW972158.1 EST_HUMAN 12750 2.25 1.1E-01 AW972158.1 INT 12751 2.25 1.1E-01 AW821909.1 EST_HUMAN 12754 2.25 1.1E-01 AW821909.1 EST_HUMAN 12754 2.25 1.1E-01 AW821909.1 EST_HUMAN 13221 0.8 1.1E-01 F675251 INT 13224 0.8 1.1E-01 F675251 INT 1322 23123 1.54 1.1E-01 F675251 INT 13450 23246 0.94 1.1E-01					AI561003.1	EST_HUMAN	tn18d08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167983 3'
10535 20344 3.38 1.1E-01 AA569006.1 EST_HUMAN 10956 20799 1.53 1.1E-01 AA569006.1 EST_HUMAN 10985 1.29 1.1E-01 AL161560.2 NT 12866 20899 4.06 1.1E-01 AW972158.1 EST_HUMAN 11137 20990 1.72 1.1E-01 D64004.1 NT 11408 21267 2.47 1.1E-01 AU140363.1 EST_HUMAN 1250 1.72 1.1E-01 AU140363.1 EST_HUMAN 1250 2.25 1.1E-01 AU140363.1 EST_HUMAN 12754 2.25 1.1E-01 AW821609.1 EST_HUMAN 12754 2.2546 1.84 1.1E-01 AW821609.1 EST_HUMAN 13221 0.8 1.1E-01 F03265.1 EST_HUMAN 13222 22717 0.8 1.1E-01 F03265.1 EST_HUMAN 13223 23248 1.1E-01 F03265.1 INT 13450 23246 0.94 1.1E-01 W07695.1 INT 1362 23348 1.23 1.1E-01 W07695.1 <t< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td>rim08g11.s1 NOL CGAP Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_rna1</td></t<>							rim08g11.s1 NOL CGAP Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_rna1
10956 20799 1.53 1.1E-01 BF697308.1 EST HUMAN 10985 1.29 1.1E-01 AL161560.2 NT 12886 20899 4.06 1.1E-01 AW972158.1 EST HUMAN 11137 20990 1.72 1.1E-01 D64004.1 NT 12653 1.72 1.1E-01 AW972158.1 EST HUMAN 12750 2.25 1.1E-01 AU140363.1 EST HUMAN 12754 2.25 1.1E-01 AV821609.1 EST HUMAN 12754 2.2546 1.84 1.1E-01 AW821609.1 EST HUMAN 12754 2.2546 1.84 1.1E-01 AW821609.1 EST HUMAN 13221 0.8 1.1E-01 AW821609.1 EST HUMAN 13222 22717 0.8 1.1E-01 AW821609.1 EST HUMAN 13223 232092 3 1.1E-01 AW819412.1 NT 13450 23248 1.23 1.1E-01 AW819412.1 NT 13925 23698 1.31 1.1E-01 AW819412.1 EST HUMAN 13926 23699 1.31 1.					AA569006.1	EST HUMAN	HEME OXYGENASE 1 (HUMAN);
10985 1.29 1.1E-01 AL161560.2 NT 12686 20899 4.06 1.1E-01 AW972158.1 EST HUMAN 11137 20990 1.72 1.1E-01 D64004.1 NT 11408 21267 2.47 1.1E-01 AU140363.1 EST HUMAN 1250 2.25 1.1E-01 AU140363.1 EST HUMAN 1254 2.25 1.1E-01 AW821809.1 EST HUMAN 12754 22546 1.34 1.1E-01 AW821809.1 EST HUMAN 12754 22546 1.84 1.1E-01 AW821809.1 EST HUMAN 13221 0.8 1.1E-01 AW821809.1 EST HUMAN 13222 22717 0.8 1.1E-01 AW821809.1 INT 13223 23092 3 1.1E-01 AW82180.1 INT 13450 23246 0.94 1.1E-01 AW819412.1 INT 1362 23698 1.31 1.1E-01 AW819412.1 EST HUMAN 13926 23699 1.31 1.1E-01 AW819412.1 EST HUMAN			`		BF697308.1	EST_HUMAN	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5
12686 20899 4.06 1.1E-01 AW972158.1 EST HUMAN 11137 20990 1.72 1.1E-01 D64004.1 NT 11408 21267 2.47 1.1E-01 AD140363.1 EST HUMAN 12503 2.25 1.1E-01 6756215 NT 12754 22546 1.1E-01 AW821809.1 EST HUMAN 12754 22546 1.84 1.1E-01 S82418.1 NT 13221 0.8 1.1E-01 F03265.1 EST HUMAN NT 13222 22717 0.8 1.1E-01 F03265.1 EST HUMAN 13223 23092 3 1.1E-01 F03265.1 EST HUMAN 13283 23092 3 1.1E-01 F03265.1 NT 13450 23246 0.94 1.1E-01 NT NT 1362 23348 1.23 1.1E-01 NT NT 1362 23698 1.31 1.1E-01 NW819412.1 EST HUMAN						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
11137 20990 1.72 1.1E-01 D64004.1 NT 11408 21267 2.47 1.1E-01 AU140363.1 EST HUMAN 12150 2.25 1.1E-01 6756215 NT 12653 1.17 1.1E-01 6978676 NT 12394 1.17 1.1E-01 6978676 NT 12754 22546 1.84 1.1E-01 882418.1 NT 13221 0.8 1.1E-01 F03265.1 EST HUMAN NT 13221 0.8 1.1E-01 F03265.1 EST HUMAN NT 13222 22717 0.8 1.1E-01 F03265.1 NT 13283 23092 3 1.1E-01 F03265.1 NT 13450 23246 0.94 1.1E-01 Y07695.1 NT 1362 23348 1.23 1.1E-01 X62708.1 NT 13926 23698 1.31 1.1E-01 X678132.1 EST HUMAN 13926					1	EST_HUMAN	EST384142 MAGE resequences, MAGL Homo saplens cDNA
11408 21267 2.47 1.1E-01 AU140363.1 EST HUMAN 12150 2.25 1.1E-01 6756215 NT 12534 1.17 1.1E-01 6978676 NT 12754 22546 1.84 1.1E-01 882418.1 NT 1221 0.8 1.1E-01 82418.1 NT NT 13221 0.8 1.1E-01 675323.1 NT 13283 23092 3 1.1E-01 8533186.1 EST HUMAN 13280 23246 0.94 1.1E-01 X62135.1 NT 13562 23348 1.23 1.1E-01 X62135.1 NT 13562 23348 1.23 1.1E-01 X62135.1 NT 13652 23598 1.31 1.1E-01 X6203.1 NT 13925 23698 1.31 1.1E-01 X62135.1 NT 13926 23698 1.31 1.1E-01 X62132.1 ST HUMAN					D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
12150 2.25 1.1E-01 6756215 NT NT 12653 1.17 1.1E-01 6978676 NT NT 12394 1.17 1.1E-01 6978676 NT NT 12754 22546 1.84 1.1E-01 882418.1 NT 13221 1.39 1.1E-01 F03265.1 EST HUMAN NT 13223 23092 3 1.1E-01 F03265.1 EST HUMAN 13322 23123 1.54 1.1E-01 RE393186.1 EST HUMAN 13450 23246 0.94 1.1E-01 W07695.1 NT 13622 23348 1.23 1.1E-01 W07695.1 NT 1362 235698 1.31 1.1E-01 WW1919412.1 EST HUMAN 13926 23699 1.31 1.1E-01 AW819412.1 EST HUMAN							AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
12653 1.17 1.1E-01 6978676 NT 12394 1.17 1.1E-01 AW821909.1 EST HUMAN 12754 22546 1.84 1.1E-01 S82418.1 NT 13221 0.8 1.1E-01 F03265.1 EST HUMAN EST HUMAN 13223 23092 3 1.1E-01 ES33186.1 EST HUMAN 13322 23123 1.54 1.1E-01 X62135.1 NT 13450 23246 0.94 1.1E-01 Y07695.1 NT 13622 23348 1.23 1.1E-01 X62708.1 NT 13926 23698 1.31 1.1E-01 X62708.1 NT 13926 23698 1.31 1.1E-01 XM819412.1 EST HUMAN		2150	2.25		6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA
12394 1.17 1.1E-01 AW821909.1 EST HUMAN 12754 22546 1.84 1.1E-01 S82418.1 NT 12925 22717 0.8 1.1E-01 F03265.1 EST HUMAN 13221 1.39 1.1E-01 F03265.1 EST HUMAN 13222 23123 1.54 1.1E-01 RE393186.1 EST HUMAN 13450 23246 0.94 1.1E-01 Y07695.1 NT 13662 23348 1.23 1.1E-01 X52708.1 NT 13926 23698 1.31 1.1E-01 AW819412.1 EST HUMAN 13926 23699 1.31 1.1E-01 AW819412.1 EST HUMAN		2653	1.17		6978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
12754 22546 1.84 1.1E-01 582418.1 NT 12925 22717 0.8 1.1E-01 F03265.1 EST HUMAN 13221 1.39 1.1E-01 F6753231 NT 13293 23092 3 1.1E-01 BE393186.1 EST HUMAN 13450 23246 0.94 1.1E-01 Y07695.1 NT 13562 23348 1.23 1.1E-01 X52708.1 NT 13925 23698 1.31 1.1E-01 AW819412.1 EST HUMAN 13926 23699 1.31 1.1E-01 AW819412.1 EST HUMAN					-		RC0-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
12925 22717 0.8 1.1E-01 F03265.1 EST HUMAN 13221 1.39 1.1E-01 6753231 NT 13293 23092 3 1.1E-01 BE393186.1 EST HUMAN 13322 23123 1.54 1.1E-01 X62135.1 NT 13450 23246 0.94 1.1E-01 Y07695.1 NT 13562 23348 1.23 1.1E-01 X52708.1 NT 13925 23698 1.31 1.1E-01 AW819412.1 EST HUMAN 13926 23699 1.31 1.1E-01 AW819412.1 EST HUMAN			,			NT	interleukin-12 p35 subunit [mice, Genomic, 700 nt, segment 4 of 5]
13221 1.39 1.1E-01 6753231 NT 13293 23092 3 1.1E-01 BE393186.1 EST_HUMAN 13322 23123 1.54 1.1E-01 X62135.1 NT 13450 23246 0.94 1.1E-01 Y07695.1 NT 13562 23348 1.23 1.1E-01 X52708.1 NT 13925 23698 1.31 1.1E-01 AW819412.1 EST_HUMAN 13926 23699 1.31 1.1E-01 AW819412.1 EST_HUMAN	l'				F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
13293 23092 3 1.1E-01 BE393186.1 EST HUMAN 1332 23123 1.54 1.1E-01 X62136.1 NT 13450 23246 0.94 1.1E-01 Y07695.1 NT 13562 23348 1.23 1.1E-01 X52708.1 NT 13925 23698 1.31 1.1E-01 AW819412.1 EST HUMAN 13925 23699 1.31 1.1E-01 AW819412.1 EST HUMAN		3221	1.39		6753231	F	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
13322 23123 1.54 1.1E-01 X62135.1 NT C.reinhardtil nuclear gene on linkage group XIX 13450 23246 0.94 1.1E-01 Y07695.1 NT A.immersus gene for transposase 13562 23348 1.23 1.1E-01 X52708.1 NT G.gallus gene encoding non-histone chromosomal protein HMG-14b, 13925 23698 1.31 1.1E-01 AW819412.1 EST_HUMAN MR3-ST0290-290100-025-907 ST0290 Homo sapiens cDNA					BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5
13450 23246 0.94 1.1E-01 N07695.1 NT A.immersus gene for transposase 13562 23348 1.23 1.1E-01 X52708.1 NT Gaallus gene encoding non-histone chromosomal protein HMG-14b, 13925 23698 1.31 1.1E-01 AW819412.1 EST_HUMAN MR3-ST0290-290100-025-907 ST0290 Homo sapiens cDNA 13926 1.31 1.1E-01 AW819412.1 EST_HUMAN MR3-ST0290-290100-025-907 ST0290 Homo sapiens cDNA					X62135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
13925 23698 1.31 1.1E-01 AW819412.1 NT G gallus gene encoding non-histone chromosomal protein HMG-14b, MR3-ST0290-290100-025-907 ST0290 Homo sapiens cDNA 13925 23698 1.31 1.1E-01 AW819412.1 EST_HUMAN MR3-ST0290-290100-025-907 ST0290 Homo sapiens cDNA					Y07695.1	LN	A.immersus gene for transposase
13925 23698 1.31 1.1E-01 AW819412.1 EST_HUMAN 13926 23699 1.31 1.1E-01 AW819412.1 EST_HUMAN						NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
13925 23699 1.31 1.1E-01/AW819412.1 EST_HUMAN					AW819412.1	EST HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
	Ш		-		AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Heart

	Top Hit Descriptor	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, Iysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2). CREB-RP, and tenascin X (TNX) genes, complex	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSR1 protein (WSB1) genes, complete cds	The second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of th	l apa-1=integral membrane protein TATA-1 [integ. D cell jumphonis integral cont.]	A.immersus gene for transposase	Synechocystis sp. PCCb803 complete genome, 10/27, 1100000-1011204	nx76a03.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone iMAGE:1208140 similar to contains Aug repentive element.contains element MER35 repetitive element;	S nombe ste8 dene encoding profein kinase	Providencia retroeri penicillin G amidase gene	The sections I CAN The representations and the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the sections of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of th	HOMO Sapiens LOWIDZD gard	M3-F10024-13000-004-112-10024-10110-34201	RC3-C10254-2809999-011-a01 C10234 from sapiens CDNA clone R1 43	AF035/46 Human salaray gland cell intel 150 i dino saprens con recommendate (NOTIVATING ENZVME)	CETYL-COENZYME A SYN THE LASE (ACETATE—COALLOAGE) (ACTEDATED COENTRY)	Homo sapiens syntaxin 4 binding protein Civic (Civic) IIII va., compress case	Homo saplens bnospiratulyintositul giryeti, crass u (r Jou), iii. www.	602/409/6F1 NIH MIGG 40 Homo sapiens CONA clare IMAGE 4302019 5	6021409/6FT NIM _WGC_40 Hollid Sapirals Contraction (Contraction)	TRAB PROTEIN	and 1 both st. Scares_paramyroid_tumor_norms_septens_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_color_c	nh04n10 s1 NCI CGAP Thy1 Homo sapiens oDNA clone IMAGE: 943362	Third State of MCI COAD Third Home series CDNA clone IMAGE 943362		H. sapiens II. 19 gene	PM4-ST0270-080200-001-109 ST0270 Homo sapiens cDINA	DKFZp547P194_r1 547 (synon)/m: nipri) nomo sapiens conve cione DNI zpo411 154 5	Pediococcus aciditactici H plasmid pSMB/4 pediocin Acri production (pap), gene cluster papa, papa, papa, and papD genes, complete cds
Serio Lyon aigino	Top Hit Database Source	Z Z O		T HUMAN					NT	EST HIMAN					HOMAN	T		ISSPROT	LN.	NT	HOMAN	T	SWISSPROT		FOT LIMAN	Т	HUMAN		\Box	EST_HUMAN	LN LN
שונים -	Top Hit Acession No.	1 1E-01 AF030001.1		- 1		1.1E-01 AF064564.2	1.1E-01 S44957.1		1.1E-01 D90908.1	4 4E 04 AAZAZZIR 1	1.1E-01 ANT+1210.1	A08651.1	1.1E-01 M86533.1	1.1E-01 AJ007973.1	1.1E-01 BE769152.1	1.1E-01 AW853699.1	AF035746.1	1.1E-01 O69635	1.1E-01 AF032922.1	11432372	1.1E-01 BF684628.1	1.1E-01 BF684628.1	1.1E-01 P41067			1.1E-01 AA4935/4.1	1.1E-01 AA493574.1	1.1E-01 X91233.1	1.1E-01 AW817918.1	1.1E-01 AL134349.1	1.1E-01 U02482.1
	Most Similar (Top) Hit BLAST E Value	1 TE-01	4 Th	1.1E-01.	1	1.1E-01	1.1E-01	1.1E-01	1.1E-01	4 40 04	1.15-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.1E-01		1.1E-01	1.1E-01											
	Expression Signal	200	100	58.7		0.91	2.02	1.26	1.25		1.43	1.54	4.73	1.46	1.79	7.01	1.39	3.48	2.9	2.21	7.05	7.05	1.74				1.57	1.22	124	1.78	2.19
	ORF SEQ ID NO:		+	10000	73807	24150	24214		24487				25570	25681	25697					26198	26474	26475	26550			3 26845	3 26846	26872		1 26934	
	Exon SEQ ID NO:	0000	13930	14059	-	14360	-	1	ı	1	ı		15494	L_	15596	<u>L</u>	ł	1		l_	16309	16309		1		16656	16656	16682	ì	1_	1 1
	Probe SEQ ID NO:		4027	4159	4189	4466	4539	4725	7840	2	5479	5562	5579	5672	5687	5697	5876	6985	6027	6068	6448	6448	6513		6531	6777	67777	6803	8826	6862	7118

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Table 4
Single Exon Probes Expressed in Heart

Organ Lyon Flores Expressed III Tealt	Top Hit Descriptor	Leptosphæria maculans beta-tubulin mRNA, complete cds	Leptosphaeria maculans beta-tubulin mRNA, complete cds	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'	Aloe arborescens mRNA for NADP-malic enzyme, complete cds	Homo sepiens fibroblast growth factor receptor 3 (achondroplesia, thanatophoric owarfism) (FGFR3) mRNA	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)	EST366546 MAGE resequences, MAGC Homo sapiens cDNA	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE.254788 3'	wx78b08.x1 NCI_CGAP_Ov38 Homo saplens cDNA clone IMAGE:2549747 3' similar to gb:X52851_rna1 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (H.IMAN):	Mus musculus ligatin (Lgtn) mRNA, partial cds	oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'	oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:16784853'	Proteus mirabilis fimbrial operon, strain HI4320	EST378303 MAGE resequences, MAGI Homo sapiens cDNA	RC5-BT0254-031099-011-a03 BT0254 Homo sapiens cDNA	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5'	601434080F1 NIH_MGC_72 Homo saplens cDNA clone IMAGE:3919363 5'	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162	zu91g01.s1 Scares_testis_NHT Hono sapiens cDNA clone IMAGE:745392.3'	ym19h03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:48653 3'	601563355F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832908 5'	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA	Lycopersicon esculentum polygalacturonase isoenzyme 1 beta subunit gene, complete cds
שוני ווטאם פוני	Top Hit Database Source	1 LN	NT IN	EST HUMAN 6	NT TN		T_HUMAN	SWISSPROT	EST_HUMAN_E	N	EST_HUMAN y	EST_HUMAN y	EST HUMAN		EST HUMAN	EST_HUMAN o	TZ TZ	EST_HUMAN E	EST_HUMAN F	EST_HUMAN 6	EST HUMAN A	EST_HUMAN 6	- LN	ΤN	NT IN	NT	SWISSPROT	NT N	EST_HUMAN z		EST_HUMAN 6	T_HUMAN	NT
	Top Hit Acession No.	9.8E-02 AF257329.1	9.8E-02 AF257329.1	9.8E-02 BF037421.1	9.7E-02 AB005808.1	4503710 NT	9.7E-02 BE168660.1	099795	9.7E-02 AW954476.1	9.7E-02 Z99119.1	9.7E-02 N22798.1	9.7E-02 N22798.1	9.7E-02 Al953984.1	9.7E-02 U58337.1	9.6E-02 AI080721.1	9.6E-02 Al080721.1	9.6E-02 Z32686.2	9.6E-02 AW966230.1	9.6E-02 BE061729.1	9.6E-02 BE910039.1	9.6E-02 AV687898.1	9.6E-02 BE894895.1	9.6E-02 AJ243211.1	9.6E-02 AJ243211.1	9.6E-02 AB013985.1	9.6E-02 AB013985.1	P08174	Z79702.1	9.6E-02 AA625755.1	9.6E-02 H14599.1	9.6E-02 BE728219.1	5.1	9.5E-02 U63374.1
	Most Similar (Top) Hit BLAST E Value	9.8E-02	9.8E-02	9.8E-02	9.7E-02	9.7E-02	9.7E-02	9.7E-02 Q99795	9.7E-02	9.7E-02	9.7E-02	9.7E-02	9.7E-02	9.7E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02 P08174	9.6E-02 Z79702.1	9.6E-02	9.6E-02	9.6E-02	9.5E-02	9.5E-02
	Expression Signal	6.67	29'9	2.1	1.16	0.98	2.37	3.56	1.39	4.27	1.59	1.59	1.32	1.97	1.27	1.27	6.02	0.94	0.8	2.72	1.51	1.84	1.75	1.75	1.59	1.59	3.29	6.51	1.8	1.38	1.26	2.25	0.87
	ORF SEQ ID NO:	23805	23806	28148	21092		22004		25669	26345	26731	26732	27207		21753	21754	23921	24579	24738	_	27580		27855	27856	27933	27934	27980	28260	29058		25212	23694	24704
	Exon SEQ ID NO:	14031	14031	17904	11235	11471	12100	13811	15572	16184	16535	16535	17014	18403	11862	11862	14147	14810	14963	15621	17371	17527	ı	17622	_			18013	18764	19312	19344	$_{\perp}$	14932
	Probe SEQ ID NO:	4131	4131	8755	1328	1567	2214	3901	5661	6321	6655	999	7137	8531	1969	1969	4248	4932	5093	5713	7502	7677	7772	7772	7839	7839	7886	8125	8957	9798	9848	4012	5062

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	Top Hit Descriptor	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE.4291917 5'	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds	M.capricolum DNA for CONTIG MC073	Mus musculus coding region determinant-binding protein (Crdbp), mRNA	Acinetobacter sp. cysD, cobQ, sodM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes	Human BRCA1, Rho7 and vall genes, complete cds, and ipi35 gene, partial cds	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds	Human pephBGT-1 betaine-GABA transporter mRNA, complete cds	Homo sapiens BA11-associated protein 3 (BAIAP3) mRNA	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'	601655988R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'	HYPOTHETICAL PROTEIN KIAA0032	HYPOTHETICAL PROTEIN KIAA0032	UI-H-BI1-afx-h-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'	Photobacterium damselae subsp. damselae partial gyrB gene for DNA gyrase B subunit	hd28h12.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887.3'	Mus musculus major histocompatibility locus class II region; Fas-binding protein Dax (DAXX) gene, partial	cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-	galactosyl transferase (beta1,3-galactosyl tr>	Molluscum contagiosum virus subtype 1, complete genome	Molluscum contagiosum virus subtype 1, complete genome	Molluscum contagiosum virus subtype 1, complete genome
	Top Hit Database Source	TN	NT	EST_HUMAN 6	EST_HUMAN 6	EST_HUMAN 6	EST_HUMAN 6	EST_HUMAN 6	Г	IN	NT N	NT	- LN	LN LN	LN	TA			EST_HUMAN 6	HUMAN	EST_HUMAN 6	EST_HUMAN_A	EST_HUMAN 6	SWISSPROT	SWISSPROT	EST_HUMAN L		EST_HUMAN h	2		NT			NT
	Top Hit Acession No.	9.5E-02 AB003473.1	9.5E-02 AL161538.2	9.5E-02 BF035861.1	9.5E-02 BF035861.1	9.5E-02 BF035861.1	9.5E-02 BF035861.1	9.4E-02 BF671063.1	9.4E-02 U55944.1	9.4E-02 U55944.1	9.4E-02 Z33059.1	6753517	9.4E-02 Z46863.1	9.4E-02 L78833.1	9.4E-02 U31815.1	9.4E-02 U27699.1	4809280 NT	6912525 NT	9.3E-02 BF575511.1	9.3E-02 BE391943.1	9.3E-02 BE391943.1	9.3E-02 AV732224.1	9.3E-02 BE962631.2	Q15034	Q15034	9.3E-02 AW 206117.1		9.3E-02 AW468850.1			9.3E-02 AF100956.1			9.2E-02 U60315.1
	Most Similar (Top) Hit BLAST E Value	9.5E-02	9.5E-02	9.5E-02	9.5E-02	9.5E-02	9.5E-02	9.4E-02	9.4E-02	9.4E-02	9.4E-02	9.4E-02	9.4E-02	9.4E-02	9.4E-02	9.4E-02	9.3E-02	9.3E-02	9.3E-02	9.3E-02	9.3E-02	9.3E-02	9.3E-02	9.3E-02 Q15034	9.3E-02 Q15034	9.3E-02	9.3E-02	9.3E-02			9.3E-02	9.2E-02	9.2E-02	9.2E-02
	Expression Signal	3.72	7.46	2.59	2.59	3.29	3.29	3.86	0.86	0.86	4.34	0.89	2.62	2.69	3.36	1.42	1.83	5.39	2.03	3.51	3.51	1.88	2.24	3.52	3.52	3.74	1.85	8.62	-	-	1.95	4.32	4.32	4.32
}	ORF SEQ ID NO:	26348	26494	26666	26667		28207	21565				24621		26505		25182				23738				27949										20010
	Exon SEQ ID NO:	16186	16327	16479	16479		17957	11690	11717	11717		14855	16876	16338	19603	19411	12887	12921	13142	13962	_	14516						19555						10197
	Probe SEQ ID NO:	6323	6467	6659	6290	8066	9908	1792	1820	1820	3804	4980	6669	8304	9083	9943	2960	2993	3218	4060	4060	4628	7599	7855	7855	7913	9343	9704			9886	228	228	228

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hi: Descriptor
2180	12067		2.2	9.2E-02	9.2E-02 R54156.1	EST_HUMAN	yg98f07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE.41618 5'
3142	13067	22866	4.53	9,2E-02 Q28631		SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3265	13188	22986	1.16		9.2E-02 AA534354.1	EST_HUMAN	nf79e01.s1 NCI_CGAP_Co3 Homo saplens cDNA clone IMAGE:926136 3'
3537	13453		1.12		6755215 NT	N	Mus musculus pre T-cell antigen receptor alpha (Ptora), mRNA
4145	14045		1.34	9.2E-02		NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4211	14109		1.02	9.2E-02	2.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE.2960176 5'
4538	14431	24213	1.86	9.2E-02	9.2E-02 X96402.1	LN	G.gallus Mia-CK gene
6670	16550	26746	. 1.86		9.2E-02 T49920.1	EST_HUMAN	ya99c09.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE 69808 5' similar to similar to gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
6756	16635	26823	2.07	9.2E-02	9.2E-02 X95256.1	N	H.vulgare xylose isomerase gene
417	9984	19776	2.77	9.1E-02	9.1E-02 X77665.1	LN	O. cuniculus k12 keratin gene
2365	12245	22139	1.01	9.1E-02 P78985		SWISSPROT	6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)
3618			1.14	9.1E-02	9.1E-02 AW372569.1	EST_HUMAN	PM2-BT0349-161299-001-f02 BT0349 Homo sapiens cDNA
4383	14279	24058	1.81	9.1E-02	9.1E-02 AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5507	15425	25487	1.73		9.1E-02/AF129756.1	L	Homo sapiens MSH55 gene, pertial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AlF-1, 1C7, LST-1. LTB, TNF, and LTA genes, complete cds
6372			11.89		3.1	EST HUMAN	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7958	17808		1.65			EST HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3'end
9021	18815		1.29	9.1E-02	9633494 NT	NT	Bacteriophage Mu, complete genome
9256	19692		1.52	9.1E-02	9.1E-02 AA179901.1	EST_HUMAN	zp38h12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA;
9785	19548		5.63	9.1E-02	9.1E-02 AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
			······································				FOLATE RECEPTOR ALPHA PRECURSOR (FR.ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED
727	10659	20490	3.36	9.0E-02 P15328		SWISSPROT	ANTIGEN MOV18) (KB CELLS FBP)
1617	11521	21379	6.45		9.0E-02 BE220482.1	EST_HUMAN	hv39g10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2772	12634	22528	1.11	9.0E-02	9.0E-02 AF138522.1	LZ	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2772	12634	22629	1.11	9.0E-02	9.0E-02 AF138522.1	FN	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3294	13216	23018	0.92	9.0E-02	9.0E-02 AF279135.1	N	Dictyostelium discoideum spore coat structural protein SP65 (cotE) gene, complete cds
4202			8.0	9.0E-02		NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4202	{		0.8	9.0E-02	.1	LV	corticosterold-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4321	14218	24001	1.2	9.0E-02 P55268		SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)

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Table 4
Single Exon Probes Expressed in Heart

					יוני פווני	JIE EXUIT FIVE	Single Extended Expressed Intreate
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4568	14460	24248	1.79	9.0E-02	9.0E-02 X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5142	15009	24780	1.06	9.0E-02 Q24597	Q24597	SWISSPROT	REGULATORY PROTEIN ZESTE
	L			1			za68a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone iMAGE:297694 5' similar to
5647	15560	25653		9.0E-02	W 56037.1	ESI HUMAN	PIX.502111 502111 Sitial G procein - Indinati
2966	19428		15.35	9.0E-02	11431759 NT	. 1	Homo sapiens chromosome 16 open reading frame 5 (C16ort5), mRNA
1419	11325	21189	2.15	8.9E-02	8.9E-02 BF701593.1	EST HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 57
1419	11325		2.15	8.9E-02	8.9E-02 BF701593.1	EST HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5
2338	12218	22117	1.41	8.9E-02	8.9E-02 BE153572.1	EST HUMAN	PM0-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA
4104	14004		1.71	8.9E-02	8.9E-02 AF286055.1	NT	Africhum angusfatum AtranFlo2 protein (AtranFlo2) gene, partial cds
4534	14427	24208	0.92	8.9E-02	8.9E-02 AA424887.1	EST HUMAN	zw03d04.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:768199 3'
5569	15485		3.3	8.9E-02	8.9E-02 AW 452122.1	EST HUMAN	UI-H-BI3-alo-f-08-0-UI.s1 NOI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5569	L				8.9E-02 AW 452122.1	EST_HUMAN	UI-H-Bi3-alo-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5576	1	25568	3.13		11433478 NT	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
	1_						FOLD BIFUNCTIONAL PROTEIN (INCLUDES: METHYLENETETRAHYDROFOLATE
6270	16135	26290	1.56	8.9E-02 P47259	P47259	SWISSPROT	DEHYDROGENASE; METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE]
6460	16320		1.83	8.9E-02	8.9E-02 Z79021.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8
8669	16875	27066	5.28		8.9E-02 AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9228	18949		4.03		8.9E-02 BF696918.1	EST_HUMAN	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
1351	11257	21113	1.25		8.8E-02 Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3828	13740		96.0		8.8E-02 AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
	L						TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII-135) (TAFII135) (TAFII-130)
3948	13856		3.24		8.8E-02 C00268	SWISSPROT	(TAFII130)
4205	14104		1.13	8.8E-02	4580423 NT	LN	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
7195	17072	27280	1.83		8.8E-02 AA151872.1	EST HUMAN	zne9a05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
8461	18334	28596	3.19		8.8E-02 BE264455.1	EST HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5
8461	18334	28597	3.19		8.8E-02 BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
8585	18453				8.8E-02 AL040129.1	EST_HUMAN	DKFZp434D1313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5'
9302	L		1.38		8.8E-02 Z71561.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL285w
							Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN)
3636	13550	23337	3.02		8.7E-02 U82695.2	LN L	genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3636	13550	23338	3.02		8.7E-02 U82695.2	F Z	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PWGA3) gene, partial cds
	ı						

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Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	Top Hit Descriptor	zh68a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:417194 5' similar to contains element MER12 repetitive element;	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds	Methanobactenium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the	complete genome	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end	Gluconobacter oxydans iRNA-lle and tRNA-Ala genes	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease	Mus musculus nidogen 2 (Nid2), mRNA	Homo sapiens Xq pseudoautosomal region; segment 2/2	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds	Dictyostellum discoideum adenylyl cyclase (acrA) gene, complete cds	Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region	Homo sapiens LCN1b gene	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5	Archaeoglobus fulgidus section 34 of 172 of the complete genome	Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete	cds	Helicobacter pylori 26695 section 130 of 134 of the complete genome	M PROTEIN, SEROTYPE 6 PRECURSOR	Mus musculus phospholipase C-like protein mRNA, partial cds	Mus musculus myosin XV (Myo15), mRNA
le Exon Probe	Top Hit Database Source	EST HUMAN CO					EST_HUMAN z			I	NT	H H	EST_HUMAN 6	TN	NT		H	NT TN				NT .	NT L	EST_HUMAN 6	EST_HUMAN 6		8		NT H	ISSPROT		
Sing	Top Hit Acession No.	8.7E-02 W87841.1	8.7E-02 AF178636.1				8.7E-02 AA286875.1		8.7E-02 AJ007763.1		6679057	8.6E-02 AJ271736.1	8.6E-02 BE408667.1		8.6E-02 AF153362.1				100440.1	5730066 NT	5730086	8.6E-02 AF206551.1	8.6E-02 AF206551.1	8.6E-02 BF305606.1	8.6E-02 BF305606.1				8.5E-02 AE000652.1			6754779 NT
	Most Similar (Top) Hit BLAST E Value	8.7E-02	8.7E-02		8.7E-02	8.7E-02	8.7E-02	8.7E-02 L04758.1	8.7E-02	8.7E-02 X17116.1	8.7E-02	8.6E-02	8.6E-02	8.6E-02 L05468.1	8.6E-02	8.6E-02 U68179.1	8.6E-02 Y10826.1	8.6E-02 J00440.1	8.6E-02 J00440.1	8.6E-02	8.6E-02	8.6E-02	8.6E-02	8.6E-02	8.6E-02	8.6E-02		8.6E-02	8.5E-02	8.5E-02 P08089	8.5E-02	8.5E-02
	Expression Signal	0.82	1.22		1.06	5.41	5.41	2.58	1.77	2.58	1.81	7.05	2.22	2.94	3.07	0.87	4.38	1.51	1.51	1.26	1.26	1.98	1.98	3.63	3.63	4.71		1.73	2.87	1.8	5.34	1.93
	ORF SEQ ID NO:	23578	24286			24951	24952		28770			20991		22876		24060	25718	25867	25868	26695	26696	28441	28442	28710	28711	28131			22124		25665	
	Exon SEQ ID NO:	13790	14497		14906	15177	15177	17985	18496	18994	19105	11139	12084	13076	13507	14281	15616	15752	15752	16508	16508	18192	18192	18442	18442	17887			12227	15419		16880
	Probe SEQ ID NO:	3879	4609		5034	5255	6255	8094	8631	9293	9484	1232	2197	3151	3593	4385	5708	5846	5846	6628	6628	8315	8315	8574	8574	8738		8828	2347	5500	5668	7003

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Single Exon Probes Expressed in Heart

						e cds		12E20 E'	1000 N			2 3' similar to TR:088312								illar to contains L1.t1 L1 L1		2 Q15332 GAMMA										
Single Exoli Plobes Expressed in Heart	Top Hit Descriptor	RC4-OT0037-200700-014-e05 OT0037 Homo sanieps cDNA	RC4-070037-200700-014-e05 070037 Homo saniens cDNA	Homo sapiens heparanase predired mRNA complete of	Streptococcus mutans gene for places 1-pheenbate middyltransference	Antirrhinum maius mRNA for MYB-related transcription factor	EST72736 Ovary II Homo sapiens cDNA 5' end	zd44e11.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMACE:342623 F	601190436F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE 3534303 F	Homo sapiens mRNA for FLJ00050 protein, partial cde	CM3-BT0790-260400-162-405 BT0790 Homo sapiens cDNA	as88910.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312 O88312 GOB-4.	Ixodes hexagonus mitochondrion complete genome	Ixodes hexagonus mitochondrion complete genome	HYPOTHETICAL LIPOPROTEIN MG309 HOMO! OG PRECI IRSOP	(th82g06.x1 Soares NhHMPu S1 Homo saniens cDNA clone MAGE: 2125226.3	th82q06.x1 Soares NhHMPu S1 Homo saniens cDNA clone IMAGE: 22270.3	Homo sapiens protocadherin 43 gene, expn 1	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dr.p.2) mBNA commission	og88g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.t1 L1 L1 Irepetitive element	og81f10.s1 NCI CGAP Kid6 Homo saniens cDNA clone MAAGE: 15027720.3	iao6h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q16332 Q15332 GAMMA SIRINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA AT DA SAMMA SIRIINIT OF SODII MA DOTA SCHIMA SIRIINIT SODII MA SAMMA SAMMA SIRIINIT SODII MA SAMMA S	Agabidousis thallana DNA chromosoma 4 contin framout No. 04	601644770F1 NIH MGC 56 Homo saniens CNN A clare 1840 CE 3020003 E	Gallus gallus mRNA for for OBCAM protein gamma isoform	Canis familiaris glutamate transporter (EAATA) mRNA complete cds	Homo sapiens chromosome 21 segment HS21Chhe	Arabidopsis thaliana DNA chromosome 4 continuent No. 10	Homo sapiens chromosome 21 segment HS21C006	LEUCOCYTE ANTIGEN CD97 PRECURSOR	LEUCOCYTE ANTIGEN CD97 PRECURSOR	LEUCOCYTE ANTIGEN CD97 PRECURSOR
	Top Hit Database Source	EST HUMAN	EST HUMAN	NT	IN	TN	EST HUMAN	EST HUMAN	EST HUMAN	NT	EST_HUMAN	EST HUMAN	N	Į.	SWISSPROT	EST HUMAN	EST HUMAN	IN	NT	EST HUMAN	EST HUMAN	EST HUMAN	LN	EST HUMAN		TN	LN	N.	LN	SWISSPROT	SWISSPROT	SWISSPROT
	Top Hit Acession No.	8.5E-02 BE833054.1	-		8.5E-02 AB001562.1	AJ005586.1	8.5E-02 AA362934.1		8.4E-02 BE267153.1	*	8.4E-02 BE095074.1	8.4E-02 AI735184.1	5835680	5835680 NT		8.3E-02 Al436797.1	8.3E-02 Al436797.1	-	+-	8.3E-02 AA865285.1	-	-		-		8.2E-02 AF167077.2	8.2E-02 AL163206.2	8.2E-02 AL161498.2	8.2E-02 AL163206.2			
	Most Similar (Top) Hit BLAST E Value	8.5E-02	8.5E-02	8.5E-02	8.5E-02	8.5E-02	8.5E-02	8.4E-02	8.4E-02	8.4E-02	8.4E-02	8.4E-02	8.3E-02	8.3E-02	8.3E-02 P75334	8.3E-02	8.3E-02	8.3E-02	8.3E-02	8.3E-02	8.3E-02	8.3E-02	8.3E-02/	8.3E-02	8.2E-02 Y08170.2	8.2E-02/	8.2E-02/	8.2E-02	8.2E-02	8.2E-02 P48960	8.2E-02 P48960	8.2E-02 P48960
	Expression Signal	3.07	3.07	11.15	4.07	1.39	3.28	4.24	7.82	1.71	8.11	4.	98.0	0.86	6.19	0.88	0.88	2.82	3.42	1.47	1.42	4.	1.94	1.55	7.82	1.21	1.78	1.26	1.11	5.36	5.36	5.36
	ORF SEQ ID NO:	27737	27738		28649			22391	24949	26053	26755	28020	21748	21749	23254	23271	23272	25859	26728			27573				21248			23615	23862	23863	23864
	Exon SEQ ID NO:	17511	17511	18369	18384	19488	19339	12728	15175	15923	16560	17781	11859	11859	13460	13481	13481	15746	16533	16551	16708	17368	17294	19695	11263	11385	12964	13645	13835	14087	14087	14087
	Probe SEQ ID NO:	7661	7661	8496	8512	9681	9841	2632	5253	6019	9680	7931	1965	1965	3544	3567	3567	5840	6653	6871	6828	7498	7506	9307	1357	1480	3036	3733	3928	4187	4187	4187

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Mus musculus zinc transporter (Zn i-3) gene, complete cds	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA	Beet necrotic yellow vein virus RNA-2	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355595 5'	Chlamydophila pneumoniae AR39, section 73 of 94 of the complete genome	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds,	alternatively spliced	Pseudomonas putida maioriate decarboxyrase gene cruster (moch, mocb, mocb, mocb, mocb, mocb, mocb, mocb, moch, moch, moch and mocM genes), complete cds	Homo saplens extracellular glycoprotein lacritin precursor, gene, complete cds	Homo sapiens chromosome 21 segment HS21C002	EST366723 MAGE resequences, MAGC Homo sapiens cDNA	Molluscum contagiosum virus subtype 1, complete genome	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)	Human gene for dihydrolipoamide succinytransferase, complete cds (exon 1-15)	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA	Synechocystis sp. PCC6803 complete gename, 17/27, 2137259-2267259	Synechocystis sp. PCC6803 complete genome, 17:27, 2137259-2267259	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'	Dictyoselium discoideum cyclic nucleotide phosphodiesterase gene, complete cds	Thermoplasma acidophilum complete genome; segment 5/5	EST378191 MAGE resequences, MAGI Homo sapiens cDNA	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA	M.musculus gene for gelatinase B	Herpesvirus saimiri transformation-associated protein (STP), and dihydrofolate reductase (DHFR) gene.s	complete cds, and small nuclear RNAs (uRNAs)	Homo sapiens ABCA1 (ABCA1) gene, complete cds	Homo sapiens ABCA1 (ABCA1) gene, complete cds	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	H.saplens AGT gene, intron 4	H.sapiens AGT gene, intron 4
le Exon Probe	Top Hit Database Source	NT	EST HUMAN		EST HUMAN		EST_HUMAN			Z	LV.			EST HUMAN	NT	NT		T HUMAN		NT	T HUMAN		NT	EST_HUMAN	LN	LN		۲	NT	L	LN	LN	N
Sing	Top Hit Acession No.			8.2E-02 AF309555.1	1		8.1	8.2E-02 AE002246.2		8.2E-02 AF275366.1	8 1F-02 AB017138 1	8.1E-02 AY005150.1	8.1E-02 AL163202.2	8.0E-02 AW954653.1	J60315.1	726535.1)26535.1	8.0E-02 BE067219.1	J90915.1	J90915.1	8.0E-02 BF246744.1	M23449.1	8.0E-02 AL445067.1	8.0E-02 AW965118.1	4503034 NT	X72794.1		8.0E-02 M28071.1	8.0E-02 AF275948.1	8.0E-02 AF275948.1	8.0E-02 AL114993.1	X74208.1	X74208.1
	Most Similar (Top) Hit BLAST E Value	8.2E-02 U76009.1	8.2E-02 E	8.2E-02	8.2E-02	8.2E-02 X04197.1	8.2E-02	8.2E-02		8.2E-02/	8 1F-02	8.1E-02/	8.1E-02/	8.0E-02	8.0E-02 U60315.1	8.0E-02 D26535.1	8.0E-02 D26535.1	8.0E-02	8.0E-02 D90915.1	8.0E-02 D90915.1	8.0E-02	8.0E-02 M23449.1	8.0E-02	8.0E-02	8.0E-02	8.0E-02 X72794.1		8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	B.0E-02 X74208.1
- - - - - -	Expression Signal	2.82	1.43	3.14	3.13	5.33	2.11	4.13		1.84	1 72	1.65	3.38	3.28	1.33	10.54	10.54	3.9	1.01	1.01	4.08	0.81	1.01	0.84	1.06	5.62		0.87	3.35	1.63	3.65	1.49	1.49
	ORF SEQ ID NO:	24655	24988	26222	27164	27598	27699	25336			24247		28894	19784	20690	21440	21441	21632	22103			20833	22591	23440					25581			27471	27472
	Exon SEQ ID NO:	14888	15193		L	17387	17479	19006	L	19480	11384	1		1_	L	12701	12701	11757	12204	12204	12298	10991	12797	13658	13887	14595		14716	15506	15506	16607		17268
	Probe SEQ ID NO:	5014	5271	6188	7094	7536	7628	9314		92/6	1470	7703	8789	5	920	1671	1671	1861	2323	2323	2421	2790	2870	3745	3980	4709		4834	5591	6261	6727	7401	7401

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						as i lieve eigine	
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8172	18060	28310	7.42		8.0E-02 AF217798.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NFIL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
9344	19023	25300	2.94		8.0E-02 AJ005375.1	NT	Drosophila orena hunchback region
9891	13887		1.47	8.0E-02	4503034 NT	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
9969	19854		3.04		8.0E-02 AJ278435.1	NT	Mus musculus Ranbp7 gene, Staf gene and Wee1 gene
2127	12015	21913	3.98		7.9E-02 BE250008.1	EST HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5
2948	12875	22673	6.43		7.9E-02 AI582029.1	EST_HUMAN	ar98c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
3776) 		6681044 NT	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3776	13688	23472	3.31	7.9E-02	6681044 NT	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4595	14483		1.06		7.9E-02 BF348454.1	EST_HUMAN	602019770F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155401 5'
4706	14592		1.16		7.9E-02 AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
6682	16562	26756	3.25		7.9E-02 U27832.1	NT	Saccharomyces cerevisiae suppressor of MIF2 Smt4p (SMT4) gene, complete cds
							ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
7762	17612	27838	5.68		7.9E-02 A1081644.1	EST HUMAN	CE08611;
27.62	17812	27839	5 68		7 9F-02 AID81644 1	FST HUMAN	ou63b05.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611 ;
	1						0059d02.y5 NCI_CGAP_Lu5 Homo saplens cDNA clone IMAGE:1570457 5' similar to contains L1.t3 L1
1192	11102	20947	1.43		7.8E-02 AI 793275.1	EST_HUMAN	repetitive element;
	1					i i	0059402.y5 NCL_CGAP_Lu5 Homo sepiens cDNA clone IMAGE:1570467 5' similar to contains L1.t3 L1
1192	_[1.8E-02 AI/932/3.1	ES HOWAIN	repaire entitin,
4688	14574	24371			7.8E-02 BE836331.1	EST_HUMAN	PM3-FN0058-140 700-005-109 FN0058 Homo sapiens cUNA
5019	13603		2.71		7.8E-02 BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5
5197	15060	24825	1.04		7.8E-02. A/418520.1	EST HUMAN	1g48g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112070 3' similar to contains MER10:13 MER10 repetitive element;
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete
7236	17113	27306	2.06		7.8E-02 AF233437.1	LN	spo
							Homo sapiens FYVE domain-containing dual specificity protein phospitatase FYVE-DSP1b mRNA, complete
7236	17113	27307	2.06		7.8E-02 AF233437.1	NT	spo
7389	17307		1.27		7.8E-02 AA469354.1	EST HUMAN	Inc68b06.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:771731
1378	12693	3 21139	-	7.7E-02	7.7E-02 AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3538	13454	11	2.09		7.7E-02 AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
6615	16495	26682	4.4		7.7E-02 AA402949.1	EST_HUMAN	zu53d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICECSOME ASSOCIATED PROTEIN.;

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Tobe E.Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q ID SE(Q 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7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-03 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-03 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02 7.6E-02	Top Hit Aces: No. No. 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 11436 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NIH, MIGC, 28 Horn captures CDNA come MARCE.3634903 5° EST HUMAN (S01316426F1 NIH, MIGC, 28 Horn captures CDNA come MARCE.3634903 5° EST HUMAN (S01316426F1 NIH, MIGC, 28 Horn captures CDNA come MARCE.3634903 5° Source EST HUMAN (S01316426F1 NIH, MIGC, 28 Horn captures CDNA come MARCE.3634903 5° NIT Horn sepiers Soulce carrier family 6 (neutrotensmitter transporter, glycine), member 9 (SLC6A9), mRNA Horn sepiers soulde carrier family 6 (neutrotensmitter transporter, glycine), member 9 (SLC6A9), mRNA Horn sepiers obtile carrier family 6 (neutrotensmitter transporter, glycine), member 9 (SLC6A9), mRNA Horn sepiers obtile carrier family 6 (neutrotensmitter transporter, glycine), member 9 (SLC6A9), mRNA Horn sepiers obtile carrier family 6 (neutrotensmitter transporter, glycine), member 9 (SLC6A9), mRNA MCDASE (HUMAN) (AUT6817 EMBA1 Horn sepiers CDNA clore IMAGE.242491 3' similar to gb Mrt 4328 ALPHA NT Horn sepiers deliver sepiers CDNA clore HAGE.283493 5' similar to gb Mrt 4328 ALPHA EST HUMAN (AUT6817 EMBA1 Horn sepiers CDNA clore IMAGE.283595 3' NT Horn sepiers deliver sepiers CDNA clore IMAGE.283595 3' Human periodic Dayorachmen protein (NAT2) gene, complete cds Human periodic Dayorachmen protein (NAT2) gene, complete cds Human periodic Dayorachmen protein (NAT2) gene, complete cds Human periodic Dayorachmen protein (NAT2) gene, complete cds Human periodic Dayorachmen protein (NAT2) gene, complete cds Human periodic Dayorachmen protein (NAT2) gene, complete cds Human periodic Dayor
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Table 4
Single Exon Probes Expressed in Heart

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Table 4
Single Exon Probes Expressed in Heart

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		T		T	T	T	1	T	T	T	Τ	T	1		T	T	T	Τ	Ī	1	Τ	Τ	T	\top	Τ	Т	\top	T	Τ	Τ	T	
	Top Hit Descriptor	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE.3883030 5'	X.Iaevis XFD2 mRNA for fork head protein	PROTEIN TRANSPORT PROTEIN HOFC HOMOLOG	Homo sapiens membrane bound aminopeptidase P (XNPEP2) gene, complete cds	ae30f02.r1 Gessler Wilms tumor Horno sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22362 MITOCHONDRIAL MATRIX PROTEIN P1 PRECI IRSOR (HI IMAM).	Homo sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds	ai75a06.s1 Soares (estis NHT Homo sapiens cDNA clone 1376626 3'	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'	MR0-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C068	Pyrococcus abyssi complete genome; segment 5/6	Pyrococcus abyssi complete genome; segment 5/6	FB4A8 Fetal brain, Stratagene Homo sapiens cDNA clone FB4A8 3'end similar to LINE-1	ah67f05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'	Mus musculus latent TGF beta binding protein (Tgfb), mRNA	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds	qg79e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE.1841406 3'	HOMEOBOX PROTEIN HOX-D4 (CHOX-A)	att 2e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW:LIN1 NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	Drosophila melanogaster cactin mRNA, complete cds	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcrints	MELATONIN-RELATED RECEPTOR (H9)	y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN 112)	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
	Top Hit Database Source	EST HUMAN	EST_HUMAN	LN L	SWISSPROT	N	EST_HUMAN	EST HUMAN	NT	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	TN	TN	NT	EST_HUMAN	EST_HUMAN	LN	NT	EST_HUMAN	SWISSPROT	EST HUMAN	NT	NT	SWISSPROT	EST_HUMAN	N	LZ.	TN	SWISSPROT	SWISSPROT
	Top Hit Acession No.	6.9E-02 BE567435.1	6.9E-02 BE567435.1	6.9E-02 X74315.1	P44621	6.9E-02 AF195953.1	6.8E-02 AA496759.1	6.8E-02 AA496759.1	6.8E-02 AF156673.1	6.8E-02 AA781996.1	6.8E-02 AA781996.1	6.8E-02 AA781996.1	6.8E-02 BE141076.1	6.8E-02 AL163268.2	6.8E-02 AJ248287.1	6.8E-02 AJ248287.1	T03214.1	6.8E-02 AA758014.1	9910585 NT	6.7E-02 AF115536.1	AI220285.1	217278	6.6E-02 AI735509.1	\	-	213585	364306.1	7108357 NT	7108357 NT	AF260225.1		361703
	Most Similar (Top) Hit BLAST E Value	6.9E-02	6.9E-02	6.9E-02	6.9E-02 P44621	6.9E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02 T03214.1	6.8E-02	6.8E-02	6.7E-02	6.7E-02 AI220285.	6.7E-02 P17278	6.6E-02	6.6E-02	6.6E-02 /	6.6E-02 Q13585	6.6E-02 R64306.1	6.6E-02	6.6E-02	6.6E-02	6.6E-02 Q61703	6.6E-02 Q61703
	Expression Signal	1.37	1.37	3.95	1.5	2.19	1.11	1,11	3.91	1.23	1.23	1.23	0.92	7.71	6.12	6.12	1.37	2.98	2.97	2.17	2.5	3.52	1.05	1.5	3.07	1.32	8.61	2.19	2.19	1.59	8.4	8.4
1	ORF SEQ ID NO:	27048					21610	21611	21635	22780	22781	22782			26894	26895					21622	23356	21089	21109	21918		23139	23154	23155	23673	24558	24559
	Exon SEQ ID NO:	16855	16855	18939	19045	19180	11736	11736	11761	12989	12989	12989	14347	16178	18701	16701	19719	18895	19284	11416	11747	13570	11233	11253	12021	13058	13335	13349	13349	13896	14784	14784
	Probe SEQ ID NO:	6978	8269	9208	9385	9598	1839	1839	1865	3062	3062	3062	4453	6315	6822	6822	9011	9140	9764	1511	1851	3656	1326	1347	2133	3133	3418	3432	3432	3989	4904	4904

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Single Exon Probes Expressed in near	Top Hit Descriptor	Amsacta albistriga nucleopolyhedrovirus AcORF17 homolog gene, complete cds	Vibrio cholerae chromosome II, section 2 of 93 of the complete chromosome	P.vulgaris mRNA for chalcone synthase	qh41d01.x1 Soeres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847233 31	Homo sapiens chemokina receptor CXCR4 gene, promoter region and complete cds	Homo sapiens EWS, gar22, rrp22 and bam22 genes	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA	Mus musculus DIPB gene (Dipb), mRNA	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5 tlanking region	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'	Homo sapiens E2F-like protein (LOC51270), mRNA	Xenopus laevis alpha(E)-catenin mRNA, complete cds	Aquifex aeolicus section 96 of 109 of the complete genome	zv46h12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);	zr32g05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:6651443'	Rabbit microsomal epoxide hydrolase	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds	A.carterae precursor of peridinin-chlorophylla-protein (PCP) gene	Mus musculus histone deacetylase 5 (Hdac5), mRNA	Mus musculus histone deacetylase 5 (Hdac5), mRNA	qe07b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249.3' similar to contains LTR8.b3 I TR8 repetitive element	Harriston aliminate bake 4.4 and only increased by environt (H.C. and 1) rane complete ride	Therefore a grant is the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of	Heterodera glycines beta-1,4 endoglucanase-1 precursor (HG-eng-1) gene, complete cds	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 31	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'	Homo sapiens mRNA for KIAA0554 protein, partial cds	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (AD A. W.) name. Rodget name, and sodium phosphale transporter (NPT3) name, complete cids.	LICATI) gene, indice gene, and social production anapora (in 19) gene, compress our
e Exon Prope	Top Hit Database Source	NT TN			EST_HUMAN of			T HUMAN		-	T HUMAN			/ IN			EST_HUMAN		NT	LN				NOMO!			EST_HUMAN		EST_HUMAN	TN	H	
Sing	Top Hit Acession No.	6.6E-02 AF204882.1	6.6E-02 AE004345.1		1	2.1		6.6E-02 BF374248.1	7991		6.5E-02 BF027639.1	8909		6.5E-02 AE000764.1		VA443991.1	6.5E-02 AA195648.1		6.5E-02 AF102993.1	(94549.1	6996923 NT	EZ69669	14040554	1191900.1	4F052733.1	4F052733.1	6.4E-02 BE97448.1	6753323 NT	4A093305.1	6.4E-02 AB011126.1	b 000000	6.4E-UZ U913Z8.1
	Most Similar (Top) Hit BLAST E Value	6.6E-02	6.6E-02 A	6.6E-02 X06411.1	6.6E-02 AI243326	6.6E-02	6.6E-02 Y07848.1	6.6E-02	6.6E-02	6.6E-02 ₽	6.5E-02	6.5E-02	6.5E-02 U47624.1	6.5E-02		6.5E-02 AA443991	6.5E-02	6.5E-02 M21496.1	6.5E-02	6.4E-02 X94549.1	6.4E-02	6.4E-02	20 11 0	0.4E-0Z/A1191900	6.4E-02/AF05273	6.4E-02 AF052733	6.4E-02	6.4E-02	6.4E-02 AA09330	6.4E-02	20 25 2	6.4E-UZ
	Expression Signal	1.34	0.84	3.09	2.93	1.48	1.37	6.28	2.08	1.46	1.91	1.75	4.17	2.16		1.76	5.61	3.53	3.73	1.53	1.35	8.78		4.	7.58	7.58	5.23	2.57	4.12	202		1.85
	ORF SEQ ID NO:	24800	24817	25998	26105	26706	27894	28457			20313	20743	21131	21474		25383	28173			20307						25728	26210		27099			29049
	Exon SEQ ID NO:	15033	15053	15873	15969	16515	17656	18207	19175	19366	10506	10895	11275	L	L	15333			L	10501	12909	15044	1		1	15625		L				18754
	Probe SEQ ID NO:	5167	5190	5968	6209	6635	7806	8330	9593	9882	287	971	1369	1702		5413	8035	9034	9393	561	4802	5180		5346	5718	5718	6079	6853	7034	7603		8946

Page 98 of 413 Table 4 Single Exon Probes Expressed in Heart

Single EXDI Probes EXPRESSED IN TREAT Top Hit Descriptor Source Source Source Human hereditary haemochromatosis region, histone 24-like protein gene, hereditary haemochromatosis region, histone 24-like protein gene, complete cds: (HLA-H) gene, Rohea gene, and sodium phosphate transporter (NPT3) gene, complete cds: (HLA-H) gene, Rohea gene, and sodium phosphate transporter (NPT3) gene, complete cds: (HLA-H) gene, Rohea gene, and sodium phosphate transporter (NPT3) gene, complete cds: (HLA-H) gene, gene, mind and sodium phosphate transporter (NPT3) gene, complete cds: (HLA-H) gene, gene, mind and sodium phosphate transporter (NPT3) gene, complete cds: (HLA-H) gene, gene, mind and sodium phosphate transporter (NPT3) gene, complete cds: (MT) Heart SHOCK PROTEIN 70 HOMCLOG SWISSPROT HEAT SHOCK PROTEIN 70 HOMCLOG SWISSPROT TRANSCRIPTIONAL REGULATORY PROTEIN ALGR (ALINATE RECULATORY PROTEIN (ALGRA (ALINATE RECULATORY PROTEIN ALGRA (ALINATE RECULATORY PROTEIN ALGRA (ALINATE RECULATORY PROTEIN ALGRA (ALINATE RECULATORY PROTEIN ALGRA (ALINATE RECULATORY PROTEIN (ALGRA (ALINATE RECULATORY PROTEIN (ALINATE RECULATORY PROTEIN (ALINATE RECULATORY PROTEIN (ALINATE RECULATORY ALINATE RECULATORY PROTEIN (ALINATE RECULATORY (ALINATE RECULATORY ALINATE RECULATORY (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATORY) (ALINATE RECULATORY) (ALINATE RECULATORY) (ALINATE R	Top Hit Database Source Source Source Source Source Source Source Source Source Source Source ST HUMAN NT NT NT NT NT NT NT NT NT NT NT NT NT	Top Hit Aces No. No. No. Herogon.1 AJZ77174.1 AJZ77174.1 AJZ77174.1 AJZ42735.1 AE00750.1 AE00750.1 AE0471.1 AT0898.1 AE12039.1 AF12039.1 AF13207.2 AF13207.2 AF13207.2	Most (To BLA	Signal	ORF SEQ ID NO: 29050 25295 25741 27825 25741 27825 25741 27625 2827 26877 26877 26877		Probe SEQ ID NO: NO: 1720 9289 9337 1752 8098 8098 9541 4479 4803 7459 9541 9541 9541 9541 9541 9541 9541 9
Mesocestoides corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-GIn, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2	NT	6.0E-02 AB031289.1					2745
Mesocestoides corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met,	1					}	
EST380924 MAGE resequences, MAGJ Homo sapiens cDNA	EST_HUMAN	6.0E-02 AW968848.1		1.57		12508	2641
Thermotoga maritima section 89 of 136 of the complete genomo	N	AE001777.1					1241
Homo sapiens chromosome 21 segment HS21C007	N-	AL163207.2		3.6			9783
S japonicum mRNA for serine enzyme	NI	X70969.1		7.17			9088
IL3-HT0618-110500-136-C06 HT0618 Homo sepiens cDNA	EST HUMAN	BE179543.1				_	8112
H.sapiens mRNA for B-HLH DNA binding protein		X99268.1					6809
Homo saplens mRNA for KIAA1464 protein, partial cds	NT	AB040897.1				L_	5150
Arabidopsis thaliana K+ inward rectifying channel protein (AtKC1) gene, complete cds	LN.	U73325.1		2.65		ļ	3909
Human mRNA, Xq terminal portion	۲	D16471.1					256
TR:09Y4S6 09Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1];	EST_HUMAN	BF112039.1					9541
7137h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to							
Aquifex aeolicus section 82 of 109 of the complete genome	۲	AE000750.1		3.53		L	9129
Metarhizium anisopilae mRNA for Chymotrypsin (chy1 gene)	IN	AJ242735.1)	8655
Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA	N	99					7459
AV705701 ADB Homo sapiens cDNA clone ADBBAB03 5'	EST_HUMAN	AV705701.1		1.22			4803
52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)	SWISSPROT	Q62191		5.41		L	4479
complete cds	F	AF271235.1		1.11			4243
Rattus norvegicus differentation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA,						J.,	
Arabidopsis thallana DNA chromosome 4, contig fragment No. 68	딩	AL161572.2	6.2E-02			1_	4157
TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3)	SWISSPROT	P15276		1.49		ļ_	9373
601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5	EST HUMAN	BF210736.1					8098
Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152	NT	AB010162.1					7752
HEAT SHOCK PROTEIN 70 HOMOLOG	SWISSPROT	P37092		2.09		13467	3552
MutS homolog, OLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes	NT	AF109905.1				11621	1720
Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23,							
Drosophila melanogaster mRNA for mod(mdg4)51.4 protein	N _T		6.4E-02			19017	9337
Homo sapiens mucin 5B (MUC5B) gene, partial cds	NT					l	9289
(HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	TN	U91328.1					8946
Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis							
Top Hit Descriptor	Database Source	No.	(Top) Hit BLASTE Value	Expression	ORF SEQ ID NO:	SEQ ID NO:	NO:
	Top Hit	Ton Life Accepton	Most Similar	i.	((Exon	Probe
es Expressed in Heart	le Exon Proc	Sing					

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Table 4
Single Exon Probes Expressed in Heart

Single Excit Plobes Explessed in read	Top Hit Descriptor	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA	RC3-BT0253-011199-013-b04 BT0253 Homo sapiens cDNA	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199.3	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 31	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exons 1-2	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exons 1-2	Homo sapiens DNA-dependent protein klnase catalytic subunit-interacting protein 2 (KIP2), mRNA	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR: O60298	O60298 KIAA0551 PROTEIN ;	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial ods; alternatively spliced	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds	Mus musculus iroquois related homeobox 5 (Drosophila) (Irx5), mRNA	Mus musculus follistatin-like (Fstl), mRNA	Homo sapiens ninein (LOC51199), mRNA	Gallus gallus HKC9 telomere junction	Thiobacillus ferrooxidans merC, merA genes and URF-1	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5	Thermotoga maritima section 87 of 136 of the complete genome	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE.1848697 3' similar to ab M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697.3' similar to qb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
e Exoli Piones	Top Hit Database Source			EST HUMAN E	EST_HUMAN 60		T HUMAN						EST HUMAN ts	NT	NT		W		T_HUMAN	NT	NT S				NT G		NT	TN⊤	EST_HUMAN w	EST HUMAN W	P NAMIN TSE	HUMAN	Π
Buic	Top Hit Acession No.	6.0E-02 AA188730.1	6.0E-02 AA372376.1	6.0E-02 AA372376.1	6.0E-02 BE964443.2		6.0E-02 AW370211.1	5174698 NT	74698	_			6.0E-02 AI623167.1		6.0E-02 AJ245365.1	11431702 NT			5.9E-02 AW934719.1	5.9E-02 AF190269.1	5.9E-02 AF006304.1	9055249 NT	6679870	11433356 NT	5.9E-02 AJ240733.1	5.8E-02 D90110.1	5.8E-02 AJ223621.1		_	5.8E-02 AW051927.1			5.8E-02 AF096264.1
	Most Similar (Top) Hit BLAST E Value	6.0E-02	6.0E-02	6.0E-02 A	6.0E-02	6.0E-02 Z67739.2	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02/	6.0E-02		6.0E-02	5.9E-02	5.9E-02	5.9E-02	5.9E-02	5.9E-02	5.9E-02	5.9E-02	5.8E-02	5.8E-02	5.8E-02	5.8E-02	5.8E-02	20 E8 R	5.8F-02	5.8E-02
	Expression Signal	1.22	1.2	1.2	6.0	1.17	3.46	2.86	2.86	1.97	2.05	1.19	1.19	1.79	1.79	1.95		1.84	3.42	2.59	0.88	1.87	2.72	3.15	1.99	4.35	1.1	1.44	4.36	4.36	10.1	4 21	2.04
	ORF SEQ ID NO:	19893	22921	22922	-	24551		24848	24849	26284	26562	27406		27486	27487				20011	22681	24443			28509				23314					
	Exon SEQ ID NO:	10076	13116	13116	13497	14773	15235	15129	15129	16130	16383	17208	17208	17278	17278	l_	١	19256	10198	12882	1	16885	18053	18260	18655	10841	12759	<u></u>		L	l		
	Probe SEQ ID NO:	2906	3191	3191	3583	4893	5314	6172	6172	6265	6524	7340	7340	7411	7411	9336		9715	229	2955	4770	7008	8165	8383	8842	917	2830	3613	4257	4257	7447	4447	4471

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Table 4
Single Exon Probes Expressed in Heart

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Table 4
Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heari	Top Hit Descriptor	Mus musculus tuftelin 1 (Tuft1), mRNA	Homo sapiens elF4E-transporter (4E-T), mRNA	Homo sapiens elF4E-transporter (4E-T), mRNA	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), diverol dehydroxqacetone (dhaK), diverol dehydroxdenase (dhaD), transcriptional activator (dhaR), d.3-propanediol	dehydrogenase (dhaT), glycerol dehydratase (dhaB),>	Oryza sativa rbbí3-1 gene for pulative Bowman Birk trypsin inhibitor	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA	Xenopus laevis homeobox protein (Vox-1) mRNA, complete cds	Mus musculus p-glycoprotein (mdrla) gene, exons 1 and 2	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds	Rana catesbiana heat shock protein 30 (HSP30) mRNA, complete cds	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA	ye37f12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01506 HLA CLASS II HISTOCOMPATIBILTY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);	Pseudomonas putida tigS gene	Drosophila melanogaster laminin B2 gene, complete cds	rosophila melanogaster laminin B2 gene, complete cds	Pseudomonas putida ttgS gene	Arabidopsis thaliana eli5 gene, exons 1-11	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds	Helicobacter pylori 26695 section 5 of 134 of the complete genome	Helicobacter pylori 26695 section 5 of 134 of the complete genome	Lymphocystis disease virus 1, complete genome	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]	Podospora anserina mitochondrial epsilon-sen DNA	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	Human steroid hormone receptor Ner-I mRNA, complete cds	Drosophila melanogaster filament protein nomolog (sep1) gene, complete cos
le Exon Probe	Top Hit Database Source	NT			NT TN	0 3	<u>, </u>		T HUMAN		NT	N N		EST_HUMAN C		Y EST_HUMAN F	TN	NT			VT LN										L	
Sing	Top Hit Acesslon No.	6755902	10947034 NT	10947034 NT	U69492.1			AJ277468.1		5.4E-02 U53528.1		5.4E-02 U20790.1					5.3E-02 AJ276408.1	5.3E-02 M58417.1	5.3E-02 M58417.1	5.3E-02 AJ276408.1	5.3E-02 AJ011048.1	5.3E-02 M80463.1	5.3E-02 AE000527.1	5.3E-02 AE000527.1	9695413 NT	5.3E-02 S78221.1	5.3E-02 X03127.1	5031908 NT	5.2E-02 AJ277661.1	1.1		5.2E-02 L33246.1
	Most Similar (Top) Hit BLAST E Value	5.5E-02	5.5E-02	5.5E-02	5.5E-02		5.5E-02 U09771.1	5.4E-02	5.4E-02	5.4E-02	5.4E-02 M96761.1	5.4E-02	5.4E-02 U44894.1	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.3E-02	5.2E-02				5.2E-02
	Expression Signal	1.58	1.3	1.3	1.48		11.56	0.95	6.34	0.92	1	1.79	1.55	1.62	1.62	18.21	3.14	3.91	3.91	4.59	1.22	7.26	1.76	1.76	3.87	1.94	1.78	439.66	2.34	2.34	3.35	1.04
	ORF SEQ ID NO:	26388	27632	27633			28508	_		24563		28223		20797			22222	22838	22639	22834		24662	24955		26145		27349		22793		23854	
	Exan SEQ ID NO:	16228	17417	1_	L	1	18259	L	15078	14787	14976	17974	<u> </u>	10955	10955	l	12324		12839	<u> </u>	L	14894	15180	1	1	1	17153	12123	13003		1	14521
	Probe SEQ ID NO:	6365	7566	7566	7619		8382	2986	3375	4908	5108	8083	9323	1037	1037	1489	2447	2912	2912	3113	4506	5021	5258	5258	6115	6353	7276	2239	3076	3076	4181	4633

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oligie Exort Topes Expressed III reals	Top Hit Descriptor	zt78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'	xg56g10 x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2632386 3'	xg56g10.x1 NCL_CGAP_Ut4 Homo sapiens cDNA clone IMAGE.2632386 3'	Rat elastase II gene, exon 6	Rat elastase II gene, exon 6	Homo sapiens prepro placental TGF-beta gene, complete cds	Homo sapiens CS box-containing WD protein (LOC55884), mRNA	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds	Human mRNA, Xq terminal portion	Human mRNA, Xq terminal portion	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds	zc49b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);	Tetrahymena rostrata histone H3II and histone H4II Intergenic DNA	S.scrofa gene for skeletal muscle ryanodine receptor	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds	MR2-ST0129-221099-012-b02 ST0129 Homo saplens cDNA	Rattus norvegicus Nestin (Nes), mRNA	yz97109.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMACE:291017 5' similar to contains Alu repetitive element;	Rat statin-related protein (s1) gene, complete CDS	B.taurus mRNA for RF-36-DNA-binding protein	H.saplens DNA for endogenous retroviral like element	Gallus gallus Wpkcl-8 gene, complete cds	B.taurus mRNA for RF-36-DNA-binding protein	Mus musculus ligand of numb-protein X (Lnx), mRNA	AV648521 GLC Homo sapiens cDNA clone GLCBKD02 3'	HOMEOBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEOBOX PROTEIN 2)	Homo sapiens partial TUB gene for tubby (mouse) honolog and LMO1 gene for LIM domain only 1 protein	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533 P90533 LIMA ;contains element LTR1 repetitive element;
ale Exort Fig.	Top Hit Database Source	EST HUMAN	EST_HUMAN	EST_HUMAN	LN	NT	NT	NT	۲	N	IN	Į.	EST_HUMAN	Z	Z	N.	EST HUMAN	NT	EST HUMAN	NT	Ę	NT	NT	NT	NT	EST_HUMAN	SWISSPROT	FN	NT	EST_HUMAN
3110	Top Hit Acession No.	4.9E-02 AA400914.1	4.9E-02 AW167821.1	4.9E-02 AW167821.1	.00122.1	.00122.1	4.9E-02 AF008303.1	8923880 NT	M19364.1	016471.1	016471.1	4.8E-02 AF003100.1	4.8E-02 W51983.1	K17144.1	254280.1	J91914.1	4.8E-02 AW388497.1	6981261 NT	4.7E-02.W01153.1	M62752.1	X15543.1	X89211.1	4.7E-02 AB026678.1	X15543.1	6754565 NT	4.7E-02 AV648521.1	>52951	4.7E-02 AJ277662.1	4.6E-02 AE000445.1	4.6E-02 Al014255.1
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	Expression	1.19	1.89	1.89	1.94	1.94	3.78	2.26	3.67	1.45	1.97	7.54	1.92.	212	1.67	1.28	1.31	0.78	3.41	1.65	9.71	1.18	2.63	7.44	1.76	2.35	2.35	1.39	2.74	1.06
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	Exan SEQ ID NO:	13459	14618	14618	15220	15220	18523	19107	19276	10287	10287	10424	12112	13097	14464	14946	16611	14818	16030	1		17056	17066	17197	18024		19743	19365	10654	11177
	Probe SEQ ID NO:	3543	4733	4733	5299	5299	8705	9490	9751	327	328	480	2227	3172	4572	9209	6731	4940	6085	6134	9800	7179	7189	7321	8136	9305	9652	9881	722	1270

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Table 4
Single Exon Probes Expressed in Heart

Top Hit Descriptor Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds. Divis aries CCAAT emhancer binding protein epsilon gene InviSNOS 1 NCI_CGAP_SS1 Homo sapiens CDNA clore IMAGE.1239221 37 Hepatitis E virus strain HEV-LUS2 polyprotein (DRF1), (DRF3), and capsid protein (DRF2) genes, complete cds ae3304.1 GeAP_SS1 Homo sapiens CDNA clore IMAGE.397631 57 Hemo sapiens within stumor Homo sapiens CDNA clore IMAGE.4107418 57 Morone savalitis myosin heavy chain FM3A (FM3A) mRNA, complete cds AVT04378 ADB Homo sapiens cDNA clore ADBACH08 67 Hemo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds PLECTIN Rat IGFII gene for insulin-like growth factor II AU133327 NTZRM2 Homo sapiens cDNA clore INTSRA200020 67 MA133327 NTZRM2 Homo sapiens cDNA clore INAGE.265684 35 similar to TR: O63291 Thermoplasma acidophilum complete genome; segment 4/6 MA133327 NTZRM2 Homo sapiens cDNA clore INAGE.265684 MA143337 NTZRM2 Homo sapiens cDNA clore INAGE.265684 MA143337 NTZRM2 Homo sapiens cDNA clore INAGE.265684 MA143337 NTZRM2 Homo sapiens cDNA clore INAGE.265694 MA143337 NTZRM2 Homo sapiens cDNA clore INAGE.265694 MA143337 NTZRM2 Homo sapiens cDNA clore INAGE.265694 MA143337 NTZRM2 Homo sapiens cDNA clore INAGE.265696 MA3501 AND NOL CGAP PIRT HOMO sapiens cDNA clore INAGE.26569 MA3610 AND NOL CGAP PIRT HOMO sapiens cDNA clore INAGE.26569 Heman mRNA for KIAA0160 genome, partial cds Legionella pneumophila cetalace peroxidase (katk) gene, complete cds Legionella pneumophila cetalace peroxidase (katk) gene, complete cds Heman mRNA for KIAA0160 gene, partial cds Legionella pneumophila cetalace peroxidase (katk) gene, complete cM174-18000000-410 BN0174 Homo sapiens cDNA		Top Hit Aces: No. No. AL1222689.1 AJ222689.1 AJ222689.1 AA736969.1 AA736969.1 AB040926.1 BE241245.1 AB040926.1 AB040926.1 AB04036.1 AL163210.2 AL163210.2 AL163210.2 AL163217.1 AL173327.1 AL123327.1 AL123327.1 AL45066.1 BE815822.1 BE815822.1	Mos J B H B H	Expres	RO		Probe SEQ ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:
PRRS Isolate PRRSV36 envelope glycoprotein gene, complete cds wt49g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'	NT EST_HUMAN			2.69	00807	11	9563
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partial cds	Z	-02/AF109907.1					4527
Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene							
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Table 4
Single Exon Probes Expressed

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3824	13736	23527	0.86	4.1E-02	BE297236.1	EST HUMAN	601177907F1 NIH MGC 17 Homo serviens cPNA close MAA OE: sesses si
4372			7.37	4.1E-02	4.1E-02 AW893484.1	EST HUMAN	QV1-NN0012-180400-164-706 NN0012 Homo saniens CDMA
6436	16297	26459	1.84	4.1E-02	7662347 NT		Homo sapiens KIAA0867 protein (KIAA0867), mRNA
6565	16423	26604	2.44	4.1E-02	4.1E-02 AF026198.1	Z	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds, putative protein 1 (PUT1) gene, partial cds, mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds, and calcitim channel subhed authorities.
9873	19682	24994	12.83	4.1E-02	4.1E-02 AJ271909.1	LZ	Brassica nabus din gane for plastid du famino auchtore
3206	13130	22932	2.68	4.0E-02	4.0E-02 AB040904.1	Z L	Homo sapiens mRNA for KIAA1471 protein, pertial cds
5304	15225	25029	4.92	4.0E-02	4.0E-02 AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6528	16387	26567	5.69	4.0E-02	4.0E-02 L23838.1	LN	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds.
7059	16936	27126	2.8	4.0E-02	4.0E-02 P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
7572	17423	.27638	2.42	4.0E-02	4.0E-02 AJ000941.1	NT	Methanobacterium thermoautofronhici im strain Marhura Thicl-furnace
8983	18788		1.94	4.0E-02		TN	Kluweromces lactis gene for Ca++ ATDece.
9196	19506	25135	4.96	4.0E-02		NT	Ovis aries mRNA for acety-coA carbondase
1104	11020	20863	2.77	3.9E-02	3.9E-02 BF516149.1	EST HUMAN	ULH-BW 1-anx-h-08-0-Ul st NC) CGAP Subz Home continue CDMA -to 11100
1322	11229	21084	3.46	3.9E-02 P41047		SWISSPROT	FAS ANTIGEN LIGAND
1918	11813	21691	3.04	3.9E-02	86.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2671	12536	-	2.29	3.9E-02	4506862 NT	LN LN	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kU (SDHC) mRNA
5105	14973	24748	96.0	3.9E-02	8924019 NT	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163) mRNIA
5105	14973	24749	0.98	3.9E-02	8924019 NT	LN	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
6581	16461	26654	1.22	3.9E-02	3.9E-02 BF239613.1	EST HUMAN	601906848F1 NIH MGC 54 Homo sapiens cDNA clone IMAGE 4134770 F
9056	19644		5.45	3.9E-02	3.9E-02 AB042553.1	Γ	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cyte.
7696	19248		1 #7	о С	0 E00001		Human germline T-cell receptor bata chain TCRBV17S1A1T, TCRBV2S31, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV34S1.
9811	19568	-	7 38	3.0E.02		2	OKBV331, JOKBV4S1411, IRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc
1909	11804	21683	0.94	3.8E-02		T HUMAN	linger protein 92, mmxq28ort 601510891F1 NIH MGC 74 Homo company CONA
						Į	COLOR OF THE COLOR OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE

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Single Exon Probes Expressed in Heart

	Top Hit Descriptor	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA	Human von Willebrand factor gene, exons 23 through 34	Homo sapiens PELOTA (PELOTA) gene, complete cds	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)	Homo saplens plasma membrane calcium ATPase Isoform 1 (ATP2B1) gene, alternative splice products, partial cds	wr85e08.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2494502.33	Homo sapiens mRNA for KIAA0718 protein, partial cds	EOMESODERMIN	601896233F1 NIH_MGC_19 Homo capiens cDNA clone IMAGE:4125584 57	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Komme3),	mRNA 2017 - Territoria	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'	Homo sapiens solute carrier family 22 (organic calion transporter), member 1 (SLC22A1), mRNA	H.vulgare Ss1 gene for sucrose synthase	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo	sapiens	Homo saplens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA	Chromatium vinosum sulfur globule protein Cv2 precursor (sgp2) gene, complete cds	nw20e05.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2TUBULIN BETA-1 CHAIN (HUMAN);	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes.	complete cds	Dictyostellum discoldeum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes.	ontile melanese time in EDNA	Orosophina metallogaster uggilli monyk, complete cos	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5	Thermotoga maritima section 85 of 136 of the complete genome
20201 1122 21	Top Hit Database Source		nH IN	된 된	SWISSPROT LA	Ho NT Par	T HUMAN	NT HO	SWISSPROT EC				T HUMAN		NT H.	유	NT	Ho NT sap	EST HUMAN CN	EST_HUMAN CM	NT	EST_HUMAN TU	Dio	NT	Dic				HUMAN	EST_HUMAN 602	NT
B	Top Hit Acession No.	E005700 NT	3.8E-02 M60675.1	3.8E-02 AF143952.2		3.7E-02 L14561.1	-	3.7E-02 AB018261.1		3.7E-02 BF312963.1		80541		3.7E-02 11418392 NT			3.6E-02 AL096806.1	3.6E-02 AL096810.1	3.6E-02 AW945516.1	3.6E-02 AW945516.1	3.6E-02 AF025952.1	3.6E-02 AA714521.1		3.6E-02 U20608.1						1	3.5E-02 AE001773.1
	Most Similar (Top) Hit BLAST E Value	3.8E-02	3.8E-02	3.8E-02	3.7E-02 P19137	3.7E-02	3.7E-02	3.7E-02	3.7E-02 P79944	3.7E-02	1	3.7E-02	3.7E-02	3.7E-02	3.6E-02		3.6E-02	3.6E-02	3.6E-02	3.6E-02	3.6E-02	3.6E-02		3.6E-02	3 RF-02/1/20/608 1	3 5E 021	2.0	3.5E-02/	3.5E-02	3.5E-02	3.5E-02
	Expression Signal	1.74	1.39	2.45	4.59	6.0	6.3	0.91	0.8	3.45			3.4	1.62	0.85		0.8	0.84	5	5	1.82	2.63	-	2.08	2.08	1 1	2 3	1.53	1.49	1.49	2.01
	ORF SEQ ID NO:	26355		28185	20746	21128	21982	22299	22733	22734		25.00	29119	25063	23306		23313	24773	26062	26063	26229	26349	-	27473	27474	20653	2000	20728	21309	21310	23798
	Exon SEQ ID NO:	16194	16910	17936	10899	11272	12077	12407	12940	12941	4000	13325	1886/	19539	13518		13526	15002	15932	15932	16080	16187		17269	17269	10803	200	10913	11449	11449	14020
	Probe SEQ ID NO:	6331	7033	8045	976	1366	2190	2533	3012	3013	0070	3408	2606	9755	3604		3612	5135	6028	6028	6214	6324		7402	7402	877		288	1544	1544	4120

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Table 4
Single Exon Probes Expressed in Heart

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Table 4
Single Exon Probes Expressed in Heart

Single Lyon Flobes Lypressed III near	Top Hit Descriptor	AU119006 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5	QV0-L10014-250200-129-h09 L10014 Homo sapiens cDNA	zs81a06.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE: 703858 5'	Enterococcus faecalis surface protein precursor, gene, complete cds	Pityokteines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product	zt65h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5	Saccharomyces cerevisiae stem-loop mutation supressor SSL2 gene, complete cds	Pseudomonas fluorescens family II aminotransferase gene, complete cds	QV2-ST0296-150200-040-e09 ST0296 Homo sapiens cDNA	EST74530 Pineal gland II Homo sapiens cDNA 5' end	601472331F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3875503 5'	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced	Homo sapiens mRNA for KIAA1573 protein, partial cds	Opprinus carpio mRNA for inducible nitric oxide synthase (iNOS gene)	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'	601512206F1 NIH MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds.	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in E-cells 1 (NFKB1) gene, complete	spo	Human dystrophin gene	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds	Thermotoga maritima section 109 of 136 of the complete genome	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1	ne87f04.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263	yh63d04.s1 Soaros placenta Nb2l IP Homo sapiens cDNA clone IMAGE:134407 3'	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA	Rattus norvegicus UDP-Gal:glucosylocramide bota 1,4 galactosyltransferase mRNA, compléte cds	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
ום ראחוו ב וחמם	Top Hit Database Source	EST_HUMAN A	EST_HUMAN Q	EST_HUMAN z	NT	_ d. ⊢N	HUMAN	NT	N		EST_HUMAN E	EST_HUMAN 6	H FN	IN	I	N	EST_HUMAN 6	EST_HUMAN 6	II O		ΝΤ		NT		H	EST HUMAN n	EST_HUMAN Y	EST_HUMAN Q	TN R	II 8	T_HUMAN
Sino	Top Hit Acesslon No.		3.1E-02 AW835313.1	3.1E-02 AA278478.1	3.1E-02 AF034779.1		3.0E-02 AA402242.1		3.0E-02 AF247644.1	1.	3.0E-02 AA364003.1	Ţ	3.0E-02 AF281074.1	3.0E-02 AF281074.1	3.0E-02 AB046793.1	3.0E-02 AJ242906.1	3.0E-02 BE889948.1	3.0E-02 BE889948.1	3.0E-02 AF213884.1		.1			3.0E-02 AE001797.1		3.0E-02 AA483216.1		3.0E-02 AW895565.1	3.0E-02 AF048687.1	2.9E-02 AF228703.1	2.9E-02 BE565644.1
	Most Similar (Top) Hit BLAST E Value	3.1E-02	3.1E-02	3.1E-02	3.1E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02/	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02/	3.0E-02	3.0E-02	3.0E-02		3.0E-02/	3.0E-02 M86524.1	3.0E-02/	3.0E-02/	3.0E-02	3.0E-02	3.0E-02 R32019.1	3.0E-02/	3.0E-02	2.9E-02	2.9E-02
	Expression Signal	0.82	66.0	2.33	2.62	2.82	1.07	1.07	2.61	96.0	1.18	68.0	6.02	6.02	2.88	2.71	3.58	3.58	1.79		1.79	1.54	2.11	1.71	3.09	7.7	1.66	4.67	2.09	1.1	1.07
	ORF SEQ ID NO:		24440		27843		22305	23234	23305			24444	24624	24625		26196	26109	26110	26101		26102	28311		28069	28701	29039	24909			22157	22687
	Exon SEQ ID NO:	14052	14652	15211	17615	11511	12415	13434	13517	13598	13777	14657	14858	14858	15233	16050	15974	15974	15967		15967	16158	16983	17828	18432	18745	19730	19273	19723	12720	12889
	Probe SEQ ID NO:	4152	4767	5290	7765	1605	2541	3518	8098	3585	3866	4773	4983	4983	5312	9909	6127	6127	6207		6207	6292	7106	7978	8562	8937	9336	9740	9780	2385	2962

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Exon SEQ ID NO: 12889 13762 14827 14827 14827 15705 16705 16705 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 16728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17728 17	R □	Signa	Most Not Not Not Not Not Not Not Not Not No	Top Hit Acession No. No. Hockerst Acession H72805.1 K65137.1 K65137.1 K65137.1 K65137.1 AW875976.1 AW875976.1 AW875976.1 AW875976.1 AF066063.1 BE741083.1 AF066063.1 AF066063.1 AF066063.1 AF066063.1 AF06896.1 AF06896.1 AL161494.2 NA7258.1 AA4903571.1 BF514858.1 AA4903571.1 AA490021.1 AA490021.1 AA490021.1 AA490021.1	Top Hit Database Source Source Source Source Source EST HUMAN NT EST HUMAN EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN NT EST HUMAN EST HUMAN EST HUMAN EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT EST HUMAN NT NT NT NT NT NT NT NT NT NT NT NT NT	Top I II Descriptor 101336428F1 NIH_MGC_53 Home capiens cDNA clone IMACE:3680656 5' 1014328F1 NIH_MGC_53 Home capiens cDNA clone IMACE:3680656 5' 1014528F1 NIH_MGC_53 Home capiens cDNA clone IMACE:3856566 5' 10144228F1 NIH_MGC_69 Home sapiens cDNA clone IMAGE:3856566 5' 10144528F1 NIH_MGC_69 Home sapiens cDNA clone IMAGE:3856566 5' 10144528F1 NIH_MGC_69 Home sapiens cDNA clone IMAGE:3856566 5' 1014528F1 NIH_MGC_99 Loda PT0014 Home sapiens cDNA 10145271 Sparse scale (FSCN2) gene, exp. 2 1014528F1 NIH_MGC_99 Home sapiens cDNA clone IMAGE:126675 5' 1014528F1 NIH_MGC_99 Home sapiens cDNA clone IMAGE:126675 5' 1014528F1 NIH_MGC_99 Home sapiens cDNA clone IMAGE:126675 5' 1014528F1 NIH_MGC_99 Home sapiens cDNA clone IMAGE:126675 5' 1014528F1 NIH_MGC_99 Home sapiens cDNA clone IMAGE:126675 5' 1014528F1 NIH_MGC_99 Home sapiens cDNA clone IMAGE:126675 5' 1014528F1 NIH_MGC_99 Home sapiens cDNA clone IMAGE:126675 5' 1014528F1 NIH_MGC_99 Home sapiens cDNA clone IMAGE:126675 5' 1014528F1 NIH_MGC_99 Home sapiens cDNA clone IMAGE:126675 5' 1014528F1 NIH_MGC_99 Home sapiens cDNA clone IMAGE:126675 5' 1014528F1 NIH_MGC_99 Home sapiens cDNA clone IMAGE:126675 5' 1014528F1 NIH_MGC_99 Home sapiens cDNA clone IMAGE:126675 5' 1014618788F1 NISH NICL CGAP_SILPT Home sapiens cDNA clone IMAGE:308250 3' 101472877289735 The IMAGE Sage Sage Sage Sage Sage Sage Sage Sage
1		1.55		AF109906.1 AW181945.1	NT EST HUMAN	Indus musculus with class in region RU gene, partial cds; bi, CZ, G94, NGZZ, G9, HOZ 70, HOZ 70, HOZ 70, HOZ 70, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes xj66f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE.2662409 3'
- 1		1.13		AW 181945.1	EST HIMAN	
		1.13		BE9089ZZ.1	ESI MUMAIN	00.10498//TKTINIT_MIGC_/4 notitio sapiens cuina cione imaget: 3433/80 3
Probe SEQ ID NO: NO: NO: 2962 2962 3851 4950 4950 6298 7568 7568 7568 7568 7568 7568 7568 756		Exon SEQ ID ID NO: 12889 13762 14827 14719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 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17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719 17719	Exon SEQ ID ID NO: Signa NO: 12889 22588 13762 23555 14827 24593 147419 27636 17419 27636 10494 13241 23047 14112 15293 25140 115726 26990 19574 13241 23048 13241 23048 13241 23048 13241 23049 19574 19574 19574 19579 19500 25134 10499 20305 12198 22096 12198 22096 13794 13794 13794 13794	Exon NO: CRF SEQ Expression Signal Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid Fluid 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Single Extent Flobes Expressed in near	Top Hit Descriptor	Chicken dorsalin-1 mRNA, complete cds	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1	xa52b04.x1 NCL_CGAP_Sar4 Homo sepiens cDNA clone IMAGE:2570383.3' similar to SW:Y069_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069;	qg27f11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA	Homo sapiens KIAA1070 protein (KIAA1070), mRNA	Homo sapiens chromosome 21 segment HS21C103	zs84c02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'	UI-HF-BN0-akj e-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'	602015501F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150944 5'	on26f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'	on26f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'	Rattus norvegicus rabphilin-3A mRNA, complete cds	H.carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1	H.carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA	ht36h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015.3'	7e30e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1 t1 L1	repetitive element ;	601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5	602070562F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213406 5'	602070562F1 NCL CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213406 5	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I	Bos taurus partial stat5B gene, exons 17-19	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II a pha	chain (IAapha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like (NG9),	Homo sapiens gene for LEGT2, complete cds
DIE EXUII F 10	Top Hit Database Source	NT	NT	EST HUMAN	EST HUMAN	EST_HUMAN	TN	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	Z	ΙZ	EST_HUMAN	EST HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	L		FZ	N.
	Top Hit Acession No.	2.6E-02 L12032.1	2.6E-02 AE002014.1	2.6E-02 AW241154.1	2.6E-02 AI206030.1	2.6E-02 BE621748.1	6981271	11432020 NT	2.6E-02 AL163303.2	2.6E-02 AA279351.1	2.6E-02 AW 500547.1	2.6E-02 BF343827.1	2.5E-02 AI793130.1	2.5E-02 AI793130.1	2.5E-02 BE974314.1	BE974314.1	2.5E-02 U12571.1	2.5E-02 X99897.1	2.5E-02 X99697.1	2.5E-02 BE701165.1	2.5E-02 BE701165.1	2.5E-02 AW592114.1		2.5E-02 BE670128.1	2.5E-02 BE746888.1	2.5E-02 BF526722.1	22.1			2.5E-02 AJ237936.1	i	2.5E-02 AF050157.1	2.5E-02 AB007546.1
	Most Similar (Top) Hit BLAST E Value	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02		2.5E-02	2.5E-02	2.5E-02	2.5E-02	2.5E-02 Q10335	2.5E-02 Q10335	2.5E-02		2.5E-02	2.5E-02
	Expression Signal	3.69	1.67	2.06	6.95	2.08	60.9	1.19	4.87	2.1	1.89	1.55	1.45	1.45	12.83	4.77	2.59	4.4	4.4	1.09	1.09	5.07		4.48	3.86	1.57	1.57	2.45	2.45	3.38		3.33	1.74
	ORF SEQ ID NO:	24481	24637	24667		25895	26113	27512	28038		28949		20274		20262			22652	22653		23644	23788					Ì	28320	28321	28370			
	Exon SEQ ID NO:	14695	14873	14898	15678	15776	15977	17306	17798	18579	18660	19715	10463	10463	10721	10778	12597	12853	12853	15070	15070	14011		15667	15674	16378	16378	18071	18071	18118		18135	18783
	Probe SEQ ID NO:	4811	4998	5025	5771	5870	6130	7388	7948	8692	8848	9320	521	521	792	851	2735	2926	2926	3959	3959	4111		5759	2767	6219	6519	8185	8185	8238		8255	8978

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ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top H it Acession No.	Top Hit Database Source	Top Hit Descriptor
	2.19	2.5E-02	11420078 NT	LN	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
	1.63	2.5E-02	11433220 NT	LN	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
25271	2.39		2.5E-02 BE973327.1	EST_HUMAN	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
19956	1.01	2.4E-02	2.4E-02 AI378582.1	EST_HUMAN	to72c07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3
21344	1.89		2.4E-02 H65884.1	EST_HUMAN	w75f11.r1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone (MAGE:211149 5'
21784	2.22	2.4E-02 P01901	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(3))
21785	2.22	2.4E-02 P01901	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
23948	1.4	2.4E-02	2.4E-02 J05110.1	۲	T.thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
24099	1.43	2.4E-02 P01901	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
24100	1.43	2.4E-02 P01901	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
	11.51	2.4E-02	2.4E-02 AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
27032	10.36		2.4E-02 N69442.1	EST HUMAN	2a35g11 s1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA done IMAGE 294596 3' similar to oblK02909IRATSR7K Rat (rRNA) contains A3R b1 A3R renetitive element
27714	217		2.4E-02 AV692954.1	EST HUMAN	AV692954 GKC Homo sapiens cDNA clone GKCDSC03 6
27808	2.98	2.4E-02	2.4E-02 AA493894.1	EST_HUMAN	nh07b12.s1 NCI_CGAP_Thy1 Homo saplens cDNA clone IMAGE:943583 similar to cortains Alu repetitive element; contains element PTR5 repetitive element;
0		L	2000	<u> </u>	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23,
00697	1.90	2.4E-02	Z.4E-UZ AF109905.1	Z	Muts nomaco, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
28957	1.96	2.4E-02	2.4E-02.4F109905.1	F Z	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog CLCP NG24 NG25 and NG26 genes, complete and improve general
	1.95	2.4E-02	9627909 NT	IN	Bacteriophage bIL67, complete genome
25357	2.72	2.4E-02	6753635 NT	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
25326	2.03	2.4E-02	2.4E-02 BE928869.1	EST_HUMAN	MR0-FT0175-310800-202-a06 FT0175 Homo sapiens cDNA
	1.27	2.4E-02	2.4E-02 AF163864.1	TN	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
	3.87	2.4E-02	2.4E-02 AB008569.1	LN	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete eds
	1.6	2.4E-02	2.4E-02 N42980.1	EST HUMAN	ly08a06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270610 5'
	1.38	2.4E-02	2.4E-02 BF679477.1	EST HUMAN	602153281F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294173 5'
	1.59	2.4E-02 P54643	P54643	SWISSPROT	SPORE COAT PROTEIN SP87 PRECURSOR (PL3 PROTEIN)
	5.79	2.3E-02	2.3E-02 W05340.1	EST_HUMAN	za84g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE: 299294 5
	7.89	2:3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, excn 4
22081	2.52	2.3E-02	2.3E-02 Z74293.1	LN	S.cerevisiae chromosome IV reading frame ORF YDI 245

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The special properties of the special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special special	Most Similar Top Hit Acession (Top) Hit Top Hit Acession (Top) Hit Top Hit Acession (Top) Hit Descriptor Signal BLASTE No. Signal Value	23329 4.79 2.3E-02 Z20377.1 EST_HUMAN	23735 1.19 2.3E-02 L24799.1 NT	23736 1.:9 2.3E-02 L24799.1 NT	24002 1.26 2.3E-02 AW899107.1 EST_HUMAN	24027 0.81 2.3E-02 BE935225.1 EST_HUMAN	24028 0.81 2.3E-02 BE935225.1 EST_HUMAN	24029 0.94 2.3E-02 AW593693.1 EST_HUMAN	24030 0.94 2.3E-02 AW593693.1 EST_HUMAN	24155 1.75 2.3E-02 BE143150.1 EST_HUMAN	24171 2.39 2.3E-02 BF026487.1 EST_HUMAN 601672279F1 NIH_MGC_	24172 2.39 2.3E-02 BF026487.1 EST_HUMAN	24591 1 2.3E-02 AI793177.1 EST_HUMAN	24592 1 2.3E-02 AI793177.1 EST_HUMAN	25027 3.57 2.3E-02 U86303.1 NT	26018 4 2.3E-02 AL161505.2 NT	26665 5.67 2.3E-02 U63610.1 NT	27841 1.51 2.3E-02 AE000199.1 NT			4 41 23E-02 BE 278331.1 EST HUMAN	25219 1.94 2.3E-02 U39394.1 NT	2.27 2.3E-02 U11077.1 NT		20482 3.09 2.2E-02 AF0182	1.53	21752 1.78 2.2E-02 Z82001.1	22448 1.4	1.93 2.2E-02 AA577785.1 EST_HUMAN	3.27 2.2E-02 AF083094.1 NT	23477 1.05 2.2E-02/AW601317.1 EST_HUMAN PM0-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
		23329	23735	23736	24002	24027	24028	24029	24030	24155	24171	24172	24591	24592	25027	26018	26665	27841	27842	28302		25219					21752	22448			23477
	Exon SEQ ID NO:	13542	7 13959	7 13959	3 14220	7 14244	7 14244	8 15072	15072	14366	14384	14384	14825	L	2 15223	15895	8 16478	4 17614	4 17614		\perp	L	7 19756	L		L	_	1_		Н	13691
	Probe SEQ ID NO:	3628	4057	4057	4323	4347	4347	4348	4348	4472	4490	4490	4948	4948	5302	5990	6598	7764	7764	0462	9201	9713	79767	9961	720	1713	1968	2695	3388	3595	377

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Single Extra Figures Expressed in real	Top Hit Descriptor	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1{1p36.33} of Homo	Septens Homo sanians hymothetical protein El (10379 (El 110370) mRNA	Homo serviens hypothetical protein FI J10379 (FI J10379) mRNA	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32	7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similer to contains MER1 t3 MER1 repetitive element;	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	(Sema6b), mRNA	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds	P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end	Homo sapiens chromosome 21 segment HS21C078	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'	Japanese encephalitis virus envelope protein mRNA, partial cds	wa17b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298315 3'	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32	601478819F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881477 5'	yd04c09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE.24675 5	nf19a07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.t1 L1	repetitive element;	EMPTY SPIRACLES HOMEOTIC PROTEIN	Homo sapiens chromosome 21 segment HS21C103	Homo sapiens chromosome 21 segment HS21C103	Arabidopsis thallana DNA chromosome 4, contig fregment No. 50
The Exoll Floor	Top Hit Database Source		T HUMAN	LN	Į.						EST HUMAN	1	NT	NT	LN		THUMAN		EST_HUMAN	NT	NT	LN T		THUMAN	LN	EST_HUMAN	EST_HUMAN		\neg	SWISSPROT	NT	NT	NT
Sills	Top Hit Acesslon No.	6753635 NT	2.0E-02 AA456538.1	6753635 NT	2 OE 02 AL 006005 4	ALUSGOUS. I	8922391	8922453 NT	8922453	2.0E-02 AL161532.2	2.0E-02 BF002932.1		7305474 NT	2.0E-02 AF095588.1	2.0E-02 M18095.1	2.0E-02 AL163278.2	2.0E-02 AA456538.1	2.0E-02 U70408.1	2.0E-02 A1640342.1	273966.1	2.0E-02 D88184.1	10947055 NT	10947055 NT	2.0E-02 AA456538.1	2.0E-02 AL161532.2	2.0E-02 BE786595.1	T80037.1		1.9E-02 AA572764.1	P18488	1.9E-02 AL163303.2	1.9E-02 AL163303.2	1.9E-02 AL161550.2
}	Most Similar (Top) Hit BLAST E Value	2.0E-02	2.0E-02	2.0E-02	CO 30 C	2.0E-02/	2.0C-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02		2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02 Z73966.1	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02	2.0E-02 T80037.1		1.9E-02	1.9E-02 P18488	1.9E-02	1.9E-02	1.9E-02
	Expression Signal	2.63	2.62	1.75	0.07	1.97	5	2.31	2.31	1.75	1.96		1.16	3.33	1.5	0.99	66.0	1.8	1.59	2.01	2.55	3.09	3.09	1.41	1.56	1.72	4.08		1.68	0.84	2.52	2.52	0.87
	ORF SEQ.			20550	00000	2003		21600			19795				23614		24730		28019				28032						20432	21364			22230
	Exon SEQ ID NO:		10256	10711	40004	14002	11002	11727	1	12630		<u> </u>	{	13114	13834	14949	14955	17529	17780		18566		18739	14955	12630	19536	19404			11504			12335
	Probe SEQ ID NO:	259	292	781	4074	1181	1184	1830	1830	2768	3040		3105	3189	3925	6209	2802	7679	7930	8037	8678	8931	8931	9019	9481	9558	9935		678	1599	1993	1993	2458

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Table 4
Single Exon Probes Expressed in Heart

Top Hit Descriptor	nw04f05.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'	AV648669 GLC Homo sapiens cDNA clone GLCBLH07 3'	Urotrichus talpoides mitochandrial gene for cytochrome b, complete cds	yz28b02.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284331 3'	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'	qn04c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive	element;	Mycoplasma imitans VIhA1 precursor (vIhA1) and VIhA2 precursor (vIhA2) genes, partial cds	HOMEOTIC BICOID PROTEIN (PRD-4)	HOMEOTIC BICOID PROTEIN (PRD-4)	t/48d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to	alleans All reprouve Continents	Arabiopois Inaliana DIAA cirionosome 4, contiguidament no. 50	Meleagris gallopavo paraoxonase-2 (PON2) mKNA, complete cds	Neisseria meningitdis serogroup A strain Z2491 complete genome; segment 3/7	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'	Hirudo medicinalis intermediate filament gilarin mRNA, complete cds	hn52c06.x1 NCL_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element. MFR29 renetitive element :	AD1894329F1 NIH MGC 17 Home saniens cDNA clone IMAGF 4139983 5	H.francisci mRNA for myelin basic protein (MBP)	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome	te52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'	MR1-0T0011-280300-009-g04 OT0011 Homo sapiens cDNA	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA	HYPOTHETICAL PROTEIN DJ845024.2	qm06b04.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881007 3'	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW S'REGION	aj62f09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb:L11672 ZINC FINGER PROTEIN 91 (HUMAN);
Top Hit Database Source	HUMAN	T HUMAN		EST_HUMAN	EST_HUMAN		EST_HUMAN	LNT	SWISSPROT	SWISSPROT	North	NEWDL					EST_HUMAN	LN		EST HIMAN	7	N.	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	SWISSPROT	EST_HUMAN	SWISSPROT	EST_HUMAN
Tap Hit Acession No.	1.9E-02 AA713856.1	1.9E-02 AV648669.1	1.9E-02 AB033611.1	N52250.1	1.9E-02 BE738088.1		1.9E-02 Al301183.1	1.9E-02 AF141940.1	P09081	P09081	1 0000 TV	1.9E-02 A1452999.1	1.9E-02 AL161550.2	1.9E-02 L47572.1	1.9E-02 AL162754.2	1.9E-02 BF316129.1	1.9E-02 BF695832.1	1.9E-02 AF101065.1	1 8E 02 AW777104 1	1.0C-02 AVVIVIOR	1.8F-02 X17664.1	1.8E-02 AF243382.1	AE004544.1	1.8E-02 AI805829.1	1.8E-02 AW879122.1	1.8E-02 AW879122.1	1.8E-02 AA861446.1	1.8E-02 AW936363.1	1.8E-02 O60810	1.8E-02 AI288701.1	1.8E-02 P14310	1.8E-02 AA897543.1
Most Similar (Top) Hit BLAST E Value	1.9E-02	1.9E-02	1.9E-02	1.9E-02	1.9E-02		1.9E-02	1.9E-02	1.9E-02 P09081	1.9E-02 P09081	L	1.9E-02	1.9E-02	1.9E-02	1.9E-02														ĺ			
Expression Signal	7.08	1.53	0.82	1.25	5.75		0.98	1.14	1.47	1.47		7.51	1.9	1.29	1.29	1.47	1.31	2.55	77.	† † *	134	1 23	1.51	0.89	1.09	1.09	1.15	1.44	1.05	1.06	3.96	2.49
CRF SEQ ID NO:		22650					23355		23777	23778				25105		27452	27859	25137	20447						23513			24011				
Exon SEQ ID NO:	12802	12850	13146	13474	13658		13568	13868	13999	13999		14335	12335	15276	16862	17246	17627	19516	4000	10307	11057	11323	12512		13724	L	<u> </u>	1.	_	L	ł.	17411
Probe SEQ ID NO:	2875	2923	3222	3560	3644		3654	3961	4039	4099		4441	4944	5356	6985	7377	7777	9234		24.5	1144	1417	2645	3174	3812	3812	3996	4332	4873	4887	6075	7560

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Single Exon Probes Expressed in Heart

ייין אין פסטטער	Top Hit Descriptor	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866963 51	L. stagnalis mRNA for myomodulin neuropeptide precursor	Homo sapiens mRNA for KIAA0339 protein, partial cds	Homo sapiens mRNA for KIAA0339 protein, partial cds	Pyrococcus horikoshii OT3 gencmic DNA, 1166001-1485000 nt. position (6/7)	Zea mays acidic ribosomal protein P2a-3 (rpp2a-3) mRNA, partial cds	Drosophila melanogaster projectin (projectin) gene, partial cds	601310626F1 NIH MGC 44 Homo sapiens cUNA clone IMAGE: 3632730 5 ministrations	hf34e03.xf Soares_NFL_I_GBC_S1 Homo sapiens convergence.zess/40 seriman to contains. L1.ft L1 repetitive element;	h34a03.x1 Soares NFL T GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains	L1.t1 L1 repetitive element;	Homo sapiens chromosome 21 segment HS21C004	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mKNA	ob22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982.3	hm45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains	MER19.b1 MER19 repetitive element;	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	ac19f04.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Aiu	repetitive element;contains element MER24 repetitive element ;	ye86f08.rt Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element ;	Messenger RNA for anglerfish (Lophius americanus) somatostatin II	ov51e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE.1640858 3'	Murid herpesvirus 4 complete genome	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 2367113 3' similar to	contains Alu repelitive element;	Homo sapiens nebulin (NEB), mRNA	Homo sapiens hyperion gene, exons 1-50	DKFZp434I0314_r1 434 (synonym: htes3) Homo sapiens cDNA clone UKr-2p434I0314 5	CM4-NN1030-040400-130-106 NN1030 Homo sapiens culva	OIL-OPECIFIC EXTENSIN-LINE PROTEIN PALOGNOSTIVI CLA /
Single Exoli Flores Explosed in	Top Hit Database Source	EST_HUMAN 60	N.1						EST_HUMAN 60	FST HUMAN (L1	7	EST_HUMAN L1		NT O		EST HUMAN qb	1	_			EST HUMAN re	EST HUMAN ye	EST HUMAN L1		EST HUMAN OV		M	EST_HUMAN co		_	EST_HUMAN D	\neg	SWISSPROT
ignic	Top Hit Acession No.	1.8E-02 BE778274.1 E		1.8E-02 AB002337.2 N	1.8E-02 AB002337.2	1.8E-02 AP000006.1		1.8E-02 AF047475.1	1.7E-02 BE394869.1	1 7E_02 AW573183 1		1.7E-02 AW573183.1			7657495 NT	1 7E-02 A1147615.1		1.7E-02 AW827368.1			Ξ.	1.7E-02 R02506.1	1 7E-02 AW573183.1		-	-		1.7E-02 AI769247.1	8400716	AJ010770.1		1.7E-02 AW903482.1	Q03211
	Most Similar (Top) Hit BLAST E Value	1.8E-02	1.8E-02 X96933.1	1.8E-02	1.8E-02	1.8E-02/	1.8E-02 U62749.1	1.8E-02 /	1.7E-02	1 7E_02	, , , , , ,	1.7E-02	1.7E-02	1.7E-02	1.7E-02	1 7F-02		1.7E-02	1.7E-02 P04929		1.7E-02	1.7E-02	1.75-02	1 7F-02	1.7E-02	1.7E-02			1.7E-02	1.7E-02			
	Expression Signal	1.51	1.23	1.78	1.78	1.76	3.12	1.29	1.29	VC C	7.7	2.24	3.08	13.03	1.35	0 0	76.0	4.17	0.88		86.0	1.78	1 24	14	527			1.53	2.31	1.81	1.48		1.96
	ORF SEQ ID NO:	27873	27966	28126	28127	28991	29000		20662	7	81017	21520				72805	CEOST						0440			24612		25735			27659	24995	
•	Exon SEQ ID NO:	17640	17721	17884	17884	18697	18706	19496	10814	_	2001	11650	L	1.		1	L	13383	\perp	1_	13980	L	<u> </u>	1	1		丄	15632		L	17443		19352
	Probe SEQ ID NO:	0622	7871	8735	8735	8886	8897	9912	888	35.	1/20	1750	182R	2066	2603	9000	2002	3467	3573		4078	4105	7,07	44.46	4708	4067	Det	5725	6276	6554	7592	9781	9861

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Single Exon Probes Expressed in Heart

	Top Hit Descriptor	Mycobacterium tuberculosis H37Rv complete genome, segment 13/162	Treponema maltophilum flaB2, flaB3 and filD genes for flagellin subunit proteins and CAP protein homologue	LIVER CARBOXYLES LERASE 22 PRECURSON (EGASTIN) (ESTERASE-22)	VER CARBOARLES I ERRASE 22 PRECORSON (CONSTIN) (CONSTIN)	Homo sapiens KVLQ 11 gene	ne81d06.s1 NC_CGAP_Ew1 Homo sapiens cUNA clone IMAGE.91000/	Homo sapiens mRNA for KIAA0634 protein, partial cds	[L3-C102/9-160200-063-C07 CT0219 Homo sapiens CDNA	Mus musculus major histocompatibility complex region NG27 , NG28, KP-S28, NADH oxidoreducterse, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, NG29, 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P29294 TELOKIN. [1];	nf19g03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT	P29294 TELOKIN. [1];	G gallus microsetelitie DNA (LEI∪Zo∪ (=1 tolite 11))	Arabidopsis thaliana DNA chromosome 4, contigurant in a contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contiguration and contigurat	Arabidopsis thaliana UNA chromosome 4, contig fragment No. 20	4296e10.x1 Soares pregnant uterus Nahrru Homo saptens cunna ciulle ilvina ci. 2042442 3	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASTN) (ESTERASE-22)	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASTN) (ESTERASE-22)	R.norvegicus gene for choline acetyltransferase, exon 1 (non codIng)	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mKNA	Homo sapiens transcription factor (HSA130894), mRNA	yv27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3	Arabidopsis thaliana DNA chromosome 4, contig tragment No. 90	Homo sapiens CACNA1F gene, exons 1 to 48	Homo sapiens CACNA1F gene, exons 1 to 48
Page Hove Pignio	Top Hit Database Source	NT NT		\exists	IISSPROT		T HUMAN	\Box	EST_HUMAN II	23	LN LN	T HUMAN					1 N	EST HUMAN F	Γ	T HUMAN			LN			SWISSPROT	N			EST_HUMAN	IN		LZ.
2 -	Top Hit Acession No.	1.6E-02 AL021929.1				1	1.6E-02 AA484872.1	- .	1.6E-02 AW850652.1		4 RE-02 AE110520 1	-	TIM SETATABINIT	1.0E-UZ 007.17.13			1.6E-02 AF079764.1	1.6E-02 AA572818.1		1.6E-02 AA572818.1	1.6E-02 Z94828.1	1.6E-02 AL161508.2	1.6E-02 AL161508.2	1.6E-02 Al373558.1	1.6E-02 Q64176	1.6E-02 Q64176	1.6E-02 X92751.1	11417966 NT	8923734 NT	1.5E-02 N39521.1	1.5E-02 AL161594.2	1.5E-02 AJ006216.1	1.5E-02 AJ006216.1
-	Most Similar (Top) Hit BLAST E Value	1.6E-02	1.6E-02 Y18889.1	1.6E-02 Q64176	1.6E-02 Q64176	1.6E-02/	1.6E-02	1.6E-02	1.6E-02		4 6F-02	1 65-02	10.1	1.0E-02	1.05-02	1.6E-02	1.6E-02	1.6F-02		1.6E-02	1.6E-02		1.6E-02	1.6E-02				1.6E-02	1.5E-02	Ŀ			
	Expression Signal	1.58	1.13	1.13	1.13	0.98	1.47	1.14	3.83		c	27.10	+	1.31	2.11	4.01	2.71	1.47		1.47	2.17	2.52	2.52		1.35	1.35	2.3	1.42	24.9				1.44
	ORF SEQ ID NO:		21399	21990	21991	22284			23202						26032			77080		28045	28401		L							21879			1 22744
	Exon SEQ ID NO:	10443	11539	12089	12089		1						-	\perp		16637	17623	L	Л.	17804	19473	1_	L			L	\perp	1		L		_l_	Ш
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Single Exon Probes Expressed in Heart

		Т	Т	T	Τ	1	Τ	Τ	Т	Τ	Τ	Ţ	T	T	T	Т	Т	\top	Т	1	1	T	T	٦		T	T	Τ	Т	Т	Τ	Т	
Origin Lydrosod III Idai.	Top Hit Descriptor	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA	zq40g10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632226 5'	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I	Cyanophora paradoxa cyanelle, complete genome	Homo sapiens KIAA1009 protein (KIAA1009), mRNA	Homo sapiens chromosome 21 segment HS21C103	Homo sapiens valyf-tRNA synthetase 2 (VARS2), mRNA	602019135F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154504 5'	Saccharomyces cerevisiae chromosome VI plasmid GapC	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's	RC4 CN0049-140100-011-c11 CN0049 Homo sapiens cDNA	AU134730 PLACE1 Homo sapiens cDNA clone PLACE1000374 5'	Chlamydophila pneumoniae AR39, section 58 of 94 of the complete genome	Homo sapiens NESH protein (LOC5/225), mRNA	Haemophilus influenzae Rd section 115 of 163 of the complete genome	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds	Homo sapiens headpin gene, complete cds	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'	Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (agil.)	genes, complete cds, and n-acetyglucosamine/xytose repressor protein (nagC/xytR) gene, partial cds	Wousdoy X1 NCL CGAP GU1 Home sapiens cUNA clone IMAGE:2575/93 3	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA	EST374761 MAGE resequences, MAGG Homo sapiens cDNA	EST374761 MAGE resequences, MAGG Homo sapiens cDNA	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
פון ווסעד פול	Top Hit Database Source	EST HUMAN	EST_HUMAN	NT	SWISSPROT	LN	TN	NT	LN	EST_HUMAN	LN	EST_HUMAN	EST HUMAN	INT	EST_HUMAN	EST_HUMAN	NT	NT	TN	NT	NT	EST_HUMAN	ŀ	N I	ES HOMAN	NT	LN	NT	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN
	Top Hit Acessíon No.		1.5E-02 AA160967.1	1.5E-02 AF260225.1	209711	11467282 NT	11418713 NT	1.5E-02 AL163303.2	11417739 NT	1.5E-02 BF345554.1	044606.1	32667.1	32667.1	40609.1	1.5E-02 AW750834.1	1.5E-02 AU134730.1	1.4E-02 AE002230.2	7705980 NT	1	167779.1	1.4E-02 AF216854.1	1.4E-02 AV723785.1					1.4E-02 AL161586.2	4503628 NT	6996918 NT	W962688.1	1.4E-02 AW962688.1	1.4E-02 BE733142.1	1.4E-02 BE733142.1
	Most Similar (Top) Hit BLAST E Value	1.5E-02 E	1.5E-02]/	1.5E-02	1.5E-02 Q09711	1.5E-02	1.5E-02	1.5E-02/	1.5E-02	1.5E-02	1.5E-02 D44606.	1.5E-02 R32667.	1.5E-02 R32667.	1.5E-02 L40609.1	1.5E-02	1.5E-02	1.4E-02/	1.4E-02	1.4E-02 U32800.	1.4E-02 U67779.1	1.4E-02	1.4E-02	L	1.4E-02 /	1.45-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02	1.4E-02 AW9626	1.4E-02	1.4E-02 B	1.4E-02 E
	Expression Signal	0.9	1.23	0.91	1.91	1.66	1.36	1.53	3.44	1.23	2.07	1.25	1.25	2.5	1.32	1.47	1.45	3.58	1.35	2.82	0.94	96.0	•	6.0	0.99	5.21	5.21	0.98	6.16	7.29	7.29	6.7	6.7
	ORF SEQ ID NO:	23365	23727	24048	25819			26664	26668	27195	27545	27717	27718	28647				20860												24062			24446
	Exon SEQ (D NO:	13577	13951	14263	15707	16195	16239	16476	16480	17003	17339	17496	17496	18380	19559	19437	10357	11018	11143	11184	11280	11405	970	13101	132/2	13356	13356	13392	13520	14283	14283	14659	14659
	Probe SEQ ID NO:	3663	4049	4367	5801	6332	6377	9659	0099	7126	7520	7646	7646	8208	9429	0866	411	1102	1236	1276	1374	1501	24.40	0/10	3322	3439	3439	3476	3606	4387	4387	4775	4775

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Table 4
Single Exon Probes Expressed in Heart

					6		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5862	15768	25887	4.62	1.4E-02	1.4E-02 AA559030.1	EST_HUMAN	nl11c04.s1 NCI_CGAP_Br2 Homo sepiens cDNA clone IMAGE:1029990 3' similar to contains Alu repet tive element;
5862	15768	25888	4.62	1.4E-02	1.4E-02 AA559030.1	EST_HUMAN	nl11c04.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
6732	16612		1.82	1.4E-02	1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 88/162
7408	17275	27481	207	1.4E-02	1.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5
9126	18885		4.79			NT	Human IFNAR gene for interferon alpha/beta receptor
9476	19102		1.55		1.4E-02 AF324985.1	LN	Arabidopsis thaliana F21J9.2 mRNA, complete cds
9753	19277		1.89	1.4E-02	11426968 NT	. 1	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1821	11718		0.86		1.3E-02 BE739263.1	EST HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'
1912	11807	21684	2.41	1.3E-02	1.3E-02 AL163201.2	LN	Homo sapiens chromosome 21 segment HS21C001
3177	13102	22906	1.99			EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3177	13102	22907	1.99		1.3E-02 BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5
3888	13799		1.41	1.3E-02	1.3E-02 AF169288.1	TN	Mus musculus beta-sarcoglycan gene, complete cds
5176	11807	21684	+	1.3E-02	1.3E-02 AL163201.2	LN	Homo sapiens chromosome 21 segment HS21C001
							Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc
5212	15135	24854	1.36		1.3E-02 AL049866.2	NT	finger protein 92, mmxq28orf
							Mus musculus chromosome X conttgB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc
5212	15135	24855	1.36		1.3E-02 AL049866.2	L	finger protein 92, mmxq28orf
6156	15114		1.35		1.3E-02 AL161546.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6156	15114	24857	1.35		1.3E-02 AL161546.2	LZ	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
							ow06g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to
6473	16332		4.77		1.3E-02 Al031593.1	EST_HUMAN	contains Alu repetitive element;
6669	16817	_	1.74		1.3E-02 AF156961.1	NT	Homo sapiens human endogencus retrovirus W gagC3.37 G gag (gag) gene, complete cds
7862	17712	27956	1.87		1.3E-02 M63707.1	NT	
8360	18237	28484	4.39		1.3E-02 AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone iMAGE::2815036 3'
8360	18237		4.39		1.3E-02 AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
9102	19705		2.92		1.3E-02 X51780.1	LN L	Yeast ABP1 gene for actin binding protein
9482	19694		1.6		1.3E-02 Z99117.1	LΝ	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
9286	19170		1.8		TN 6905596	TN	Human herpesvirus 6B, complete genome
9758	19486		28.64		1.3E-02 AF152238.1	TN	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
9949	19744	24912	1.32		1.3E-02 AF009179.1	NT	Oryza sativa replication protein A1 (Os-RPA1) mRNA, complete cds
206	10177		0.94		1.2E-02 X87344.1	ÑΤ	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes

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	Top Hit Database Top Hit Descriptor Source	Z165g01.r1 Soares retina N254HR Homo sapiens cDNA clone IMAGE:381940 5' similar to contains element EST HUMAN L1 repetitive element;	Т	qd68e12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.t1_1 = EST_HUMAN repetitive element:		T HUMAN	EST HUMAN 601068408F1 NIH MGC 10 Homo sapiens cDNA clone IMA GF 3454608 5	EST HUMAN 601068406F1 NIH MGC 10 Homo sapiens cDNA clone IMAGF 3454608 5		EST_HUMAN zm88e03.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone INA GE-545n20 5	EST_HUMAN v11b08.s1 Soares placenta Nb2HP Homo saplens cDNA clone IMAGE:138903.3		Cynons pyrthogaster Cal Nind TimRNA negliglade	T HUMAN			T_HUMAN				HUMAN			SWISSPROT PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGHT) (HPER)	SWISSPROT COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR	EST_HUMAN C18119 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GFN-557G06 5	EST_HUMAIN zm69e11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924.33		
	Top Hit Acessian No.	9.1		-	12			1.2E-02 BE538310.1 ES				TN. 1828	-			F175412.1				-			J246003.1				.1		75491.1 NT
-	Most Similar (Top) Hit BLAST E Value	1.2E-02 AA059290	1.2E-02 P38898	1.2E-02 Al183522	1.2E-02 A	1.2E-02 A	1.2E-02 B	1.2E-02 B	1.2E-02 A	1.2E-02 AA075418.1	1.2E-02 R62805.1	1.2E-02 U91328 1	1.2E-02 AB019786	1.2E-02 AV731704.1	1.2E-02 D78589.1	1.2E-02 AF175412.1	1.2E-02 AV732093.1	1.2E-02 Q11205	1.2E-02 AF193612.1	1.2E-02 AF193612	1.2E-02 T76987.1	1.2E-02 AB031013.1	1.2E-02 AJ246003	1.2E-02 015534	1.2E-02 P17139	1.2E-02 C18119.1	1.1E-02 AA070364	1.1E-02 X75491.1	1.1E-02 X75491.1
	Expression Signal	1.74	1.48	2.98	1.99	1.23	1.1	1.1	1.27	6.18	1.89	2.04	1.73	2.12	1.96	5.33	6.37	2.11	1.22	1.22	1.17	2.45	1.23	1.78	1.5	3.47	1.32	1.99	1.99
	ORF SEQ ID NO:	20128	20210	20483	21916	22167	22223	22224	22167		22971	24495		24659	25497	26216	26352	26742	26832	26833		27623	27640	25345			21004	21451	21452
	Exon SEQ ID NO:	10310	10389	10653	12018	12271	12325		١ ا		13173	14712	14849	14891	15434	16066	16190	16545	16644	16644	17029	17408	17426	18918	19575	19286	11155	11581	11581
	Probe SEQ ID NO:	352	445	721	2130	2393	2448	2448	2596	3063	3250	4830	4974	5017	5516	6180	6327	6665	6765	6765	7152	7557	7575	9177	9588	926	1248	1679	1679

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Single Exon Propes Expressed in near	Most Similar (Top Hit Acession Database BLAST E No. Source	1.1E-02 BF345263.1 EST_HUMAN 602018037F1 NCI_CGAP_Brn67 Homo sepiens cDNA clone IMAGE:4153808 5	EST_HUMAN	1.1E-02 AF055066.1 NT	1.1E-02 AI653508.1 EST_HUMAN	1.1E-02 BE144637.1 EST_HUMAN			1.1E-02 AW820281.1 EST_HUMAN	1.1E-02 BE149611.1 EST HUMAN	1.1E-02/Q61982 SWISSPROT NEUROGENIC LOCUS NOTCH 3 PROTEIN	1.1E-02 AA082578.1 EST_I1UMAN	1.1E-02 AA314665.1 EST_HUMAN	1.1E-02 11435505 NT	1.1E-02 AA668239.1 EST_HUMAN	1.0E-02 AW846120.1 EST_HUMAN	1.0E-02 AW368128.1 EST_HUMAN	1.0E-02 AA806389.1 EST_HUMAN	1.0E-02 BE835556.1 EST_HUMAN	1.0E-02 BE968999.1 EST_HUMAN	1.0E-02 AW845621.1 EST_HUMAN	1.0E-02 A1065086.1 EST HUMAN	1.0E-02 6753521 NT	1.0E-02 R96567.1 EST_HUMAN	1.0E-02 AF218910.1	1.0E-02 BE876539.1 EST_HUMAN	1.0E-02 AW577113.1 EST_HUMAN	1.0E-02 AW577113.1 EST_HUMAN	1.0E-02 Z29642.1 NT	1.0E-02 BF036331.1 EST HUMAN	1.0E-02/BF036331.1 [EST_HUMAN 601459570F1 NIH_MGC_66 Homo sapiens CLINA clone IMAGE:3853177.3
	Aost Similar (Top) Hit BLAST E Value	1.1E-02	1.1E-02	1.1E-02	1.1E-02	1.1E-02	1.1E-02	1.1E-02	1.1E-02	1.1E-02	1.1E-02	1.1E-02	1.1E-02	1.1E-02	1.1E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02
	Expression Signal	4.35	3.53	10.39	2.46	0.87	76.0	1.81	0.92	2.26	6.87	2.25	4.1	3.38	2.23	3.35	0.91	1.2	2.37	1.18	66.0	0.79	4.26	2.38	0.85	0.82	2.74	2.74	2.06	4.65	4.65
	ORF SEQ ID NO:	21778		22660	23200		-	24395		26506	27230	27785	27900	28476	-	19785	21270	-	22771	22950		23505	24345	24407	24633		25766		26178	27475	27476
	Exon SEQ ID NO:	11886	12776	12860	13394	13846	13921	14609	14704	16339	17037	17560	17660	18224	18845	9992	11411	12399	12978	13150	13380	13717	14553	l_	<u> </u> _	15016	1	15659	<u> </u>		17270
	Probe SEQ ID NO:	1992	2848	2933	3478	3937	4016	4723	4821	6480	7160	77.10	7810	8347	9064	9	1508	2525	3051	3226	3464	3805	4667	4736	4995	5149	5751	5751	6054	7403	7403

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ORF SEQ Expression (Top) Hit Top Hit Acession Signal RLASTE No. Signal BLASTE No. Signal BLASTE No. Signal BLASTE No. Signal RLASTE No. Signal Signal Albert No. Signal RLASTE No. Signal 1.0E-02 AF157559.1 NT 1.0E-02 AF15759.1 NT 1.0E-02 AW935521.1 EST_HUMAN 1.0E-02 AW935521.1 EST_HUMAN 1.0E-02 SY0330.1 NT 1.0E-02 SY0330.1 NT 1.0E-02 SY0330.1 NT 1.0E-02 SY0330.1 NT 1.0E-02 SY0330.1 NT 1.0E-02 SY0330.1 NT 1.0E-03 AL161559.2 NT 1.0E-03 AL161559.2 NT 1.0E-03 AL161559.2 NT 1.0E-03 AL161559.2 NT 1.0E-03 AL161559.2 NT 1.0E-03 AL161559.2 NT 1.0E-03 AL161559.2 NT 1.0E-03 AL161569.2 NT 1.0E-03 AL161569.1 NT 1.0E-03 AL161569.1 NT 1.0E-03 AL161569.1 NT 1.0E-03 AL161569.1 NT 1.0E-03 AL163261.1 NT 1.0E-03 AL163261.1 NT 1.0E-03 AL163261.1 NT 1.0E-03 AL163261.2 NT 1.0E-03 AL163261.2 NT 1.0E-03 AL163283.2 NT 1.0E-03 AL1								
18454 2.1 1.0E-02 AF157559.1 NT I 1852 28846 2.03 1.0E-02 AV760016.1 EST HUMAN 19762 1.7 1.0E-02 Q62203 SWISSPROT 19536 2.96 1.0E-02 GAV93551.1 EST HUMAN 19530 2.24 1.0E-02 SV3350.1 NT 19645 2.24 1.0E-02 SV3350.1 NT 1150 2.2123 3.26 9.0E-03 AV35727.1 NT 12265 2.2356 1.08 9.0E-03 AL243727.1 NT 12803 2.2567 0.83 9.0E-03 AL243727.1 NT 14703 2.2568 0.83 9.0E-03 AL243727.1 NT 14703 2.268 9.0E-03 BE74744.1 EST HUMAN 15045 2.2749 1.17 9.0E-03 BE747940.1 NT <	Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
19562 28846 2.03 1.0E-02 (AV760016.1) EST_HUMAN 19762 1.7 1.0E-02 (AV2603.3) SWISSPROT 19762 1.7 1.0E-02 (AV935521.1) EST_HUMAN 19590 2.44 1.0E-02 (AV935521.1) RT 19591 2.24 1.0E-02 (AV935521.1) RT 19592 2.24 1.0E-02 (AV935521.1) RT 19645 2.24 1.0E-02 (AV935521.1) RT 11500 2.2123 3.26 9.0E-03 (AL76159.2) NT 12226 2.2356 1.08 9.0E-03 (AL76159.2) NT 12803 2.2356 1.08 9.0E-03 (AL76159.2) NT 12803 2.2356 1.08 9.0E-03 (AL7614.1) EST_HUMAN 12803 2.2557 0.83 9.0E-03 (AL7744.1) EST_HUMAN 14793 2.4568 1.17 9.0E-03 (AL7340.1) NT 15045 2.2567 0.83 9.0E-03 (AL7340.1) NT 15045 2.749 1.47 9.0E-03 (AL7640.1)	8586	1		2.1	1.0E-02	-		Crithidia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochcndrial gene for nitochondrial product
19762 1,7 1,0E-02 (362203) SWISSPROT 19535 25061 2,95 1,0E-02 (370330.1) NT 19546 2,24 1,0E-02 (370330.1) NT 19847 2,651 1,27 6,0E-03 (370330.1) NT 10801 20551 1,17 6,0E-03 (370330.1) NT 11550 22123 3,26 9,0E-03 (370330.1) NT 12226 222356 1,08 9,0E-03 (37077.1) NT 12803 22356 1,08 9,0E-03 (37077.1) NT 12803 22557 0,83 9,0E-03 (37074.1) NT 14793 24568 1,17 9,0E-03 (37074.1) NT 15045 256 9,0E-03 (37074.1) NT 15045 2,458 1,17 9,0E-03 (37074.1) EST HUMAN 17523 27749 1,47 9,0E-03 (370909.1) EST HUMAN 15045 1,47 9,0E-03 (370909.1) EST HUMAN 15045 1,27 9,0E-03 (370909.1) EST HUMAN <td>8674</td> <td></td> <td></td> <td>2</td> <td>1.0E-02</td> <td>_</td> <td>HUMAN</td> <td>4V760016 MDS Homa saplens cDNA clone MDSBDC10 5'</td>	8674			2	1.0E-02	_	HUMAN	4V760016 MDS Homa saplens cDNA clone MDSBDC10 5'
19535 25061 2.95 1.0E-02 AW935521.1 EST HUMAN 19545 5.22 1.0E-02 S70330.1 NT 19645 2.44 1.0E-02 X62654.1 NT 10801 2.0651 1.7 9.0E-03 AI796128.1 EST HUMAN 1150 1.97 9.0E-03 BE781889.1 EST HUMAN 12265 22123 3.26 9.0E-03 AJ243727.1 NT 12803 22356 1.08 9.0E-03 AJ243727.1 NT 12803 22587 0.83 9.0E-03 AJ243727.1 NT 14763 22588 0.83 9.0E-03 AJ243727.1 NT 14793 22588 0.83 9.0E-03 AJ243727.1 NT 14793 22588 0.83 9.0E-03 AJ243727.1 NT 14793 24568 1.17 9.0E-03 AJ243727.1 NT 14793 24588 1.17 9.0E-03 BF73744.1 EST HUMAN 15045 2.56 9.0E-03 AJ28727.1 NT 16477 1.18 9.0E-03 AJ28728.1 EST HUMAN <td>9142</td> <td><u> </u></td> <td></td> <td></td> <td>1.0E-02</td> <td>062203</td> <td></td> <td>SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)</td>	9142	<u> </u>			1.0E-02	062203		SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
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19215 25259 1.52 9.0E-03 AL163267.2 NT 19341 27.64 9.0E-03 BF351141.1 EST HUMAN 10436 3.2 8.0E-03 AA723007.1 EST HUMAN 10897 20744 45.2 8.0E-03 AF106656.1 NT 12002 21900 2.38 8.0E-03 AL163283.2 NT	9562	\perp		1.27		AF137240.1	LN	Sargocentron sp. mixed lineage leukemia-like protein (Mil) gene, partial cds
19341 27.64 9.0E-03 BF351141.1 EST_HUMAN 10436 3.2 8.0E-03 AA723007.1 EST_HUMAN 10897 20744 45.2 8.0E-03 AF106856.1 NT 12002 21900 2.38 8.0E-03 AL163283.2 NT	9649	1.				AL163267.2	LN	Homo sapiens chromosome 21 segment HS21C067
10436 3.2 8.0E-03 AA723007.1 EST_HUMAN 10897 20744 45.2 8.0E-03 AF106656.1 NT 12002 21900 2.38 8.0E-03 AL163283.2 NT	9843						EST HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
10436 3.2 8.0E-03 AA723007.1 EST HUMAN 10897 20744 45.2 8.0E-03 AF106856.1 NT 12002 21900 2.38 8.0E-03 AL163283.2 NT	3	<u>L</u>			_			zh30e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains
12002 21900 2.38 8.0E-03 AL163283.2 NT	493			3.2		AA723007.1	EST_HUMAN	Alu repetitive element;
12002 21900 2.38 8.0E-03 AL163283.2 NT	973	<u>L</u>				AF106656.1	LN	Homo sapiens adenylosuccinate lyase gene, complete cds
	2113	12002				AL163283.2	TN	Homo sapiens chromosome 21 segment HS21C083

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Table 4
Single Exon Probes Expressed in Heart

		T	7	T	7	Т	T	T	Т	7	T	7	T	Τ.	Τ	T	T-	T	Τ-	Τ.	Т	7	Ţ	Т	1	_	T	$\overline{}$	T	7
oliigie Eauli riobes Expressed III neali	Top Hit Descriptor	Escherichia coli microcin 24 region, DNA binding protein (mdbA), immunity protein (mtfl), microcin 24 (mtfS), and microcin transport protein (mtfA, mtfB) genes, complete cds	RC1-HT0545-120200-011-b09 HT0545 Homo saplens cDNA	Homo sapiens SCL gene locus	Xonopus laevis bone morphogenetic protein 4 (BMP-4) gene, complete cds	CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoroductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds. Sacm21 gene, partial>	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (2/7)	PROBABLE PEPTIDASE Y4NA	A,californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end	Tursiops truncatus mRNA for p40-phox, complete cds	MR1-ST0111-111199-011-h06 ST0111 Homo sapiens cDNA	QV1-BT0677-040400-131-903 BT0677 Homo sapiens cDNA	601475619F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'	S.cerevisiae chromosome X reading frame ORF YJR152w	od80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232	od80a09.s1 NCI_CGAP_Ov2 Homa sapiens cDNA clone IMAGE:1374232	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds	Oryctolagus cuniculus elF-2a kinase mRNA, complete cds	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds	Cryptosporidium parvum HC-10 gene, complete cds	Cryptosporidium parvum HC-10 gene, complete cds	Glycine max glutathione S-transferase GST 21 mRNA, partial cds	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)	ab79b09.s1 Stratagene fetal retina 937202 Horno sapiens cDNA clone IMAGE:853145 3'	xv21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	UI-H-Bi3-akb-o-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
gie Exori Fro	Top Hit Datebase Source	LN LN	EST_HUMAN	NT TN	LN L	EST_HUMAN	L Z	NT	SWISSPROT	N	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	NT	TN	NT	FN	Z	LN LN	EST_HUMAN		SWISSPROT	EST HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN
<u> </u>	Top Hit Acession No.	8.0E-03 U47048.1	8.0E-03 BE171225.1	8.0E-03 AJ131016.1	8.0E-03 AF058764.1	8.0E-03 BF363327.1	8.0E-03 AF110520.1	8.0E-03 AP000002.1	P55577	M17197.1	8.0E-03 AB038267.1	8.0E-03 AW808692.1	8.0E-03 BE086509.1	8.0E-03 BE788441.1	8.0E-03 Z49652.1	8.0E-03 AA828817.1	8.0E-03 AA828817.1	8.0E-03 AF064589.1	M69035.1	8.0E-03 AB038161.1	7.0E-03 AF097183.1	7.0E-03 AF097183.1	7.0E-03 AF243376.1	7.0E-03 AV731712.1		Q61060	7.0E-03 AA668298.1	7.0E-03 AW303599.1	P04929	7.0E-03 AW 444463.1
	Most Similar (Top) Hit BLAST E Value	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03 P55577	8.0E-03 M17197.	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03 M59035.	8.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03		7.0E-03 Q61060	7.0E-03	7.0E-03	7.0E-03 P04929	7.0E-03
	Expression Signal	0.86	76.0	0.89	1.07	5.12	2.7	1.35	4.52	2.19	1.86	3.81	4.72	1.92	2.78	1.75	1.75	4.83	1.34	3.36	11.58	11.58	2.01	2.6		1.19	13.73	4.6	2.24	1.27
	ORF SEQ ID NO:		22990	23039		23966	25164	25775	26081	26299		27235		28284		28858	28859	29053			20433	20434	20732	20858			21135	21251	22001	23400
	Exon SEQ ID NO:	12857	13191	13235	13704	14185	15310	19453	15951	16143	16314	17043	17567	18036	18230	18575	18575	18760	18852	18882	10612	10612	10884	11016		11247	11279	11391	12715	13616
	Probe SEQ ID NO:	2930	3270	3314	3792	4286	5391	5761	6048	6279	6453	7166	7717	8148	8353	8687	8687	8953	9075	9121	629	629	961	1100		1341	1373	1486	2210	3702

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Single Exon Probes Expressed in Heart

-					_					_						_	_		_				_					_
	Top Hit Descriptor	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete eds	xe34f09.x1 NC_CGAP_Ut1 Homo saplens cDNA clone IMAGE:2609033 3' similar to TR:Q12987 Q12987 ACIDIC 82 KDA PROTEIN ;	hh89a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2959936 5'	Homo sapiens chronosome 21 segment HS21C078	ho39h08.x1 Soares_NFI_T_GBC_S1 Homo sepiens cDNA clone IMAGE:3039807.3' similar to TR:O93434 093434 RETICULOCALBIN.;	ho39h08.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:O93434 O93434 RETICUI OCAI BIN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA	2d33f10.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:342475 5	EST30674 Colon I Homo sapiens cDNA 5' end	7g34b10.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387 Q13387 HYPOTHETICAL PROTEIN 384D8_2, contains TAR1.t2 TAR1 repetitive element;	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA	S.cerevisiae chromosome II reading frame ORF YBL077w	S,cerevisiae chromosome II reading frame ORF YBL077w	RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA	BETA-GALACTOSIDASE PRECURSOR (LACTASE)	BETA-GALACTOSIDASE PRECURSOR (LACTASE)	AV687379 GKC Homo sapiens cDNA clone GKCAFC07 5'	Bos taurus mRNA for NDP52, complete cds	yd 5h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains	Alu repettive element;	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5	RC0-SN0052-110400-021-a04 SN0052 Homo sapiens cDNA	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224.3' similer to SW:PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR;	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224.3' similar to SW:PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR;	Danio rerio odorant receptor gene cluster	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772.3'	ah78e11.s1 Soares_testis_NHT Homo sapiens cUNA clone 1321772.3'
011100000000000000000000000000000000000	Top Hit Database Source	Z	EST_HUMAN	EST_HUMAN	N	EST_HUMAN	EST HIMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT.	NT	EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	NT	1	ESI HOMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	7.0E-03 AF196344.1	7.0E-03 AW117711.1	7.0E-03 AW630888.1	7.0E-03 AL163278.2	7.0E-03 BE044191.1	7 0F-03 BE044191 1	AW861059.1	7.0E-03 W68251.1	7.0E-03 AA327129.1	7.0E-03 BE857385.1	7.0E-03 BE928133.1	7.0E-03 Z35838.1	7.0E-03 Z35838.1	7.0E-03 BE175667.1	P48982	7.0E-03 P48982	7.0E-03 AV687379.1	7.0E-03 AB008852.1		7.0E-03 H94065.1	7.0E-03 BE263253.1	7.0E-03 AW868110.1	6.0E-03 AW511148.1	6.0E-03 AW511148.1	6.0E-03 AF112374.1	6.0E-03 AA759135.1	AA759135.1
	Most Similar (Top) Hit BLAST E Value	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0F-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03		7.0E-03	7.0E-03	7.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03
	Expression Signal	1.01	1.23	1.01	1.76	1.1	.	5.07	1.49	3.46	1.3	2.39	4.98	4.98	2.29	2.53	2.53	1.27	3.36		1.55	1.88	1.83	9.29	9.29	1.09	3.11	3.11
	ORF SEQ ID NO:	23436				24683	24684		25831		25980	26127	26466	26467	26792	27670	27671		28337					20979	20980	22499		22582
	Exon SEQ ID NO:	13653	14329	14389	14795	14910	14910	19452	15718	15844	15859	15992	16302	16302	16603	17456	17456	17756	18086		19750	19194	19425	11129	11129	12606	12790	12790
	Probe SEQ ID NO:	3741	4434	4495	4916	5038	4038	5717	5813	5939	5954	6210	6441	6441	6723	7605	7605	7906	8201		6096	9615	9962	1220	1220	2744	2862	2862

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Table 4
Single Exon Probes Expressed in Heart

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3208	13132		2.06	6.0E-03	6.0E-03 H75690.1	EST_HUMAN	yr77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3264	13187		0.82	6.0E-03	6.0E-03 AF190338.1	NT	Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3336	13256	23062	1.24	6.0E-03	6.0E-03 U90880.1	TN	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3336	(23063	1.24	6.0E-03	6.0E-03 U90880.1	LN	Fugu rubripas zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3499	13416		1.05	6.0E-03		EST HUMAN	zc13a11.r1 Soares, parathyroid, tumor, NbHPA Homo sapiens cDNA clone IMAGE:3221725'
3610	13524	23311	3.62	6.0E-03	6.0E-03 BF510986.1	EST_HUMAN	UI-H-BI4-apm-c-08-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3711	13624	23407	1.28	6.0E-03	6754029 NT	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpi), mRNA
3846	13757		0.93		6.0E-03 AW847284.1	EST_HUMAN	RC0-CT0204-240999-021-b10 CT0204 Homo sapiens cDNA
3873	13784		1.18	6.0E-03	6.0E-03 BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Horno sapiens cDNA clone IMAGE:2959513 5'
4231	14129		0.87	6.0E-03	6.0E-03 N58946.1	EST_HUMAN	yy62h10.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:2781793
4267	14166		1.37	6.0E-03	6.0E-03 AI016833.1	EST_HUMAN	ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4597	14485	24271	6.82		6.0E-03 AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5115	14983	24758	1.83	6.0E-03	6.0E-03 AL163281.2	IN	Homo sapiens chromosome 21 segment HS21C081
5129	14996	24767	0.89	6.0E-03	6.0E-03 AA889972.1	EST_HUMAN	aj95g09.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404256 3'
9059	16365	26542	1.97	6.0E-03	6.0E-03 AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
							ow13a04.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE::1646670 3' similar to
9829		26657	7.04	6.0E-03	6.0E-03 Al033980.1	EST_HUMAN	contains MEK10.b1 MEK10 repetitive element;
6650	16530	26724	2.44	6.0E-03		EST_HUMAN	RC0-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
6689	16569		1.41	6.0E-03	6.0E-03 BF038198.1	EST HUMAN	601454915F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3858626 5'
2509	17297	27506	8.21	6.0E-03	6.0E-03 D10548.1	INT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
							#22c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW.R13A. HUMAN
1776	17626		1.94	6.0E-03	.1	EST_HUMAN	P40429 60S RIBOSOMAL PROTEIN L13A;
7849	17789	28039	1.5	6.0E-03	6.0E-03 X68366.1	N	M.thermoformicicum complete plasmid pFV1 DNA
8127	18015	28263	2.23	6.0E-03	AW962164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapions cDNA
8186	18072		2.21	6.0E-03	11545814 NT	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
							te91c12.x1 NCL CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 000519
8220	18102	28356	1.89	6.0E-03	6.0E-03 Al420786.1	EST_HUMAN	FALLY ACID AMIDE HYDROLASE.;
							te91c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 000519
8220	_[28357			6.0E-03 AI420786.1	EST_HUMAN	FATTY ACID AMIDE HYDROLASE.;
8350	İ				6.0E-03 U14556.1	Ľ.	Mus musculus zinc-finger protein mRNA, complete cds
8351	18228	28479	3.54		6.0E-03 BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Rhodobacter capsulatus strain SB1003, partial genome	Methanobacterium thermoautotrophicum from bases 429192 to 450296 (section 39 of 148) of the complete genome	Anguilla japonica mRNA for activin B, complete cds	Pneumocystis carinil f. sp. rattl guanine nucleotide binding protein alpha subunit (bca1) gene complete cds	601482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5	Brassica napus slg gene for S-locus glycoprotein, cultivar T2	Chlamydia trachomatis partial ORFB; aminoacy/-tRNA synthase, complete cds; complete ORFA, and grpElike protein, complete cds	Chlamydia trachomatis partial ORFB; aminoacyl-IRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds	Chlamydia trachomatis partial ORFB; aminoacy-tRNA synthase, complete cds; complete ORFA, and grpE-	like protein, complete cds	Arabidopsis thaliana mRNA for DEAD box RNA helicase RH3	qd79d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735689 3'	Homo sapiens mRNA for KIAA1180 protein, partial cds	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'	yc81f09.s1 Soares infant brain 1NIB Homo sapions cDNA clone IMAGE:22395 3'	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3	y/86g02.s1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:155666 3'	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds	Citrus sinensis seed storage protein citrin mRNA, complete cds	EST12218 Uterus tumor I Homo sapiens cDNA 5' end	yu79g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE: 240055 5'	Citrus sinensis seed storage protein citrin mRNA, complete cds	Homo sapiens SOL gene locus	5c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA cione NHTBC cn15c02 random	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
lle Exon Probes	Top Hit Database Source	NT	Me NT		NT Pn	EST_HUMAN 60	NT	NT FA	PN N	PN NT		NT		EST_HUMAN qd	NT	EST_HUMAN 60	EST_HUMAN ye	NT	T_HUMAN		NT Ps	П	EST_HUMAN ES		NT	NT Ho		SWISSPROT SC
Sing	Top Hit Acession No.	6.0E-03 AF010496.1	6.0E-03 AE000833.1		6.0E-03 U30790.1	6.0E-03 BE788019.1	6.0E-03 AJ245480.1	5.0E-03 L25105.1	5.0E-03 L25105.1	5.0E-03 L25105.1						5.0E-03 BE266057.1	T87623.1	.2			5.0E-03 AF147449.2		5.1	5.0E-03 H78355.1	5.0E-03 U38914.1	5.0E-03 AJ131016.1	57.1	
	Most Similar (Top) Hit BLAST E Value	6.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03	6.0E-03	5.0E-03	5.0E-03	5.0E-03	1	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03	5.0E-03 P35500
	Expression Signal	1.59	3.6	1.34	2.21	1.57	1.34	2.0	9.1	2.92		2.92	1.38	0.91	3.44	0.95	4.08	1.75	1.04	1.08	4.16	0.83	1.38	0.93	0.91	0.94	2.49	5.34
	ORF SEQ ID NO:		_					20406	20407	20406		20407	20854	_	22405	22629	22820		22853		23341	23396		23886	23396	24181	24296	25528
	Exon SEQ ID NO:	18922	19519		19583	19262	19274	10589	10589	10589		10589	11012	11457	12515	12832	13024	13041	13054	13163	13555	13612	13801	14106	13612	14396	14507	15458
	Probe SEQ ID NO:	9185	9310	9372	9392	9722	9741	653	653	654	i.	654	1096	1552	2648	2905	3097	3116	3129	3240	3641	3698	3890	4207	4209	4503	4619	5541

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Table 4
Single Exon Probes Expressed

Single Exon Probes Expressed in Heart	xon ORF SEQ Expression (Top) Hit Top Hit Acession (Top) Hit Top Hit Acession No. Signal BLASTE No. Source Source	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN THIOLESTERASE Y) (TAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)	6.17 5.0E-03 BE300091.1 EST HUMAN	24877 6.02 5.0E-03 AB025024.1 NT	26605 6.26 5.0E-03 AB016816.1 NT	26865 1.97 5.0E-03 P48982 SWISSPROT	6.92 5.0E-03 M61132.1 NT	7.44 5.0E-03 T19586.1 EST HUMAN	28435 3.17 5.0E-03 AW170334.1 EST HUMAN	28436 3.17 5.0E-03.AW1703341 FST HIMAN	28527 1.95 5.0E-03 T49153.1 FST HIMAN	28563 1.77 5.0F-03 10946753 NT	3.73 5.0E-03 BE048055 1 FST HIMAN	5.04 5.0E-03 AF047874.1 NT	8.65 5.0E-03/AF067253 1 NT	1.55 5.0E-03 L10347.1	1 2R R DE 02 AAAKGED74	4.16 5.0E-03 BF572337 FET HIMAN	25197 1.94 5.0E-03/AW449109.1 EST HIMAN	1.4 5.0E-03 Q02388 SWISSPROT	1.41 5.0E-03 AIG68709.1 EST HI IMAN	20015 2.97 4.0E-03 AW 500196.1 EST HUMAN	20097 2.18 4.0E-03 R46482.1 EST HUMAN	20203 0.94 4.0E-03 P54675 SWIS	20333 3 4.0E-03 AA939339.1 EST HUMAN	20637 1.81 4.0E-03 R46482.1 EST HUMAN	3.43 4.0E-03 AW749101.1	20889 32.55 4.0E-03 AA099777.1 EST HUMAN	20910 1.58 4.0E-03 AW794740.1 EST HUMAN
						-	3	3											Ш										
	Exon SEQ ID NO:		_			- 1		17993	18187	18187	18275	18307	18508		19091	19153	19174	19529	Ш		19400				_ :		\Box	_1	11066
	Probe SEQ ID NO:	5685	5977	6094	6566	6794	7006	8103	8310	8310	8399	8433	8644	9327	9460	9555	9592	9616	9791	9808	9929	232	318	436	588	829	893	1133	1153

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	zs59a01.11 NCL CGAP GCB1 Homo saniens clova close M46 CE-704726 51	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5	Aptis nonvenicies have a setronide and alfondow limbs	zl81a08 rt Stratanene orlon (#63/200/) Homo conjunction and a contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contract	601304161F1 NIH MGC 21 Homo seniens CONA Alma NAA CE america cu	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens CDNA	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR)	CDM protein (CDM), adrenoleukodystrophy protein >	Homo sapiens polyglutamine-containing C14ORF4 gene	Homo sapiens polyglutamine-containing C14ORF4 gene	Homo sapiens chromosome 21 segment HS21C084	98f04.xl NCI CGAP Co18 Homo saplens cDNA clone IMA GE "2665723".	xj98f04.x1 NCI_CGAP_Co18 Homo saniens cDNA clone IMA CE: Jace 270.21	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR) IKE BROTEIN OF 51	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLFA)	Mus musculus tumor susceptibility protein 101 (tsg101) gene. complete cds	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)	ab 18a08.x5 Stratagene lung (#837210) Homo saplens cDNA clone IMAGE:841142.3' similar to contains Alu	Fort and month disease virus nearly 2 4 40 440.1	constant mount unsease into sell otipe A-1. I lead capsid protein VP3	Drosopina inerariogaster anonzuz (anonzuz / mRNA, complete cds	Hartas III Vagicus Deta-cateriin Dinding protein mKNA, complete cds (HPRC)	A IOP SI IDEANE I ABEL ED TENENINGZOITE TESTER	Rafflis persections and a second of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the firs	MAZEA45E4 NIH MCC 42 LI	Ukopersicon esculentim knotted 3 profeio (TV-2) m DNA	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)	Dictyostelium discoideum AX4 development protein DG1122 (DG1122) gene, partial cds
gle Exon Probe	Top Hit Database Source	EST HUMAN	Т	_ <u>u</u>	7	EST HUMAN	Т	Z H O					ΝΤ	EST_HUMAN x	EST HUMAN X	SWISSPROT	SWISSPROT	Г	T L	B NAMIN TOT	A LONG			TOBOSI	Τ	Τ	T HIJMANI	NICINIO	SWISSPROT	NT
Sin	Most Similar (Top) Hit Acession BLASTE No. Value	4.0E-03 AA284374.1	4.0E-03 AV708305.1	4.0E-03 U33472.1	17	-	4.0E-03 AW 794740.1	4.0E-03 U52111.2						4.0E-03 AW188426.1	4.0E-03 AW188426.1	4.0E-03 Q13606	4.0E-03 Q13606	1	4.0E-03 AJ011712.1	4 0F-03 AI732754 1		-				-	-			4.0E-03 AF111944.1
	Expression (1.33	1.31	2.2	20.87	1.66	1.46	98.1	Ç	90.0	2.80	7.80	1.02	0.94	0.94	0.8	0.83	0.85	1.79	13	13.17	1.66	19.53	4.23	1.5	3.23	1.76	1.52	4.14	3.61
	ORF SEQ ID NO:	21040		21480	21757		22019	22290	70000	16777	22414	CI 477	22418	23207	23208	23278	23278	23556		24190	24796	24916	25039	25527	25529		25827	26190	26291	26762
	Exon SEQ ID NO:	11189	11472	11610	11864	12087	12117	12400	13400	12526	12520	0707	12530	13403	13403	13486	13486	13763	13823	14402	15030	15149	15236	15457	15459	15612	15714	16045	16136	16570
	Probe SEQ ID NO:	1281	1568	1709	1971	2200	2232	2526	2526	2650	2650	5003	2664	3487	3487	3572	3836	3852	3914	4509	5164	5225	5315	5540	5542	5704	5809	6062	6271	9690

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Single Exon Probes Expressed in Heart

Top Hit Descriptor	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA	te49b11.x1 Soares_NFL_T_GBC_S1 Homo saptens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element:	Homo sapiens chromosome 21 segment HS210009	Homo sapiens chromosome 21 segment HS210078	Homo sapiens chromosome 21 segment HS210006	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens c/DNA	601118164F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:3028095 51	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains Alu repetitive element MFR31 repetitive alement contains element MFR31 repetitive alement.	hh02c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932.3' similar to contains element	LIK5 repetitive element;	RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1	nc73c05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive	Homo canions MHC class 1 region	S. Geraale (cv. Halo) mRNA for trios enhants is smerzes	Mus musculus intestinal trefoil factor gene, partial cds	Mus musculus Intestinal trefoil factor gene, partial cds	Arabidopsis thaliana rpoMt gene	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'	IL2-UM0076-240300-056-D03 UM0076 Hamo sapiens cDNA	Mus musculus alpha-1(XVIII) collagen (COL 18A1) gene, exon 1 and 2	C.elegans samdc gene	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'	ah04f09.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE 1155689 5	S.cereale (cv. Halo) mRNA for triosephosphate isomerase	Rattus norvegicus gdmf gene	xu8.P10.H3 conorm Homo sapiens cDNA 3'	DKFZp761B0712_11 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B0712 5
Top Hit Database Source		te EST HUMAN re		N FN	TN TN	EST HUMAN PI	EST_HUMAN 60	EST HUMAN et	\top		HUMAN		NT	NT	OU PEST HIMAN	N. C. C.			NT	NT	EST_HUMAN 60	EST_HUMAN IL		NT C.		Γ			NT Ra	EST_HUMAN xu	EST HUMAN DK
Top Hit Acession No.	7662067 NT	4.0E-03 AI553983.1		4.0E-03 AL163278.2	4.0E-03 AL163206.2	4.0E-03 BE815173.1	4.0E-03 BE298290.1	4.0E-03 BF224125.1		_	4.0E-03 AW819141.1	11436955 NT		3.0E-03 AF011920.1	3.0E-03 AA468110 1					_	1	37.1			3.0E-03 AV762392.1	3.0E-03 AV762392.1	3.0E-03 AI792278.1		3.0E-03 AJ0114321		
Most Similar (Top) Hit BLAST E Value	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	L	4.05-03	4.0E-03/	4.0E-03	3.0E-03/	3.0E-03/	3.0E-03/	3 0F-03 /	3.0E-03 Z32521.1	3.0E-03 U46858.1	3.0E-03 U46858.1	3.0E-03 Y09006.	3.0E-03	3.0E-03 /	3.0E-03 U34606.1	3.0E-03 Y12500.1	3.0E-03/	3.0E-03	3.0E-03	3.0E-03 Z32521.1	3.0E-03 A	3.0E-03 A	3.0E-03
Expression Signal	2.02	7.4	4.41	3.38	5.64	3.95	2.25	8		/6.	1.57	1.52	1.62	7.66	184	0.87	3.9	1.12	1.12	0.84	4.53	2.62	1.95	6.75	7.43	7.43	1.58	1.34	11.91	4.37	0.88
ORF SEQ ID NO:	26841	27123		27229	28609					+	200	20102	20146	20638	21401		-	22029	22030		22765	22833	23089		23591	23592	23632		23978	24096	24309
Exon SEQ ID NO:	16653	16933	17028	17036	18345	19725	19009	19202	10840	200	19236	13410	10323	10787	11542	12097	12132	12133	12133	12890	12971	13037	13290	13297	13805	13805	13858	13960	14194	14311	14518
Probe SEQ ID NO:	6774	7056	7151	7159	8472	9295	9317	9628	9890	2500	6/96	OCSS S	367	861	1638	2211	2248	2249	2249	2963	3044	3112	3371	3379	3895	3895	3920	4058	4296	4417	4630

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Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	Top Hit Acession Database Top Hit Descriptor No. Source	ab18a08.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu EST HUMAN repetitive element;	1 EST_HUMAN	4506414 NT	4506414 NT	8922499 NT	1 NT	.1 EST_HUMAN	3.0E-03 AJ011419.1 NT Kluyveromyces marxianus pcpl3 gene for purine-cytosine permease	S.1 NT	3.0E-03 N92580.1 EST HUMAN 2b27b04.s1 Soares, parethyroid tumor, NbHPA Homo sapiens cDNA clone IMAGE:304783.3	SWISSPROT	3.0E-03 AL163268.2 NT Homo sapiens chromosome 21 segment HS21C068	3.0E-03 Q9QM81 SWISSPROT NONSTRUCTURAL PROTEIN V	hh80f10.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969131 3' similar to contains L1.t1 L1 a.s. repetitive element:	LN		31.1 EST_HUMAN	3.0E-03 P08672 SWISSPROT CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; SWISSPROT ENDONUCI FASE]	SWISSPROT	3.0E-03 AL163303.2 NT Homo sapiens chromosome 21 segment HS21C103	5803028 NT	NT	L N	- NT	3.0E-03 AF094481.1 NT Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds	3.0E-03 P11369 RETROVICLEASE REVERSE TRANSCRIPTASE SWISSPROT ENDONUCLEASE	3.0E-03 A1525056.1 EST_HUMAN promina-5.E07.r bytumor Homo sapiens cDNA 5'	3.0E-03 AA993154.1 EST_HUMAN contains L1.t3 MER26 repetitive element;
	Top Hit Ac	AI732754.1	BE787945.	4	*		AJ249981.	AA456701.	AJ011419.	AB021736.	N92580.1	P51989	AL163268.	Q9QM81	AW613774	AL161589.		AI016731.1	P08672	P11369	P51989	AL163303.	35	AF009222.	AF266285.	AF094481.	AF094481.	P11369	AI525056.1	AA993154.
	Most Similar (Top) Hit BLAST E Value	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03		3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03
	Expression	1.54	60.7	1.11	1.11	3.17	1.41	9.97	1.54	3.71	2.01	1.29	1.57	1.38	8.52	4.1		8.9	3.48	1.29	1.46	4.05	2.69	2.11	2.01	3.06	3.06	1.93	2.02	1.54
	ORF SEQ ID NO:	24399	24416	24733	24734	24837	25380	25974	26297	26468	26809	27001	27011			27297		27317		27768	27813	27931		28856	28137	28877	28878	28942		28780
	Exon SEQ ID NO:	14613	14630	14959	14959	15143	15330	15851	16141	16303	16620	16806	16818	16868	17076	17107	-	17121	17449	17544	17592	17686	18104	18573	17893	18590	18590	18654	19542	18870
	Probe SEQ ID NO:	4727	4745	5089	5089	5220	5410	5946	6277	6442	6741	6928	6940	6991	7199	7230		7244	7598	7694	7742	7836	8222	8685	8744	8773	8773	8841	8906	9103

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Single Exon Probes Expressed in Heart	Top Hit Acession Database No. Source	LV	Į.		TORISSIMS	EST HUMAN		EST HUMAN	LN	SWISSPROT	Homo sapiens procollagen-tysine, 2-oxoglutarate 5-dioxygenase (tysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA	Homo sapiens procellagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers Danios syndrome	SWISSPROT	EST HIMAN	L	Z NT	EST HIMAN	EST HUMAN	EST	Z	TN.	SWISSPROT	LN	LN	TN	<u> </u>	EST HIMAN	NT	- NT	-
	Тор Н	3.0E-03 AB009668 1	3.0E-03 A.1298282 4	2.0E-03 Q04652	2.0E-03 Q04652	2.0E-03 T70874.1	2.0E-03 M20783.	2.0E-03 AA661605.1	2.0E-03 AF284446.1	2.0E-03 P48509	2.0E-03	2.0E-03	2.0E-03 P29400	2.0E-03 AA450138 1	2.0E-03 AF30269	2.0E-03 AL163302	2.0E-03 AW1377821	2.0E-03 AA450138.1	2.0E-03 BF568955.1	2.0E-03 X87344.1	2.0E-03 AB040802	2.0E-03 P03374	E-03 U68491.1	2.0E-03 L42512.1	2.0E-03 L42512.1	2 0F-03 AF223391	2.0E-03 R87773 1	2.0E-03 AJ245167	2.0E-03 AY005150	2.0E-03 AY005150
	Most Similar (Top) Hit BLAST E Value										2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	20	2.0	2.0	20.5	2.05	2.0E	2.0	2.0E
	Expression Signal	1.35	2.33	0.89	0.89	7.01	1.93	1.59	12.6	1.11	1.91	1.91	4.94	1.38	2.17	1.04	4.62	4.03	1.02	4.87	0.92	2.15	9.77	1.93	1.93	0.94	1.7	0.82	1.04	1.04
	ORF SEQ ID NO:		25296				21104		21115	21243	21263	21264		21502	21731	21992		23088	23093	23315	23572	23703		24130	24131	24285			24820	24821
	Exon SEQ ID NO:	19668	19019	10446	10446	12677	11246	11249	11259	11379	11404	11404	11477	11634	11845	12090	12409	13289	13294	13520	13780	13927	14027	14340	14340	14496	14500	14947	15057	15057
	Probe SEQ ID NO:	9159	8339	504	504	768	1340	1343	1353	1474	1500	1500	1573	1733	1950	2203	2535	3370	3376	3615	3869	4024	4127	4446	4446	4608	4612	5077	5194	5194

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	Top Hit Descriptor	601876385F1 NIH MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5	Homo sapiens mRNA for KIAA0693 protein, partial cds	Xenopus laevis xefiltin mRNA, complete cds	ATP-DEPENDENT NUCLEASE SUBUNIT B	ATP-DEPENDENT NUCLEASE SUBUNIT B	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)	Lesculentum mRNA for lysyl-tRNA synthetase (LysRS)	wu36h09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element MSR1 repetitivo cloment;	CM4-BT0366-061299-054-d01 BT0365 Homo sapiens cDNA	ht37b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60976 Q60976 JERKY:	xx42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE.264442.3' similar to contains L1.b2.L1 repetitive element:	yx42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element;	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150- 225) (TENASCIN-C) (TN-C)	2s10a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'	ene	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA	H.sapiens variable number tandem repeat (VNTR) locus DNA	ty65h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G;	Homo saplens SEL1L (SEL1L) gene, partial cds	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region	
	Φ		Homo sapiens mi	Xenopus laevis xe									[Γ	Π					Homo saplens St	Camelus dromed	
,	Top Hit Database	EST_HUMAN	٦ ۲	N	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	SWISSPROT	LN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	EST_HUMAN	N	SWISSPRO	EST_HUMAN	ΤN	EST_HUMAN	NT	IN	
	Top Hit Acession No.	2.0E-03 BF241410.1	2.0E-03 AB014593.1	U63711.1	P23477	P23477	Q95203	Q95203	2.0E-03 BF308187.1	O9UKP4	2.0E-03 X94451.1	2.0E-03 Al991089.1	2.0E-03 BE067986.1	2.0E-03 AW592004 1	2.0E-03 N20287.1	2.0E-03 N20287.1	P24821	2.0E-03 AA251376.1	2.0E-03 M86524.1	P07354	2.0E-03 BF330909.1	2.0E-03 Z11740.1	2.0E-03 AI625745.1	AF157516.2	2.0E-03 AJ245167.1	
	Most Similar (Top) Hit BLAST E Value	2.0E-03	2.0E-03	2.0E-03	2.0E-03 P23477	2.0E-03 P23477	2.0E-03 Q95203	2.0E-03 Q95203	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2.0E-03 P24821	2.0E-03	2.0E-03	2.0E-03 P07354	2.0E-03	2.0E-03	2.0E-03	2.0E-03	2:0E-03	
	Expression Signal	1.37	1.76	1.87	3.25	3.25	1.82	1.82	7.14	2.2	1.95	1.36	2.88	2.11	5.19	5.19	3.12	5.41	2.78	1.78	1.7	12.17	2.07	2.88	4.48	
	ORF SEQ ID NO:	25128	25438	_	25725	25728	25846	25847	25849	25874			26129	26763			27508			26520		28936		29115		-
	Exen SEQ ID NO:	15292	19445	15420	15624	15624	15735	15735	15737	16756		15884	15994	16571	ì		17301	17625	18256	16350	18642	18649	18835	18847	14947	
	Probe SEQ ID NO:	5372	5457	5501	5716	5716	5829	5829	5831	5850	5861	5979	6212	6691	6784	6784	7513	7775	8379	8779	8829	8836	9052	9066	9113	

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Table 4
Single Exon Probes Expressed i

Single Exon Probes Expressed in Heart	Top Hit Descriptor	Rattus norvegicus transformation related prodein 63 / Traces months		T	T	APOI IDADDOTEM A Washington and a 1-27, complete cds	T	X laeds mRNA for CASE postering	Т	T ILINE-1 REVERSE TRANSCRIPTAGE DOMAN COMA clone (MAGE:126691 5'	Homo saplens prion probin (PrD) and	Т	In85a08 x1 NCI CGAP 112 Home spained 2014	Г	Homo sapiens prion protein (PrP) nene complete ad-	Homo sapiens chromosome 21 pages 11572021	Home spring the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the	Т	\top	\top	T	Т	7	Т	1	Homo sapiens ensions, treatise and the left of the sapiens ensions, treatise and the sapiens ensions, treatise and the sapiens ensions, treatise and the sapiens ensions, treatise and the sapiens ensions, treatise and the sapiens ensions, treatise and the sapiens ensions, the sapiens ensions are sapiens ensions.	Homo sapiens CCR8 chemoking months (CCR8 chemoking months) (CR8 chemoking months)	T	DKFZ0586M2024 11 586 (SINGELLE IN LESTINE (FRUCTOSE TRAINSPORTER)	Т	1	\top	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
igle Exon F	Top Hit Database Source	ΓN	HAMINA H	EST HIMAN	CAIO LA	SWISSPROT	LN	E	EST HUMAN	SWISSPROT	F	EST HUMAN	EST HUMAN	LN	NT	FZ	L	EST H IMAN) L	EST LEBANN	NAME TO THE	FST HIMAN		EST HUMAN	L	LN LN	NT	SWISSPROT	EST HUMAN	ST HUMAN	Z L	EST HUMAN	SWISSPROT
nis	Top Hit Acession No.	3 9507208 NT	1.0E-03 Al347355 1	1.0E-03 BE780572 1	9.0E-04 L11910 1	9.0E-04 P06727	9.0E-04 AB037203 1	8.0E-04 X96469.1	8.0E-04 R07008.1	8.0E-04 P08547				7.0E-04 L41825.1	_	7.0E-04 AL163210.2	4885170	7.0E-04 AI769331.1	7 0F-04 178027 4		1-		6005855	6.0E-04 A1862525.1			6.0E-04 U45983.1		6.0E-04 AL048507.2			347.1	
	Most Similar (Top) Hit BLAST E Value	1.0E-03	1.0E-0	1.0E-0	9.0E-04	9.0E-04	9.0E-04	8.0E-04	8.0E-04	8.0E-04	8.0E-04	8.0E-04	8.0E-04	7.0E-04	7.0E-04	7.0E-04	7.0E-04	7.0E-04	7.0F-04	7.0E-04	7.0E-04	7.0E-04	7.0E-04	6.0E-04	6.0E-04	6.0E-04	6.0E-04	6.0E-04 P46408	6.0E-04	6.0E-04	6.0E-04	6.0E-04	6.0E-04 Q01768
	Expression Signal	1.95	2.15	4.2	0.81	1.56	1.42	1.39	1.27	4.2	2.39	2.08	2.16	1.61	1.13	3.26	1.03	2.24	3.2	2.61	3.29	2.72	3.28	1.34	0.85	0.85	3.28	4.35	3.13	2.24	2.07	6.32	2.45
	ORF SEQ ID NO:	25287		24904	24769	-			23548		24332			21562	22127	22437	22965			28973				23576	23680	23681	23769			27887	28881	28950	
	Exon SEQ ID NO:	19108	19687	19707	14998	15404	17412	11377	13754	13989	14542	18358	18483	11684	12230	12547	13166	15828	18663	18683	19155	19300	19321	13788	13905	13905	13992	16470	17583	17650	18593	18664	18714
	Probe SEQ ID NO:	9491	9517	9626	5131	5485	7561	1472	3843	4089	4656	8485	8616	1/86	2350	7807	3243	5923	8851	8871	9558	9260	9813	3877	3999	3999	4092	9290	7733	7800	8776	8852	8906

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	RC1-HT0269-261199-012-d08 HT0269 Homo sapiens c/NNA	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11) TONIA	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)	nk27e11.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu		Bos faurus micromolar calcium activated neutral protease 1 (CAPN1) gene expres 11 20	Zo33b08.r1 Strategene colon (#937204) Homo sapiens cDNA clone IMAGE:588663 5'	dd13f06.x1 Soares, placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1723619.3'	(HUMAN);contains Alu repetitive element:	aj56h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE-1204257 a.	xs06e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE 2268868 2	DKFZp586M2024_11 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M3034	+707M000d-	bos latinus micromolar calcium activated neutral protease 1 (CAPN1) nene excess 11 20	ntronu2.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:913875	AIT (109-XI NC) CGAP Kid11 Homo sapiens cDNA clone IMAGE:2697273 3'	b018/b534F1 NIH MGC 55 Homo sapiens cDNA clone IMAGE:4104897 5	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clinia MACE 3224000 at	Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE	Q13825 AU-BINDING PROTEIN/FNOVI COA LICENATA CON INA GE:2334039 3' similar to TR. Q13825	RC3-CT0254-130100-023-f01 CT0254 Home senions CDNA	Homo sapiens chromosome 21 segment HS21Cn78	DKFZp434D059_r1 434 (synonym: htes3) Homo sapiens cDNA close DKE2_220000000000000000000000000000000000	SERICIN-2 (SILK GUM PROTEIN 2)	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively sninger	AV036624 GKC Homo sapiens cDNA clone GKCFFH07 5' nh10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T.CEII SPECIFIC RANTES PROTEIN PRESIDENTIALS	CONTROL OF THE CONTROL (HUMAN);
gle Exon Prob	Top Hit Database Source	T_HUMAN	1000	EST HUMAN				NA HOMAN			EST HUMAN	7	EST HUMAN D	_ A	1000	\top	ECT LI MAN			T		T HUMAN			ISSPROT	1 1 1 1 1 1	HUMAN	٦
Sin	Top Hit Acession No.	AW3805	5.0E-04 040344	5.0E-04 AW851844.1	5.0E-04 AA548931.1	5 0F-04 AF2480E4 4	T	5.0E-04 M23604.1			5.0E-04 AA846545.1		7	5.0E-04 AF248054.1	-							2						
	Most Similar (Top) Hit BLAST E Value	6.0E-04	5.0F-04	5.0E-04	5.0E-04	5.05.04	5.0E-04	5.0E-04		3.0E-04	5.0E-04	50E 04	0.00-04	5.0E-04	5.0E-04	5.0E-04	4.0E-04	4.0E-04 U32748.1	4 0F-04 7		4.0E-04	4.0E-04 A	4.0E-04 AL163278.	4 0F-04 ALU46/04.1	4 05 04	4.0E-04A	4.0E-04 A	
	Expression Signal	2.26	5.82	1.83	1.42	2.19	5.72	13.6	n n	20:07	4 60	417		17.6	227	1.46	1.13	1.42	1.57		1.57	3.92	1 10	2.73	1.89	0.84	2.75	
	ORF SEQ ID NO:	25170	20385		23085	25113	26026	26387	26710	27412	27606			25113				20410	20606	20607	21218	21823	+	22348	22850	23041	23900	
	S	19598	10572	11390	13286	15281	15901	16227	16519	17213	17394	18220		15281	19530	19413	10333	10592	10756	10756	11354	11928	11976	12457	13052	13237	14126	
	Probe SEQ ID NO:	9225	635	1485	3367	5361	5996	6364	6839	7345	7543	8343	-	8950	9164	9944	386	657	828	828	1449	2037	2086	2586	3127	3316	4228	

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Top Hit Descriptor	nh10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);	zn61c08.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'	yy78b10.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE.279843 3' similar to contains Alu repetitive element:	yx39e12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IN/AGE:264112 5'	ov87h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced	FORMIN (LIMB DEFORMITY PROTEIN)	DKFZp761J221_r1 761 (synonym: hamy2) Homo saplens cDNA clone DKFZp761J221 5'	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2	th23a02.x1 NCL_CGAP_Pr28 Homo saplens cDNA clone IMAGE:2119082 3'	INTERNALIN B PRECURSOR	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)	Homo sapiens Xq pseudoautosomal region; segment 1/2	PM0-H10339-190200-007-912 HT0339 Homo sapiens cDNA	QV3-DT0045-221299-046-d09 DT0045 Homo sapiens cDNA	V.carteri gene encoding volvoxopsin	Homo sapiens chromosome 21 segment HS21C081	Homo sapiens chromosome 21 segment HS21C078	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)	zx48d08.r1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:795471 5' similar to gb:M62762 VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN):	ag24905.s1 Soares_tests_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L'7A (HUMAN):	nc38e04.r1 NCI CGAP Pr2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains 1 112 11	repetitive element;	Homo sapiens mRNA for KIAA0749 protein, partial cds	DKFZp547L185_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547L185 5	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
Top Hit Database Source	EST HUMAN S	EST_HUMAN Z	EST_HUMAN 6	EST HUMAN	Т			H IN	SWISSPROT	EST_HUMAN D		H		SWISSPROT	SWISSPROT	H H		EST_HUMAN Q	NT V	H	H	SWISSPROT	EST HUMAN V		T	EST_HUMAN re	IN IN	EST_HUMAN D	TN g
Top Hit Acession No.	4.0E-04 AA576331.1	4.0E-04 AA086324.1	4.0E-04 BE560660.1	4.0E-04 N48313.1	4.0E-04 N25507.1	4.0E-04 AI025699.1	5.1	4.0E-04 AF254822.1	Q05860	3.0E-04 AL119426.1	P49259	3.0E-04 U83991.1	3.0E-04 A1399674.1	P25147	P49448		3.0E-04 BE153778.1	3.0E-04 AW937723.1	3.0E-04 Y11204.1	1.2		P22607	3.0E-04 AA454055.1	AA781201.1		3.0E-04 AA228301.1	3.0E-04 AB018292.1	3.0E-04 AL134483.1	2.0E-04 AF217798.1
Most Similar (Top) Hit BLAST E Value	4.0E-04	4.0E-04	4.0E-04	4.0E-04	4.0E-04	4.0E-04	4.0E-04	4.0E-04	4.0E-04 Q05860	3.0E-04	3.0E-04 P49259	3.0E-04	3.0E-04	3.0E-04 P25147	3.0E-04 P49448	3.0E-04	3.0E-04	3.0E-04	3.0E-04	3.0E-04 AL16328	3.0E-04	3.0E-04 P22607	3.0E-04	3.0E-04 AA78120		3.0E-04	3.0E-04	3.0E-04	2.0E-04
Expression Signal	2.75	1.28	3.72	6.0	1.62	2.79	1.44	1.52	1.84	3.04	2.22	1.27	1.16	3.37	3.63	1.18	4.5	0.85	1.34	4.82	5.88	3.49	1.42	3.66		2.33	4.32	2.01	1.18
ORF SEQ ID NO:	23901	24121	24661	24770						19942	19977	20639		22988	23581			24456			26166	26875	27780			24908	25068		19957
Exon SEQ ID NO:	14128	14332	14893	14999	L	17439	17512	19505	19479	10124	10160	10788	11707	13190	13793	13876	14597	14669		15843	16026	16685	17555	17827		19726	19576	19361	10141
Probe SEQ ID NO:	4228	4437	5020	5132	6972	7588	7662	9256	2296	150	188	862	1810	3268	3882	3969	4711	4784	5052	5735	6081	9089	7705	7161		9118	9483	9874	169

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Table 4
Single Exon Probes Expressed in Heart

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Table 4
Single Exon Probes Expresses

Single Exon Probes Expressed in Heart	Most Similar (Top) Hit Acession Top Hit BLAST E No. Source Source	2 0F-04 AEnonena 4	2 0F-04 RF140303 4 EST	2.0E-04/AA465777 1 EST 1.11,141.	2.0E-04 AV730373 1 FEET LINAAN	2.0E-04 AJ243213.1 NT	2 0F-04 Aldanoses 4	2.0E-04 AW136740 1 FEST HUMAN	1.0E-04 H99646.1	4 OE 04 D44020	1 0F-04 AW043847 4 FOT 1 1	1.0E-04 AW013847 1 EST	1.0E-04 U62918 1 NIT	1.0E-04 AF148805.1 NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene partial rde: and ODE co.	1.0E-04 AF148805 1 NT	1.0E-04 AB048342.1 NT	1.0E-04 AF195953.1 NT	1.0E-04 AF195953.1 NT	1.0E-04 BE218833.1 FST HIMAN	1.0E-04 BE218833.1 EST HUMAN	1.0E-04 Q62203 SWISSPROT	0 E O E O E	1 0F-04 M14042 4	1 0F-04 AVEA7727 4	1.0E-04 P08547	1.0E-04 7662015 NT
		2 0F-04 AE020F	2 0F-04 RF140	2.0E-04 AA4057	2.0E-04 AV7305	2.0E-04 AJ2432	2 0F-04 A144028	2.0E-04 AW136	1.0E-04 H99646	4 OF 04 0440ED	1 0F-04 AW0138	1.0E-04 AW0135	1.0E-04 U62918	1.0E-04 AF14880		1.0E-04 AF14880	1.0E-04 AB04834	1.0E-04 AF19595	1.0E-04 AF19595	1.0E-04 BE21883	1.0E-04 BE21883	1.0E-04 Q62203	1 OF 04 A1440.000	1 DE-04 M14042 4	1 0F-04 AVEA779	1.0E-04 P08547	
	Expression Signal	2.29	1.46	1.71	6.14	1.88	5.57	2.94	86.0	2.43	3.87	3.87	2.97	3.24		3.24	1.67	1.29	1.29	1.15	1.15	1.04		1.78	1.08	0.85	1.56
	ORF SEQ ID NO:	27054	27801		28360		28762	28866	20516	20819	20855	20856		21374		21375	21594	22363	22364	22411	22412	22969	23376	23654	23675	24043	24671
	Exon SEQ ID NO:	16859	17579	17604	}	18387	18490	18582	10680	10976	11014	11014	11216	 11515		11515	11714	12469	12469	12522	12522	13170	13589	13878	13898	14258	14901
	Probe SEQ ID NO:	6982	7729	7754	8225	8515	8625	8726	750	1059	1098	1098	1310	 1610		1610	1817	2600	7200	2655	2655	324/	3675	3971	3991	4362	5028

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Table 4
Single Exon Probes Expressed in Heart

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SEQ ID ORF SEQ Expression (Top) Hit Top Hit Acession LPMIN NO: ID NO: Signel BLASTE NO. Source NO: ID NO: Signel BLASTE NO. Source 19589 3.45 8.0E-05 AA27933.1 EST HUMAN 10303 20119 2.9 7.0E-05 AW847445.1 EST HUMAN 10466 20302 1.05 7.0E-05 L49075.1 EST HUMAN 10466 20303 1.05 7.0E-05 L49075.1 EST HUMAN 1057 20800 2.22 7.0E-05 L49075.1 EST HUMAN 1057 7.0E-05 L49075.1 EST HUMAN 1057 7.0E-05 L49075.1 INT 14241 24023 0.82 7.0E-05 L49075.1 INT 14723 24506 0.84 7.0E-05 L49075.1 INT 14724 24023 0.84 7.0E-05 L496750.1 INT 14729 27506 0.84 7.0E-05 L496750.1 INT 11874 21767 <	H 112
19589 3.45 8.0E-05 AA279333.1 EST_HUMAN 10303 20118 2.9 7.0E-05 AW847445.1 EST_HUMAN 10496 20302 1.05 7.0E-05 AW847445.1 EST_HUMAN 10496 20302 1.05 7.0E-05 L48075.1 EST_HUMAN 10496 20303 1.05 7.0E-05 L48075.1 EST_HUMAN 10496 20303 1.05 7.0E-05 L48075.1 EST_HUMAN 12551 22440 5.24 7.0E-05 AL63278.2 NT 13046 22843 5.78 7.0E-05 AR009080.1 NT 14775 23633 1.27 7.0E-05 AR009080.1 NT 14721 24023 0.84 7.0E-05 AR85170 NT 11874 21767 1.57 6.0E-05 AR85170 NT 11874 21767 1.57 6.0E-05 AR85170 NT 12519 22410 0.89 6.0E-05 AR85170<	
10303 20118 2.9 7.0E-05 AW847445.1 EST_HUMAN 10303 20119 2.9 7.0E-05 AW847445.1 EST_HUMAN 10496 20302 1.05 7.0E-05 L49075.1 EST_HUMAN 10496 20302 1.05 7.0E-05 L49075.1 EST_HUMAN 10857 22843 5.24 7.0E-05 AL8075.1 EST_HUMAN 12651 22843 5.78 7.0E-05 AL8078.2 NT 14723 22440 5.24 7.0E-05 AL60300.1 NT 14724 24023 0.84 7.0E-05 AL60300.1 NT 17296 27505 0.84 7.0E-05 AB67800.1 NT 11874 21766 1.57 6.0E-05 AB65241.1 EST_HUMAN 11874 21767 1.57 6.0E-05 A865241.1 EST_HUMAN 12519 22409 0.89 6.0E-05 A865241.1 EST_HUMAN 12519 22509 3.33 6.0E-05 A865241.1 EST_HUMAN 12519 22600 3.33 6.0E-05 A86500.1 NT <td></td>	
10303 20119 2.9 7.0E-05 AW847445.1 EST HUMAN 10496 20302 1.05 7.0E-05 L49075.1 EST HUMAN 10496 20303 1.05 7.0E-05 L49075.1 EST HUMAN 10957 20800 2.32 7.0E-05 AL163278.2 NT 13046 22843 5.24 7.0E-05 AL163201.2 NT 14775 22843 5.78 7.0E-05 AL06300.1 NT 14723 24506 0.84 7.0E-05 AL06300.1 NT 14724 24023 0.82 7.0E-05 AL06300.1 NT 14725 24506 0.84 7.0E-05 AB00908.1 NT 14724 24023 0.82 7.0E-05 AB06908.1 NT 14729 24506 0.84 7.0E-05 AB0690.1 NT 11874 21767 1.57 6.0E-05 AB655241.1 EST HUMAN 12519 22409 0.89 6.0E-05 AB5650.1 NT 12519 22409 0.89 6.0E-05 AB6560.1 NT 15519 <td>EST_HUMAN</td>	EST_HUMAN
1096 20302 1.05 7.0E-05 L49075.1 EST_HUMAN 10967 20303 1.05 7.0E-05 L49075.1 EST_HUMAN 12551 22440 5.24 7.0E-05 AL162278.2 NT 13046 22843 5.78 7.0E-05 AL163201.2 NT 14775 22843 7.2 7.0E-05 AL163201.2 NT 14724 24023 0.82 7.0E-05 AL163201.2 NT 14723 24506 0.84 7.0E-05 A3867812.1 EST_HUMAN 17296 27505 0.84 7.0E-05 A3867817.0 NT 18374 21766 1.57 6.0E-05 A885170 NT 18374 21767 1.57 6.0E-05 A885170 NT 18374 21767 1.57 6.0E-05 A885170 NT 1837 22409 0.89 6.0E-05 A885170 NT 15519 222409 0.89 6.0E-05 A88506.	EST
10956 20303 1.05 7.0E-05 L49075.1 EST HUMAN 10957 20800 2.32 7.0E-05 Q22949 SWISSPROT 12551 22440 5.24 7.0E-05 AL163278.2 NT 14076 22843 5.78 7.0E-05 AB009080.1 NT 14724 22953 1.27 7.0E-05 B00980.1 NT 14723 24506 0.82 7.0E-05 B00980.1 NT 14723 24506 0.84 7.0E-05 B009850.1 NT 14724 24506 0.84 7.0E-05 A88510.0 NT 14874 21767 1.57 6.0E-05 A885170 NT 11874 21767 1.57 6.0E-05 A885170 NT 12519 22409 0.89 6.0E-05 A885170 NT 12519 22410 0.89 6.0E-05 A885170 NT 15519 22599 3.33 6.0E-05 A885070	HUMAN
10957 20800 2.32 7.0E-05 Q22949 SWISSPROT 12551 22440 5.24 7.0E-05 AB009080.1 NT 13046 22843 5.78 7.0E-05 AB009080.1 NT 14475 23953 1.27 7.0E-05 AB009080.1 NT 14241 24023 0.82 7.0E-05 U60980.1 NT 14723 24506 0.84 7.0E-05 U60980.1 NT 15065 27505 0.84 7.0E-05 B845300 NT 17296 27505 3.04 7.0E-05 A865300 NT 18374 21767 1.57 6.0E-05 A885170 NT 11874 21767 1.57 6.0E-05 A885170 NT 12519 22409 0.89 6.0E-05 A885170 NT 10598 20415 2.45 6.0E-05 A885170 NT 15519 25599 3.33 6.0E-05 A785060 NT </td <td>HUMAN</td>	HUMAN
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17354 27558 1.28 6.0E-05 T94149.1 EST_HUMAN 18019 28267 3.68 6.0E-05 R75639.1 EST_HUMAN	SWISSPROT C4B-BINDING PROTEIN PRECURSOR (C4BP)
18019 28267 3.68 6.0E-05 R75639.1 EST_HUMAN	EST_HUMAN ye28c12r1 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:119062 5:
18019 2826/ 3.58 6.0E-05 R/5639.1 EST HUMAN	
	EST HUMAN
18621 28911 3.59 6.0E-05 AA044015.1 EST_HUMAN	EST_HUMAN
1	0.1

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Table 4
Single Exon Probes Expressed in Heart

סוופין ווספס באלע פספס ווויטעם	Most Similar Top Hit Acession (Top) Hit Descriptor Signal BLASTE No. Source Source	1.54 6.0E-05 BE858403.1 EST_HUMAN 7g28a08.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3307766 3	14.37 5.0E-05 AW392086.1 EST_HUMAN QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA	23891	0.88 5.0E-05 AJ251058.1 NT	2.99 5.0E-05 AJ251884.1 NT Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1	9.01 5.0E-05 X58855.1 NT	3.46 5.0E-05 AV653544.1 EST_HUMAN	2.96 5.0E-05 P49193 SWISSPROT RETINAL-BINDING PROTEIN (RALBP)	SWISSPROT	4.58 4.0E-05 U12821.1 NT Human renin (REN) gene, 5' flanking region	7.17 4.0E-05 AF202635.1 NT Homo sapiens PP1200 mRNA, complete cds	4.6 4.0E-05 AW627946.1 EST HUMAN	2.17 4.0E-05 AW117580.1 EST_HUMAN xd93e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192.3	0.84 3.0E-05 AI248061.1 EST_HUMAN	1.36 3.0E-05 AW273851.1. EST_HUMAN	1.28 3.0E-05 BF037898.1 EST_HUMAN	1.28 3.0E-05 BF037898.1 EST_HUMAN	0.91 3.0E-05 Q62234 SWISSPROT	6.89 3.0E-05 BE169211.1 EST_HUMAN	6.89 3.0E-05 BE169211.1 EST_HUMAN	1.19 3.0E-05 AA368679.1 EST_HUMAN	1.19 3.0E-05 AA368679.1 EST_HUMAN	7 0.85 3.0E-05 AF149773.1 NT Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	0.84 3.0E-05/AI248061.1 EST_HUMAN	0.97 3.0E-05 AV726630.1 EST_HUMAN	1.54 3.0E-05 11072102 NT	2.23 3.0E-05 BE733157.1	1.62 3.0E-05 AA284049.1 EST_HUMAN	1.65 3.0E-05 AW7709	1.5 3.0E-05 6912431 NT	1.33 3.0E-05/AA372562.1 EST HUMAN EST84475 Colon adenocarcinoma IV Homo saplens cDNA 5' end
	ORF SEQ ID NO:		21141	100	22550	7 23593	25165						3 28286					20871	3 22442		23965			24197			25382					27447
	Exon SEQ ID NO:	5 19427	2 11287	9 11716	1 12760	7 13807	15311	6 15559	8 19173	0 19173	6 10193	6 17356		7 18989		3 10961	5 11030	5 11030	8 12553		5 14184	5 14261	5 14261	14412			2 15332	1 16491				17247
	Probe SEQ ID NO:	3962	1382	1819	2831	3897	5392	5646	9328	9590	2776	7486	8150	9287	 999	1043	1115	1115	2688	4285	4285	4365	4365	4519	 4731	515	5412	6611	6863	7154	7158	7373

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Table 4
Single Exon Probes Expressed in Heart

Cirigio Expressed in Heart	Expression (Top) Hit Acession Top Hit Acession Top Hit Descriptor Signal Value Value Source	3.15 3.0E-05 A1769331 EST 11111111	ייייייייייייייייייייייייייייייייייייייי	2 OF OF M122024	- N - N - N - N - N - N - N - N - N - N	2.0E-05 AA160562.1 EST HUMAN	2.0E-05 BE066036.1 EST_HUMAN	2.0E-03/AF 184514.1	2 0F-05 XO5465 1	7.4 FRT UIMAN	LOI TOMAN	2 OF OF BESTRATA	2.0E-05 A 1424045	2 OF OF A 104.740	2 0F-05 AA744220 4	2 DE OF VARIOUS	2.0E-05 100920; I	ES HUMAN	2.21 2.0E-05 AF224262.1 NT (HoxA5), HoxA4 (HoxA40), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5	(HOXAZ (HOXAZ), and HoxA1 (HOXA1) genes, complete cds	2.21 2.0E-05/AE224262.1 NT Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA2), HoxA6 (11.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1	2.0E-05/A/381040.1 FET HIMANI	NIMINION	EST_HUMAN yw91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo saplens_cDNA_close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_Close_NAA_	2.45 2.0E-05 N41751.1 FST HIMAN MOLECULAR A C.	TEST HIMAN	EST HUMAN	
		0E-05/A1769	0E 0E 0	0E-05 M1220	2 1	OE-05 AA160	7E-05 BE066	F-05 VB024	15-05 X0546F	E-05 AL0391	E-05 612633	E-05 DE270	E-05 A 14240	E-05 A 1011	E-05 A 2442	E 05 V00026	E-05 A 199402	201651	-05 AF22426		-05 AF22426	-05 AI381040		-05 N41751	-05 N41751.1	-05 Al991025	-05 BE17580	
						L																				2.0E	2.0臣	
	Expressio Signal	3.	12.4	3.6	,	1	00	1		0.8	0 0	10	0.8	145	215	2 15	8.04		2.21		2.21	2.3	2 4 5	7.42	2.45	2.42	2.93	
	ORF SEQ ID NO:		22058	22302		22821	23027	23050			24191		24453	25502	26022	26108	-		26260		26261	26671	28116		28117		28141	
	Exon SEQ ID NO:	17421	12160	12412	12546	13025	13225	13243	13366	13649	14403	14480	14666	15438	15898	15972	15983		16109		16109	16483	17874		17874	15983	17897	1951
	Probe SEQ ID NO:	7570	2276	2538	2681	3008	3304	3323	3449	3737	4510	4592	4782	5520	5993	6125	6136		6243		i	6603	8024	1.	╝	- 1	8/48	9335

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Top Hit Descriptor Source	xa89e03.x1 NC_CGAP_Co17 Homo sepiens cDNA clone IMAGE:2573932 3' similar to contains L1.b3 L1 EST_HUMAN repetitive element;	VT Homo sapiens ABCA1 (ABCA1) gene, complete cds	EST_HUMAN AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'	NT Homo sapiens chromosome 21 segment HS21C082	NT Drosophila melanogaster strain Lamto 120 Suppressor of Hairless (Su(H)) gene, partial cds	SWISSPROT MOSAIC PROTEIN LGN	NT Homo sapiens chromosome 21 seginent HS21C003	EST_HUMAN zw69g04.r1 Soares_testls_NHT Homo sapiens cDNA clone IMAGE:7781494 5	EST_HUMAN xy49g11.x1 NC _CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'	NT Homo sapiens chromosome 21 segment HS21C046	NT Homo sapiens Spast gene for spastlin protein	T HUMAN		SWISSPROT [52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))	NT Homo sapiens chromosome 21 segment HS21C027	zx35h12.s1 Soares_total_fetus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:788519 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);	Π			EST_HUMAN UI-H-BI2-agk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3		EST HUMAN repetitive element;	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis	NT (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds		Human hereditary haemochromatosis region, histone 2A like protein dene, hereditary haemochromat	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	T_HUMAN
Top Hit Acession No.	AW074604.1	2.0E-05 AF275948.1	2.0E-05 AU131513.1	1.0E-05 AL163282.2	1.0E-05 AF088273.1	P81274	AL163203.2	1.0E-05 AA431119.1	1.0E-05 AW419134.1	1.0E-05 AL163246.2	1.0E-05 AJ246003.1	AA64184	4505844 NT	P19474	1.0E-05 AL163227.2	1.0E-05 AA452578.1		1.0E-05 AA236110.1	1.0E-05 AW 291521.1	1.0E-05 AW 291521.1		1.0E-US AW 405995.1		1.0E-05 U91328.1			1.0E-05 U91328.1	1.0E-05 U91328.1 9.0E-06 Al583811.1
Most Similar (Top) Hit BLAST E Value	2.0E-05	2.0E-05	2.0E-05	1.0E-05	1.0E-05	1.0E-05 P81274	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05 P19474	1.0E-05	1.0E-05		1.0E-05	1.0E-05	1.0E-05	10	1.0E-US		1.0E-05			1.0E-05	1.0E-05 9.0E-06
Expression Signal	3.73	2.25	1.81	1.61	1.67	9.24	1.09	2.01	2.15	4.46	1.42	3.54	6.45	1.8	2.18	2.48		11.8	1.2	1.2	,	1./8		2.2	 		22	22
ORF SEQ ID NO:			25257	22417	23301	23583	23761	23853	24413	24539	26082	26128	26228			27312		27420	27778	27779				28414			28415	28415
Exon SEQ ID NO:	19677	19503	19208	12729	13513	13797	13984	14080	14627	14763	15952	- 1		16430	17045	17117	l		17554	17554		1//1		18170			18170	18170
Probe SEQ ID NO:	9442	9486	9637	2663	3599	3886	4082	4180	4742	4882	6046	6211	6213	6572	7168	7240		7352	7704	7704	į	LC8/		8291		_	8291	8291 2637

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Table 4
Single Exon Probes Expressed in Heart

Probe Exon			_	_		
SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No	Top Hit Database Source	Top Hit Descriptor
19311	25204	4.74	5.0E-06	5.0E-06 Al065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
10568	20380	4.41	4.0E-06	4.0E-06 R16267.1	EST_HUMAN	ya48c03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53254 5 similar to contains Alu repetitive element; contains L1 repetitive element;
40755	2060	C	00.00	4 OE OE A18(4000E4 4	MALM IN TOR	xc69g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu
1312 11218		5	4.0E-06	4.0E-06/AI334928.1	EST HUMAN	repeatable desired, contents element with the legicity element, the same same than the same same than the same same than the same same than the same same than the same same than the same same than the same same than the same same than the same same than the same same than the same same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the same than the
1			4.0E-06	4.0E-06 Al334928.1	EST HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3
1458 11363	21227		4.0E-06	4.0E-06 BF365612.1		QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
	22008	1.22	4.0E-06	4.0E-06 AW015401.1		UI-H-BI0-aat-f-05-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE: 2710425 3
3025 12953	22746	1.39		4.0E-06 AF198349.1	TN	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3819 13731	23520	1.78	4.0E-06	4.0E-06 AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4702 14588	24378	1.58	4.0E-06	4.0E-06 AI886939.1	EST HUMAN	wl94c10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432552 3' similar to contains element MER22 repetitive element;
4840 14721	24504	1.02	4.0E-06	4.0E-06 AL163279.2	FN	Homo sapiens chromosome 21 segment HS21C079
7109 16986	27177	3.1	4.0E-06	4.0E-06 AF009660.1	N	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8746 17895	28139	3.74	4.0E-06	4.0E-06 AB007955.1	K	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2117 12006	21904	1.27	3.0E-06	3.0E-06 AA700562.1	EST HUMAN	z34b08.s1 Soares_fetal_liver_splean_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element;
						z/34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE 432663 3' similar to
	21905		3.0E-06		EST HUMAN	contains L1.11 L1 repetitive element;
2220 12105		1.37	3.0E-06	3.0E-06 AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2891 12818	22610	0.95		3.0E-06 AA868218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1 t3 LTR1 repetitive element;
			i			wl22a05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:060734 060734
		2.14	3.0E-06	3.0E-06/AI857779.1	EST_HUMAN	LINE-1 LIKE PROTEIN ; contains L1.t2 L1 repetitive element ;
_	23412		3.0E-06	3.0E-06 BE047094.1	EST_HUMAN	hq64d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3716 13628	23413	1.26	3.0E-08	3.0E-06 BE047094.1	EST HUMAN	hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4376 14272	24053	0.0	3.0E-06	3.0E-06 T50266.1	EST_HUMAN	yb78b10.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
1.000			1		!	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N
4461 14355	24146	4.31	3.0E-06	-	LN	terminus.)
		1.92	3.0E-06 P08548	P08548	\neg	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
		4.17	3.0E-06	3.0E-06 AW385262.1		RC0-LT0001-261199-011-A03 LT0001 Homo sapiens cDNA
195 10167		3.28	2.0E-06 P54366	P54366	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID

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Pode FORD Exercised NO. CMP. SEC Associated CMP. SEC Associated Top HI According No. Top HI According No.)	200	Single Exon Flobes Expressed in Real
11455 6.27 2.0E-06 P21414 SWISSPROT 12207 22106 2.96 2.0E-06 AI672138.1 EST_HUMAN 12295 22182 2.14 2.0E-06 P04929 SWISSPROT 12393 22286 2.0E-06 P04029 SWISSPROT 13394 23398 1.11 2.0E-06 P047555.1 EST_HUMAN 13613 23398 1.5 2.0E-06 AA173618.1 EST_HUMAN 1563 2.0E-06 AA173618.1 EST_HUMAN 1563 2.0E-06 AA173618.1 EST_HUMAN 1563 2.0E-06 AB19424.1 EST_HUMAN 1563 2.0E-06 AB19424.1 EST_HUMAN 1563 2.0E-06 AB19424.1 EST_HUMAN 1669 2.0E-06 P05125 SWISSPROT 17013 2.7206 1.0E-06 P052249 SWISSPROT 11412 2.1271 1.0E-06 P06125 SWISSPROT 11440 2.1271 1.0E-06 AA163278.2 NT 11447 2.1271 0.93 1.0E-06 AA034141.1 EST_HUMAN 11447 2.1318	Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12207 22106 296 20E-06 P04929 SWISSPROT 12295 22192 2.14 2.0E-06 P04929 SWISSPROT 12393 22285 2.69 2.0E-06 P04929 SWISSPROT 13614 23398 1.11 2.0E-06 P04929 SWISSPROT 13614 23398 1.5 2.0E-06 A1057563-1 EST_HUMAN 13623 23406 1.5 2.0E-06 A1819424-1 EST_HUMAN 15624 25904 5.08 2.0E-06 A1819424-1 EST_HUMAN 15629 2.4901 1.65 2.0E-06 A1819424-1 EST_HUMAN 16678 2.0E-06 A1819424-1 EST_HUMAN 16799 2.4901 1.0E-06 A20349 SWISSPROT 16778 2.22 1.0E-06 A20349 SWISSPROT 11442 2.1277 1.0E-06 A2034141.1 EST_HUMAN 11459 2.1318 0.93 1.0E-06 A2034141.1 EST_HUMAN 11470 1.2 1.0E-06 A2034141.1 EST_HUMAN 11447 2.1328 1.111 1.0E-06 A2035	1550			6.27	2.0E-06	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
12295 22192 2.14 2.0E-06 P04929 SWISSPROT 13391 22385 2.69 2.0E-06 P06719 SWISSPROT 13614 23386 1.5 2.0E-06 AA173518.1 EST_HUMAN 13623 23406 1.5 2.0E-06 AB030896.1 NT 13624 25304 5.08 2.0E-06 AB030896.1 NT 17013 27206 1.65 2.0E-06 AB030896.1 NT 19699 24901 1.35 2.0E-06 P625349 SWISSPROT 10578 20394 1.61 1.0E-06 AF084364.1 EST_HUMAN 10578 20394 1.61 1.0E-06 AF084364.1 NT 11440 2120 2.22 1.0E-06 AF084364.1 NT 11459 21317 0.93 1.0E-06 AA034141.1 EST_HUMAN 11450 21317 0.93 1.0E-06 AA034141.1 EST_HUMAN 11470 1.2729 4.74 <td< td=""><td>2326</td><td></td><td></td><td>2.95</td><td>2.0E-06</td><td></td><td>FST HUMAN</td><td>wa04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30 b1 MER30 repetitive element:</td></td<>	2326			2.95	2.0E-06		FST HUMAN	wa04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30 b1 MER30 repetitive element:
12383 22285 2.69 2.0E-06 P06719 SWISSPROT 13391 23196 1.11 2.0E-06 AV657555.1 EST_HUMAN 13614 23388 1.5 2.0E-06 AB030896.1 NT 13623 23406 1.5 2.0E-06 AB030896.1 NT 17013 27206 1.65 2.0E-06 AB030896.1 NT 19099 24901 1.35 2.0E-06 BE32632.1 EST_HUMAN 10018 1.9813 1.9 2.0E-06 BE32632.1 EST_HUMAN 10478 22894 1.61 1.0E-06 BE32632.1 EST_HUMAN 11340 21206 1.9 1.0E-06 BE32632.1 EST_HUMAN 114412 21271 1.0 1.0E-06 AF084364.1 NT 11442 21271 1.0 1.0E-06 AF084364.1 NT 11459 21317 0.93 1.0E-06 AA034141.1 EST_HUMAN 11459 21317 0.93 1.0E-06 AA034141.1 EST_HUMAN 14844 21730 4.74 1.0E-06 AA034141.1 NT <td>2418</td> <td></td> <td></td> <td>2.14</td> <td>2.0E-06</td> <td></td> <td>SWISSPROT</td> <td>HISTIDINE-RICH GLYCOPROTEIN PRECURSOR</td>	2418			2.14	2.0E-06		SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
13391 23196 1.11 2.0E-06 AV657555.1 EST_HUMAN 13614 23388 1.5 2.0E-06 AA173618.1 EST_HUMAN 13623 23406 1.5 2.0E-06 AB030896.1 NT 17013 27206 1.65 2.0E-06 AB030896.1 NT 19059 24901 1.35 2.0E-06 P23249 SWISSPROT 10018 19813 1.9 1.0E-06 P23249 SWISSPROT 104678 20384 1.61 1.0E-06 P23249 SWISSPROT 11440 21206 2.22 1.0E-06 P09125 SWISSPROT 11459 21317 0.93 1.0E-06 AC034141.1 EST_HUMAN 11459 21317 0.93 1.0E-06 AC034141.1 EST_HUMAN 11440 21729 4.74 1.0E-06 AC034141.1 INT 14844 21730 4.74 1.0E-06 AC034141.1 INT 14915 24689 1.111 1.0E-06 AC034141.1 INT 14915 24689 1.111 1.0E-06 AC034141.1 INT <td>2519</td> <td></td> <td></td> <td>2.69</td> <td>2.0E-06</td> <td>P06719</td> <td>SWISSPROT</td> <td>KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)</td>	2519			2.69	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
13614 23398 1.5 2.0E-06 AA173618.1 EST HUMAN 13623 23406 1.5 2.0E-06 AB030896.1 NT 15784 25904 5.08 2.0E-06 AB19424.1 EST HUMAN 17013 27206 1.65 2.0E-06 P23249 SWISSPROT 19018 24901 1.35 2.0E-06 P23249 SWISSPROT 10078 246 2.0E-06 B23232.1 EST HUMAN 10578 20394 1.61 1.0E-06 AC082 SWISSPROT 11340 21206 2.22 1.0E-06 AC082 SWISSPROT 114459 21317 0.93 1.0E-06 AC084341.1 EST HUMAN 11446 21729 4.74 1.0E-06 AC084325.2 NT 11844 21729 4.74 1.0E-06 AC084141.1 EST HUMAN 11844 21729 4.74 1.0E-06 AC084141.1 NT 11844 21729 4.74 1.0E-06 AC08525.2 NT 14915 24688 1.38 1.0E-06 AC085285.2 NT 14915	3475		23196	1.11	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'
13523 23406 1.5 2.0E-06 AB030896.1 NT 15784 25904 5.08 2.0E-06 AI819424.1 EST_HUMAN 17013 27206 1.65 2.0E-06 H62051.1 EST_HUMAN 1999 24901 1.35 2.0E-06 P52249 SWISSPROT 10018 1.9813 1.35 2.0E-06 P52249 SWISSPROT 10578 20394 1.61 1.0E-06 P6082 SWISSPROT 11340 21206 2.22 1.0E-06 AF084364.1 NT 114412 21206 2.22 1.0E-06 AF084364.1 NT 114459 21317 0.93 1.0E-06 AF084364.1 NT 11440 21201 1.0E-06 AF084364.1 NT 11440 21729 4.74 1.0E-06 AF084141.1 EST_HUMAN 11844 21729 4.74 1.0E-06 AF084141.1 NT 11844 21729 4.74 1.0E-06 AF084141.1 NT 14915 24689 1.31 1.0E-06 AF084141.1 NT 14915	3700			1.5	2.0E-06	-	EST_HUMAN	zp02e05.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5
15784 25904 5.08 2.0E-06 H62051.1 EST HUMAN 19699 24901 1.65 2.0E-06 P23249 SWISSPROT 19718 2.46 2.0E-06 P23249 SWISSPROT 10018 19813 1.9 1.0E-06 P23249 SWISSPROT 10578 20394 1.0E-06 P23249 SWISSPROT 11340 21206 2.22 1.0E-06 P03125 SWISSPROT 11412 21271 1.09 1.0E-06 P03125 SWISSPROT 11459 21317 0.93 1.0E-06 P414378.2 NT 11459 21317 0.93 1.0E-06 P27625 SWISSPROT 11459 21318 0.93 1.0E-06 P27625 SWISSPROT 11470 21729 4.74 1.0E-06 P27625 SWISSPROT 11471 23949 11.11 1.0E-06 P27625 SWISSPROT 14915 24688 1.31 1.0E-06 P27625 SWISSPROT 14916 24688 1.31 1.0E-06 P27625 SWISSPROT 14916 246	3710			1.5	2.0E-06		N	Mus musculus gene for odorant receptor A16, complete cds
17013 27206 1.65 2.0E-06 H62051.1 EST_HUMAN 19699 24901 1.35 2.0E-06 P23249 SWISSPROT 19148 2.46 2.0E-06 BE328232.1 EST_HUMAN 10018 19813 1.9 1.0E-06 D76082 SWISSPROT 10578 20394 1.61 1.0E-06 D76082 SWISSPROT 11440 21206 2.22 1.0E-06 P09125 SWISSPROT 11459 21317 0.93 1.0E-06 AA034141.1 EST_HUMAN 11459 21318 0.93 1.0E-06 AF84614.1 NT 11470 21729 4.74 1.0E-06 AF84614.1 NT 14417 22949 11.11 1.0E-06 AF84614.1 NT 14915 24688 1.38 1.0E-06 AF84614.1 NT 14916 24688 1.38 1.0E-06 AF84614.1 NT 14916 24688 1.38 1.0E-06 AF84614	5878			5.08	2.0E-06	AIB19424.1	EST_HUMAN	wj90b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3
19699 24901 1.35 2.0E-06 PE3249 SWISSPROT 19018 19813 1.9 1.0E-06 O76082 SWISSPROT 10578 20394 1.61 1.0E-06 O76082 SWISSPROT 11340 21206 2.22 1.0E-06 P09125 SWISSPROT 11412 21271 1.09 1.0E-06 AL163278.2 NT 11459 21317 0.93 1.0E-06 AA034141.1 EST_HUMAN 11470 1.2 1.0E-06 AA034141.1 INT 11471 2.729 4.74 1.0E-06 AA034141.1 INT 14472 2.3949 11.11 1.0E-06 AF184614.1 NT 14915 2.4688 1.38 1.0E-06 AA184614.1 NT	7136		27206	1.65	2.0E-08	H62051.1	EST HUMAN	w37c04.r1 Sogres ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929 KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
19148 2.46 2.0E-06 BE3282321 EST HUMAN 10018 19813 1.9 1.0E-06 O76082 SWISSPROT 10578 20394 1.61 1.0E-06 P09125 SWISSPROT 11340 21206 2.22 1.0E-06 P09125 SWISSPROT 11412 21271 1.09 1.0E-06 AL163278.2 NT 11459 21317 0.93 1.0E-06 AA034141.1 EST HUMAN 11470 1.2 1.0E-06 AA034141.1 EST HUMAN 11470 1.2 1.0E-06 AA034141.1 EST HUMAN 11470 1.2 1.0E-06 AA034141.1 EST HUMAN 11470 2.729 4.74 1.0E-06 AF184614.1 NT 14471 2.2949 11.11 1.0E-06 AF184614.1 NT 14915 2.4688 1.38 1.0E-06 AL163285.2 NT 14916 2.4089 1.38 1.0E-06 AL163285.2 NT	9403			1.35	2.0E-06	P23249	SWISSPROT	PROTEIN MOV-10
10018 19813 1.9 1.0E-06 AF084364.1 NT 10578 20394 1.61 1.0E-06 AF084364.1 NT 11340 21206 2.22 1.0E-06 P09125 SWISSPROT 11412 21271 1.09 1.0E-06 AA143278.2 NT 11459 21317 0.93 1.0E-06 AA034141.1 EST HUMAN 11470 1.2 1.0E-06 AA034141.1 EST HUMAN 11844 21729 4.74 1.0E-06 AF184614.1 NT 14172 23949 11.11 1.0E-06 AF184614.1 NT 14915 24688 1.38 1.0E-06 AF184614.1 NT 14916 24688 1.38 1.0E-06 AF184614.1 NT 14517 24688 1.38 1.0E-06 AF184614.1 NT 14616 24689 1.38 1.0E-06 AF184614.1 NT 14517 24688 1.38 1.0E-06 AF184614.1 NT 14516 24689 1.38 1.0E-06 AF184614.1 NT 14517 24926	9548	Ĺ	,	2.46	2.0E-06	BE328232.1	EST HUMAN	hs92f02.xf NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.t2 L1 repetitive element:
10018 19813 1.9 1.0E-06 O76082 SWISSPROT 10578 20394 1.61 1.0E-06 AF084364.1 NT 11340 21206 2.22 1.0E-06 P09125 SWISSPROT 11412 21271 1.09 1.0E-06 AL163278.2 NT 11459 21317 0.93 1.0E-06 AA034141.1 EST_HUMAN 11470 1.2 1.0E-06 AA034141.1 EST_HUMAN 11844 21729 4.74 1.0E-06 AF184614.1 NT 14172 23949 11.11 1.0E-06 AF184614.1 NT 14915 24688 1.38 1.0E-06 AL163285.2 NT 14916 24689 1.38 1.0E-06 AL163285.2 NT 16001 26139 6.11 1.0E-06 AL163285.2 NT 16001 26139 6.11 1.0E-06 AL163285.2 NT 16001 26139 1.0E-06 AL163285.2 NT								ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22 MEMBER 5) (HIGH
10578 20394 1.61 1.0e-06 AF084364.1 NT 11340 21206 2.22 1.0e-06 P09125 SWISSPROT 11412 21271 1.09 1.0e-06 AL163278.2 NT 11459 21317 0.93 1.0e-06 AA034141.1 EST_HUMAN 11470 1.2 1.0e-06 AA034141.1 EST_HUMAN 11844 21729 4.74 1.0e-06 AF184614.1 NT 14472 23949 11.11 1.0e-06 AF184614.1 NT 14915 24688 1.31 1.0e-06 AF184614.1 NT 14916 24689 1.31 1.0e-06 AF184614.1 NT 14916 24689 1.31 1.0e-06 AF18333015.1 EST_HUMAN 16001	31			1.9	1.0E-06	076082	SWISSPROT	AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
11340 21206 2.22 1.0E-06 AL163278.2 SWISSPROT 11412 21271 1.09 1.0E-06 AL163278.2 NT 11459 21318 0.93 1.0E-06 AA034141.1 EST_HUMAN 11470 1.2 1.0E-06 P27625 SWISSPROT 11844 21729 4.74 1.0E-06 P27625 SWISSPROT 11844 21729 4.74 1.0E-06 P27625 SWISSPROT 14172 23949 11.11 1.0E-06 AF184614.1 NT 14915 24688 11.11 1.0E-06 AF184614.1 NT 14916 24688 1.38 1.0E-06 AF184614.1 NT 14916 24688 1.31 1.0E-06 AF184614.1 NT 14916 24688 1.38 1.0E-06 AF18386.2 NT 1601 26188 1.0E-06 AF18333015.1 EST_HUMAN 1601 26139 6.11 1.0E-06 AF1847010.1 EST_HUMAN 16601 26139 1.0E-06 AF184333015.1 EST_HUMAN	641			1.61	1.0E-06	<u>۲</u>	LN	Mus musculus D6MM5E protein (D6Mm5e) mRNA, canplete cds
11412 21271 1.09 1.0E-06 AAL163278.2 NT 11459 21317 0.93 1.0E-06 AA034141.1 EST_HUMAN 11470 1.2 1.0E-06 P27625 SWISSPROT 11844 21729 4.74 1.0E-06 P27625 SWISSPROT 11844 21730 4.74 1.0E-06 P27625 SWISSPROT 14172 23949 11.11 1.0E-06 AF184614.1 NT 14915 24688 11.11 1.0E-06 AF184614.1 NT 14916 24689 11.11 1.0E-06 AF183285.2 NT 14916 24689 1.38 1.0E-06 AF1833015.1 EST HUMAN 16001 26139 6.11 1.0E-06 AF333015.1 EST HUMAN 16602 26881 1.16 1.0E-06 AF333016.1 EST HUMAN	1435		21206	2.22	1.0E-06		SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
11459 21317 0.93 1.0E-06 AA034141.1 EST_HUMAN 11459 21318 0.93 1.0E-06 P27625 SWISSPROT 11844 21729 4.74 1.0E-06 P27625 SWISSPROT 11844 21730 4.74 1.0E-06 AF184614.1 NT 14172 23949 11.11 1.0E-06 AF184614.1 NT 14915 24688 11.11 1.0E-06 AL163285.2 NT 14916 24689 1.38 1.0E-06 AL163285.2 NT 16001 26139 6.11 1.0E-06 BF333015.1 EST HUMAN 16602 26139 6.11 1.0E-06 AL163285.2 NT 16601 26139 6.11 1.0E-06 BF333015.1 EST HUMAN 16602 26681 1.0E-06 AI347010.1 EST HUMAN	1507			1.09	1.0E-06	2	N	Homo sapiens chromosome 21 segment HS21C078
11459 21318 0.93 1.0E-06 AA034141.1 EST_HUMAN 11470 1.2 1.0E-06 PZ7625 SWISSPROT 11844 21729 4.74 1.0E-06 AF184614.1 NT 11844 21729 4.74 1.0E-06 AF184614.1 NT 14915 24688 11.11 1.0E-06 U07561.1 NT 14915 24688 1.38 1.0E-06 AL163285.2 NT 15157 24925 4.69 1.0E-06 BF333015.1 SWISSPROT 16001 26139 6.11 1.0E-06 BF333015.1 SWISSPROT 16692 28881 1.16 1.0E-06 AL163285.2 NT	15.54		21317	0 03	100		TOT TOTAL	206a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to
11459 21318 0.93 1.0E-06 AA034141.1 EST_HUMAN 11470 1.2 1.0E-06 PZ7625 SWISSPROT 11844 21729 4.74 1.0E-06 AF184614.1 NT 11844 21730 4.74 1.0E-06 AF184614.1 NT 14915 24688 11.11 1.0E-06 UO7561.1 NT 14915 24689 1.38 1.0E-06 AL163285.2 NT 15157 24925 4.69 1.0E-06 BF333015.1 EST HUMAN 16001 26139 6.11 1.0E-06 BR5333015.1 SWISSPROT 16692 28881 1.16 1.0E-06 AL637710.1 EST HUMAN			11017	200	1.00		EG - TOWAIN	Contains And Topenuve definent,
11470 1.2 1.0E-06 P27625 SWISSPROT 11844 21729 4.74 1.0E-06 AF184614.1 NT 11844 21730 4.74 1.0E-06 AF184614.1 NT 14172 23949 11.11 1.0E-06 AF184614.1 NT 14915 24688 1.38 1.0E-06 AL163285.2 NT 14915 24989 1.38 1.0E-06 AL163285.2 NT 15157 24925 4.69 1.0E-06 BF333015.1 EST HUMAN 16001 26139 6.11 1.0E-06 P02671 SWISSPROT 16692 26881 1.16 1.0E-06 AL163285.2 NT	1554		21318	0.93	1.0E-06	41.1	EST HUMAN	Zuodatzist Socares, retal liver spicen 1NFLS S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
11844 21729 4.74 1.0E-06 AF184614.1 NT 11844 21730 4.74 1.0E-06 AF184614.1 NT 14172 23949 11.11 1.0E-06 U07561.1 NT 14915 24688 1.38 1.0E-06 AL163285.2 NT 15157 24925 4.69 1.0E-06 BF333015.1 EST HUMAN 15001 26139 6.11 1.0E-06 BF333015.1 EST HUMAN 16692 26881 1.16 1.0E-06 AL163285.2 IMT	1565			1.2	1.0E-06		SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
11844 21730 4.74 1.0E-06 AF184614.1 NT 14172 23949 11.11 1.0E-06 U07561.1 NT 14915 24688 1.38 1.0E-06 AL163285.2 NT 15157 24925 4.69 1.0E-06 BF333015.1 EST HUMAN 16001 26139 6.11 1.0E-06 AL163285.2 NT 16001 26139 6.11 1.0E-06 BF333015.1 EST HUMAN 16692 26881 1.16 1.0E-06 AL347010.1 EST HUMAN	1949		21729	4.74	1.0E-06	-	N	Homo sapiens p47-phox (NCF1) gene, complete cds
14172 23949 11.11 1.0E-06 U07561.1 NT 14915 24688 1.38 1.0E-06 AL163285.2 NT 14915 24925 4.69 1.0E-06 BF333015.1 EST HUMAN 16001 26139 6.11 1.0E-06 BP2671 SWISSPROT 16692 26881 1.16 1.0E-06 Al347010.1 EST HUMAN	1949		21730	4.74	1.0E-06	-	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
14915 24688 1.38 1.0E-06 AL163285.2 NT 14915 24689 1.38 1.0E-06 AL163285.2 NT 15157 24925 4.69 1.0E-06 BF333015.1 EST HUMAN 16001 26139 6.11 1.0E-06 PO2671 SWISSPROT 16692 26881 1.16 1.0E-06 AI347010.1 EST HUMAN	4273		23949	11.11	1.0E-06		LN LN	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete and
14915 24089 1.38 1.0E-06 AL163285.2 NT 15157 24925 4.69 1.0E-06 BF333015.1 EST HUMAN 16001 26139 6.11 1.0E-06 P02671 SWISSPROT 16692 26881 1.16 1.0E-06 Al347010.1 EST HUMAN	5043		24688	1.38	1.0E-06	2	LN	Homo sapiens chromosome 21 segment HS21C085
15157 24925 4.69 1.0E-06 BF333015.1 EST HUMAN 16001 26139 6.11 1.0E-06 P02671 SWISSPROT 16692 26881 1.16 1.0E-06 AI347010.1 EST HUMAN	5043		24689	1.38	1.0E-06		LN	Homo sapiens chromosome 21 segment HS21C085
16001 26139 6.11 1.0E-06 P02671 SWISSPROT 16692 26881 1.16 1.0E-06 Al347010.1 EST HUMAN	5233		24925	4.69	1.0E-06	1	Γ	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
16692 26881 1.16 1.0E-06 Al347010.1 EST_HUMAN	6107		26139	6.11	1.0E-06			FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
	6813		26881	1.16	1.0E-06	1		qp54e02.x1 NCI_CGAP_Co8 Homo saplens cDNA clone IMAGE.1926842 3'

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Table 4
Single Exon Probes Exonormal

Single Exon Probes Expressed in Heart	lit Top Hit Acession Top Hit Descriptor Top Hit Source	1.0E-06.41287878.1 FST HIMAN MIR reporting clement	L L	LN	1.1		LO LO	FST HIMAN	LN	1.0E-06 AF184614.1 NT Homo sepiens 847-phox (NCE1) zero complete cds	L	N	NT		EST HUMAN		SWISSPROT	8.0E-07/AF135416.1 NT Home can large LIDE client CONTAINS. PRO LEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE I	EST HUMAN	27	H	8.1 FST HIMAN		٦	SWISSPRO	EST HUMAN	-r	TOT TOTAL	FST HIMAN	
-	Top Hit	-06 AI287878	-06 U82668.	-06 U82668.	-06 AA13261	-06 AA44925	-06 At 16320	-06 AW8909	-06 L78810.1	-06 AF18461	06 AF18461	07 AF00352	07 AF00352	07 AL163281	07 AI288596.	07 AI288596.	07 P21414	07 AF135416	07 T07770.1	07 AL163280		7 AW85555		7 P41470	10000	7 A14/00200	7 A1831903	7 A A 3 B D E 3 D	7 Al831893.1	
	Most Similar (Top) Hit BLAST E Value							L	L												7.0E-		u U	6.0E-/	8 05	9.0E-	0.0F	5.05	5.0E-0	
	Expression Signal	1.53	3.72	3.72	4.86	3.73	1.52	4.81	2.99	1.84	1.84	1.49	1.49	2.38	4.49	4.49	7.45	7.89	7.2	4.15	0.94	2.36	241	1.65	1 25	187	3.55	2.9	0.87	
	ORF SEQ ID NO:	27013		27648	27676				25280	21729	21730	20134	20135	28708	24336	24337					21599	21641	22217		27351		-	_		
	Exon SEQ ID NO:	16822	17433	17433	17460	17488	17839	18720	19077	11844	11844	10314	10314	18440	14547	14547	15504	16547	18703	18838	11719	11766	12319	13802	17156	19653	10284	10959	12923	
	Probe SEQ ID NO:	6944	7582	7682	7609	7637	7989	8912	9440	9536	9536	357	357	8572	4661	4661	5589	2999	8893	9055	1822	1870	2442	3891	7279	9303	323	1041	2995	

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Table 4
Single Exon Probes Expressed in Heart

1	ı	J	1	1		ı	1	1	1	1	1	ł	1 -	1-1		7	1	17		7	-	_	_	_		7-7-		
Top Hit Descriptor	Homo sapiens NOD1 protein (NOD1) gene exems 4 through 11	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiers CDNA clock INAGE:2107953 3' similar to contains Alu	tg06b05.x1 NCI_CGAP_CLL1 Homo sapients cDNA clone IMAGE:2107953 3' similar to contains Alurepetitive element contains element A3R repetitive allowers.	xa31a02.x1 NCI_CGAP_Br18 Horro sapiens cDNA clone IMAGE:2568362 3' similar to gb:X15341	CM-BT178-220400 014 BT178 U.	COLLAGEN A DUA 44/ CHAIN CHAIN COLLAGEN CONA	Homo seriens Vancanda Line (1) challe Prescursory	OVO-CT0383-210,000 201 443 CT0303-11	ws84h05 v1 NCI CGAD Over Liver Septemble CDNA	MAGN11 v1 NCT CCAB 1 :24 4 1.	Wi8thing of NOT COAD CLASS. I Homo saplens cDNA clone IMAGE:2856548 3	wild those of NCI COART IN 12 Homo sapiens cDNA clone IMAGE 2399703 3	PM1. RNINGS 03000 002 - 40 EN 2000 11	Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively, solinged	Untranslated exons	nomo sapiens Aq pseudoautosomal region; segment 1/2	numan polymorphic microsatellite DNA	nisoboes 1 NCI_CGAP_Ovz Homo sapiens cDNA clone IMAGE:980825 similar to contains Ali	element; contains L1.t3 L1 repetitive element;	Human polymorphic microsatellite DNA	MRG-BN0115-020300-001-f11 BN0115 Homo saplens cDNA	Mrd-BN0113-020300-001-f11 BN0115 Homo sapiens cDNA	MODITION SOCIETIES Spleen 1NFLS Homo sepiens cDNA clone IMAGE 111695 5'	AVERGRA OF U.S. B. B. B. D. PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR	Wasterford Source NET Tions Cone GLCCD013'	yor1409.st Statagene lung (#937210) Homo sapiens cDNA clone IMAGE:2347967 3'	yo.wozacz AKACHILONATE 12-LIPOXYGENASE (HUMAN) W14h09.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMACE:80705.91 cimilar to all all all all all all all all all al	gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
Top Hit Database Source	IN	EST_HUMAN	EST_HUMAN	H. T.S.H.	EST HUMAN	SWISSPROT	LN	EST HUMAN	EST HUMAN	HIMAN	Т	┰	FST HIMAN	\neg	H				ESI HUMAN		EST HUMAN	Т	COL HOMAN	Τ.	Т			ESI HUMAN 9
Top Hit Acession No.	5.0E-07 AF149774.1	5.0E-07 Al393981.1	5.0E-07 Al393981.1	5.0E-07 AW070885.1	5.0E-07 AI908587.1	5.0E-07 P11087	5.0E-07 AJ271735.1	5.0E-07 AW862537.1			4.0E-07 AI765528.1				7 4	-				,	7.1			-	-			
Most Similar (Top) Hit BLAST E Value	5.0E-07	5.0E-07	5.0E-07	5.0E-07	5.0E-07	5.0E-07	5.0E-07	5.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	3 0F_07 110740	3 0F-07	3.0E-07 M99149	3.0E-07 M64857	0 0	3.0E.07 M00440	3 0E-07 BEODEO7	3.0E-07 BE00507	3.0E-07 T84704 1	3.0E-07 P38739	3.0E-07 AV65020	3.0E-07 AI797236.	3.0E-07 T57850 4	3 05 07 167950	0.01-0/
Expression Signal	1.44	1.71	1.71	15.93	4.11	4.31	2.06	2.02	1.98	5.29	3.84	3.84	2.05	5.01	2.38	2.19	2.23	5	1 15	17.25	17.25	0.85	1.82	7.05	0.89	1.47	1 47	
ORF SEQ ID NO:	24223	26096	26097	26373	28021	28909			23608	27305	28432	28433		20200	20314	21114			22026	22194	22195	22718	22844	24302	24329	24634	24635	
Exon SEQ ID NO:	14440	15963	15963	16211	17782	18619	18675	19556	13827	17112	18185	18185	18422	10379	10507	11258	11513	11893	12126	12297	12297	12926	13047	14512	14540	14871	14871	
Probe SEQ ID NO:	4547	6203	6203	6348	7932	8805	8863	9712	3918	7235	8308	8308	8552	434	268	1352	1608	2000	2242	2420	2420	2998	3122	4624	4654	4996	4996	
		_			_										_	ب			ــــ					1			L	1

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Table 4
Single Exon Probes Expressed in Heart

-				Most Similar			
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5476	15396	25462	10.26	3.0E-07 O88807	088807	SWISSPROT	PROTEIN ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6026	15930		5.32	3.0E-07	3.0E-07 AA815175.1	EST_HUMAN	0c04c10.s1 NCI_CGAP_GCB1 Hamo saplens cDNA clone IMAGE:1339890.3'
6433	16294	26456	8	3.0E-07	3.0E-07 AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-902 UM0036 Homo sapiens cDNA
8918			3	3.0E-07	3.0E-07 AF029308.1	N.	Homo saplens chromosome 9 duplication of the T cell receptor beta locus and transingual remaining
6630	19408		2.76	3.0E-07	3.0E-07 AJ132352.1	LN⊤	Raftus norvegicus mRNA for 45 kDa secretory protein, partial
26			2.62	2.0E-07	2.0E-07 AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA complete cds
148			4.75	2.0E-07	2.0E-07 L77569.1	L	Homo sapiens DiGeorge syndrome critical region, telomeric end
148			4.75	2.0E-07	2.0E-07 L77569.1	N	Homo sapiens DiGeorge syndrome critical region, telomeric end
175			116.1	2.0E-07	2.0E-07 U38849.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
731			1.71	2.0E-07	2.0E-07 AF003530.1	-N	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete rds and flanking reposit requires
731	10663	20496	1.7.1	2.0E-07	2.0E-07 AF003530.1	TN	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
928	10853	20701	3.11	2.0E-07	2.0E-07 AA223260.1	EST HUMAN	zr08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' stmilar to gb:L31860 GLYCOPHORIN A PRECURSOR (H1MAN) contains all repositive alcohome.
929	10854	20702	3.38	2.0E-07	2.0E-07 T63042 1	FST HIMAN	yc15g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element
1147	11060		1.28	2.0E-07 Q26768	026768	SWISSPROT	I/G AUTOANTIGEN
1582	11486		1.84	2.0E-07 Q09701	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7 10 IN CHROMOSOME I
3633	13547	23334	14.74	2.0E-07	2.0E-07 AF125348.1	TN	Homo sapiens caveolin 1 (CAV1) gene, expn 3 and nartial cds
5078	14948	24723	0.97	2.0E-07	2.0E-07 AW070995.1	EST_HUMAN	xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1 CE00923 PROBABLE RABGAP DOMAINS;
5078	14948	24724	26.0	2.0E-07	2.0E-07 AW070995 1	FST HIMAN	X805h07.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP. C38H2.1 CED0923 PROBABI F RARGAP DOMAINS
5198	15061	24826	0.95	2.0E-07	2.0E-07 AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5277			1.73	2.0E-07	2.0E-07 AW898066.1	EST HUMAN	RC3-NN0056-260400-021-q11 NN0066 Homo sapiens cDNA
6009				2.0E-07	2.0E-07 AI208715.1	Π	9956405.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE 1839177.3
6934	_}		3.91	2.0E-07	2.0E-07 AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
7627	17478		1.61	2.0E-07	2.0E-07 AL163303.2	N FN	Homo sapiens chromosome 21 segment HS21C103
7891	17741	27984	6.48	2.0E-07	2.0E-07 AW892507.1	EST_HUMAN	CM4-NN0003-280300-124-e06 NN0003 Homo sapiens cDNA
9094	19557		1.48	2.0E-07	2.0E-07 AI732462.1	EST HUMAN	zn85h11.x5 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element:
1086	11002		1.21	1.0E-07		\sqcap	Нопо sapiens chromosome 21 segment HS21C082
					!		

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								1		T		T		T	1	T	3722			T	T	1	1		7					Π
Strigte Exon Probes Expressed in Heart	Top Hit Descriptor	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)	Homo sapiens RAB, member of RAS, oncorese familiarlike 2A (13 Apr 2A)	GLYCOPROTEIN GPV	Homo sapiens chromosome 21 segment HS210082	AV718662 GLC Homo sapiens cDNA clone GL CFNF04 5'	AV718662 GLC Homo sapiens cDNA clone GL CENFOA 5'	E43406.yf NCI CGAP Brn52 Homo saniens cIDNA clone IMAGE 2201320 E	1243d06,yl NCI CGAP BITI52 Home seniens cDN4 clone IMAGE-2204320 E	1943c07.s1 Soares fetal liver spleen 1NFLS Homo ganiens of NA clans (MACE: 245.04.5)	ENTEROPEPTIDASE (ENTEROKINASE)	ENTEROPEPTIDASE (ENTEROKINASE)	zi51e10.s1 Soares fetal liver spleen 1NFLS S1 Homo saniens cDNA clone MAACE 434348.2	602137714F1 NIH MGC 83 Homo sapiens cDNA clone IMAGE-4274426 5	EST185054 Brain IV Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C082	hr53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:095722 095722 DJ1163.11 1:	H saniens AI AD gene for nombobility and suffices	Human lambda-imminorilobilin constant review (2000)	AV734819 cdA Homo sapiens cDNA clone cdARFRAG 5'	wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similæ to contains OFR.t2 OFR repetitive element	Homo sapiens chromosome 21 segment HS21C101	Homo sapiens partial steerin-1 nene	Wd16b06.x1 Soares NFI T GRC S1 Home contains characters was conserved and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains 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and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains	٦١:	601590133F1 NIH MGC 7 Homo sapiens CDNA clone IMAGE 3043976 5	cu15c02.x1 Normal Human Trahecular Rome Calls Home conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the conjugate to the 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Jie Exon Pro	Top Hit Database Source	SWISSPROT	LN ⊢N	SWISSPROT	LN LN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	EST HUMAN	EST HUMAN	N⊤	EST HUMAN	I-Z	LX	EST HUMAN	EST HUMAN	TN	N _T	EST HUMAN	ST HUMAN	EST HUMAN	EST HUMAN	ECT UIMAN	TOWN TO TO	NT
Silic	Top Hit Acession No.	P10263	7549818 NT		1.0E-07 AL163282.2			1.0E-07 BE047871.1					3.1	4.1	1.1	2.2	0.1			9.1	-	2	\				-	,	2.4	
	Most Similar (Top) Hit BLAST E Value	1.0E-07 P10263	1.0E-07	1.0E-07 P09256	1.0E-07	1.0E-07	1.0E-07	1.0E-07	1.0E-07 BE04787	1.0E-07 N55081.1	1.0E-07 P97435	1.0E-07 P97435	1.0E-07 AA69357	1.0E-07 BF67452	1.0E-07 AA38631	1.0E-07 AL16328	1.0E-07 BE04877	1.0E-07 X64467.1	1.0E-07 X51755.1	9.0E-08 AV73481	9.0E-08	9.0E-08 AL163301	9.0E-08	8.0E-08	8.0E-08	8.0E-08	8.0E-08 AI752367	8 OF -08 A1752367	A OF-DR	8.0E-08 A
	Expression Signal	0.94	0.94	1.75	1.33	2.37	2.37	5.2	5.2	9.04	2.81	2.81	3.24	2.37	1.28	1.56	3.66	1.37	4.61	1.67	2.91	3.91	3.09	2.65	0.88	1.43	3.38	3.38	2 89	2.39
	ORF SEQ ID NO:	22110	22177	21269		23874	23875	26132	26133	26447	26850	26851	27246	27790	27792		25060			27765	28656	29025					27144	27145	27616	
	Exon SEQ ID NO:	12212	12280	11410			_	_1	15997	16285	- 1	- 1	17057	17564	17566	17830	19533	19113	19222	17539	18392	18730	19008	12671	10952	13415	16951	16951	17402	18438
	Probe SEQ ID NO:	2331	2403	2797	3684	4195	4195	6103	6103	6424	6782	6782	7180	7714	7716	7980	9364	9497	9661	7689	8520	8922	9316	591	1034	3498	7074	7074	7551	8570

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Table 4
Single Exon Probes Expressed in Heart

					<u>.</u>	ביי ווייסאם סופ	חוקה באטון וספים בארטינים וויים
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
73	10057	19874	3.27	7.0E-08 Q02357	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1338	11244	21102	12.71	7.0E-08	7.0E-08 X04809.1	LN	Rat mRNA for ribosomal protein L31
3528	13444	23240	1.09	7.0E-08 P15305	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3528			1.09	7.0E-08	7.0E-08 P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
8189	18075		4.63	7.0E-08	7.0E-08 AI535743.1	EST_HUMAN	cong3.P11.A5 conorm Homo sapiens cDNA 3'
8926	18734	29027	5.6	7.0E-08	7.0E-08 U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
9770	13444		4.54	7.0E-08	7.0E-08 P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
9770	13444	23241	4.54	7.0E-08	7.0E-08 P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
9834	19334		1.89	7.0E-08	7.0E-08 AJ131016.1	LN	Homo saplens SCL gene locus
800	10729	20569	2.84		6.0E-08 AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
800	10729	20570	2.84	6.0E-08	6.0E-08 AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2312	12193	22092	1.73	6.0E-08	6.0E-08 BE144398.1	EST_HUMAN	MR0-HT0166-191199-004-g09 HT0166 Homo saplens cDNA
4165	1		66.0	6.0E-08	6.0E-08 AL163248.2	N	Homo sapiens chromosome 21 segment HS21C048
							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE.
8717	18534	28818	2.26	6.0E-08	6.0E-08 P11369	SWISSPROT	ENDONUCLEASEJ
8819	18632		1.74		6.0E-08 AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
79	10063	19880	3.05		5.0E-08 AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
							nh03b09.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE.943193 similar to contains Alu repetitive
2189	12076	21981	1.97	5.0E-08	5.0E-08 AA493851.1	EST_HUMAN	element;
5178	15042	24809	1.12		5.0E-08 Q06278	SWISSPROT	ALDEHYDE OXIDASE
9057	18839		4.38		5.0E-08 P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
9245	18958	25317	1.94		5.0E-08 AW851878.1	EST HUMAN	QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA
1724	11625	21493	1.1	4.0E-08	4.0E-08 P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1724	11625	21494	1.1	4.0E-08	4.0E-08 P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
7278	17155	27350	1.41	4.0E-08	4.0E-08 L42571.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
							an 22d 10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE: 1699411 3' similar to contains Alu
7938	17788	28030	4.17		4.0E-08 AI050027.1	EST HUMAN	repetitive element;contains element MER22 repetitive element ;
8274	18154		1.79		4.0E-08 AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
8439	18313		3.66		4.0E-08 BF692493.1	EST HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
8439	18313	28571	3.66		4.0E-08 BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
							zd65g03.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains
9061	19680		1.54		4.0E-08 W 76159.1	ESI_HUMAN	L.1.11 L.1 repentive element
9703	19252		1.46		4.0E-08 Al343353.1	EST_HUMAN	tb96a11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;

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Table 4
Single Exon Probes Expressed in Heart

Top Hit Database Source		EST_HUMAN PM2-HT0130-150999-001-f12 HT0130 Homo sapiens cDNA	TCBAP105232 Pediatric pre-B cell acute (ymphoblastic leukemia Baylor-HGSC project=TCBA Homo	T	UDAIL 10.5232 Pediatric pre-trice in acute lymphoblastic leukemia baylor-Higs/C project= UBA Homo EST_HUMAN sapiens cDNA clone TCBAP5232		NT Homo sapiens hyperion gene, exons 1-50	EST_HUMAN ol35a05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'	NT Homo sapiens major histocompatibility locus class III region	NT Human lambda-immunoglobulin constant region complex (germlino)	NT Human lambda-immunoglobulin constant region complex (germline)	EST_HUMAN MR4-S10240-240700-013-g04 S10240 Homo sapiens cDNA	NT Hamo sapiens chromosome 21 segment HS21C079	Г	EST_HUMAN RC5-BN1058-270400-031-C06 BN1058 Homo sapiens cDNA			EST_HUMAN CM0-NN1004-100300-273-e06 NN1004 Homo sapiens cDNA	EST_HUMAN op74d08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'	NT Homo sapiens DNA for 3-ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2,	NT Homo sapiens gene for enteric smooth muscle gamma-actin, exon 2, 3	NT Human Iysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region	EST_HUMAN 601111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'	HUMAN	n117a11.s1 NCI_CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1.t2 L1 EST_HUMAN repetitive element;	EST HUMAN PM1-HT0527-160200-001-h05 H T0527 Homo sapiens cDNA	EST_HUMAN xn85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311.3'	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA	Г
	OL POLYPROTEIN (CONTAINS: REVERS	M2-HT0130-150999-001-f12 HT0130 Homo	CBAP1D5232 Pediatric pre-B cell acute lympaniens cDNA clone TCBAP5232	CPANDADE CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CONTROLLER CO	CBAP 1D5252 Fediatric pre-E cell actre lympapiers cDNA clone TCBAP5232	lomo sapiens chromosome 21 segment HS2	forno sapiens hyperion gene, exons 1-50	135a05.s1 Soares_testis_NHT Homo sapiens	fomo sapiens major histocompatibility locus c	luman lambda-immunoglobulin constant regic	luman lambda-immunoglobulin constant regic	4R4-ST0240-240700-013-g04 ST0240 Homo	lomo sapiens chromosome 21 segment HS2	fomo sapiens chromosome 21 segment HS2	C5-BN1058-270400-031-C06 BN1058 Hom	d42e07.x1 Soares fetal heart NbHH19W H	ontains MSR1.t1 MSR1 repetitive element;	3M0-NN1004-100300-273-e06 NN1004 Hom	p74d08.s1 Soares_NFL_T_GBC_S1 Homo	domo sapiens DNA for 3-ketoacyl-CoA thiolas	lomo sapiens gene for enteric smooth muscle	luman lysosomal membrane glycoprotein-2 (L	01111173F1 NIH_MGC_16 Hcmo sapiens c	XFZp434C0514_r1 434 (synonym: htes3) H	I17a11.s1 NCI_CGAP_HSC1 Homo sapiens epetitive element;	M1-HT0527-160200-001-h05 HT0527 Homo	n85h08.x1 Soares_NFL_T_GBC_S1 Homo e	domo sapiens fibroblast growth factor recepto	Homo sapiens testis-specific kinase substrate (TSKS) gene, of
				T								HUMAN							П				HUMAN	HUMAN		T			
Top Hit Acession No.		1.0E-08 BE141959.1	1 OF 08 DE246844 4		1.0E-08 BE246844.1			1.0E-08 AID15304.1	1.0E-08 AF044083.1			1.0E-08 BF375398.1	9.2	9.2	8.0E-09 BE012076.1			_	8.0E-09 AA938892.1	-			7.0E-09 BE254850.1				84.1	4503710 NT	6.0E-09 AF200923.2
Most Similar (Top) Hit BLAST E Value	1.0E-08 F	1.0E-08 E	4 0 10 10	20.1	1.0E-08	1.0E-08 /	1.0E-08 AJ01077	1.0E-08	1.0E-08	1.0E-08 X51755.1	1.0E-08 X51755.	1.0E-08	9.0E-09 AL16327	9.0E-09 AL16327	8.0E-09		8.0E-09/	8.0E-09 AW9001	8.0E-09/	7.0E-09 D86842.	7.0E-09 D00649.	7.0E-09 L09709.1	7.0E-09	6.0E-09	6.0E-09	6.0E-09	6.0E-09 AW1957	6.0E-09	6.0E-09
Expression Signal	1.13	2.92	1 24	17:	1.24	1.43	4.05	1.84	3.66	2.01	6.3	1.76	2.98	2.98	1.07		6.12	2.71	3.06	1.68	66.0	3.27	1.84	1.06	1.06	4.44	8.19	2.26	4.06
ORF SEQ ID NO:	21257		22004		22882				28773					23824				26743			24236				23625	ļ	25030	27370	
Exon SEQ (D NO:	12696	11897	42000	-	13080			16852	18498	19074	19316	19518	14049	14049	13361	l .		16546	17073	13469	14450	17203	17700	11996	13849	14786	1 1	17170	17746
Probe SEQ ID NO:	1493	2005	945	50.00	3155	5191	5438	6975	8633	9434	9804	9894	4149	4149	3444		6307	9999	7196	3555	4558	7335	7850	2107	3941	4906	5305	7294	7896

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SEQ ID SEQ ID		Expression	(Top) Hit	Top Hit Acession	Top Hit Database	Ton H + Descriptor
	Ö Q	Signal	BLAST E Value	o Z	Source	TOP IT Descriptor
5858 15764		1.92	5.0E-09	5.0E-09 AA359454.1	EST HUMAN	EST68746 Fetal lung II Homo sapiens cDNA 5' end
7811 17661	31 27901	2.69		5.0E-09 AW799567.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
510 10452	52	1.68	4.0E-09	4.0E-09 AL163282.2	N	Homo sapiens chromosome 21 segment HS21C082
949 10873		2.31	4.0E-09	4.0E-09 AL163285.2	L	Homo sapiens chromosome 21 segment HS21C085
	38 21222	96.0	4.0E-09	9558718 NT	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2379 12259		98'9	4.0E-09	4.0E-09 AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein 90 kDa
0303	00000	Co	000	7 00000010	1	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
		3.82	3,011-09	3.0E-09 BE222239.1	ESI HUMAN	MER/18 repetitive element;
2506 12380	00 22270	1.25	3.0E-09	3.0E-09 BE222239.1	EST HUMAN	inoseces. I I NOT_COAPT_LU24 From 8 sapiens CDNA clone IMAGE:3166120 3' similar to contains MER18 t3 MER18 repetitive element :
2614 12482	12 22371	1.1	3.0E-09 P23249	P23249	SWISSPROT	PROTEIN MOV-10
						hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18 13
[3.0E-09	3.0E-09 BE222239.1	EST_HUMAN	MER18 repetitive element;
_		3.22	3.0E-09	3.0E-09 AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4AI (EIF4A1) gene, partial cds
		1.54	3.0E-09	3.0E-09 Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C210RF5 (KIAA0933)
_1		1.73	3.0E-09	3.0E-09 AL163247.2	N	Homo sapiens chromosome 21 segment HS21C047
	1 28510	3.8	3.0E-09	3.0E-09 BF109943.1	EST_HUMAN	7172c08.x1 Sogres_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA cione IMAGE:3527030 3
		3.8	3.0E-09	3.0E-09 BF109943.1	EST_HUMAN	7/72c08.xf Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
		0.93	2.0E-09	2.0E-09 X16674.1	NT	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
\perp	4 20995	5.23	2.0E-09	2.0E-09 AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
- 1		10.52	2.0E-09	2.0E-09 AL118573.1	EST_HUMAN	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710.5
ſ		2.25	2.0E-09	2.0E-09 Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C210RF5 (KIAA0933)
3858 13769	9 23561	3.65	2.0E-09 O60241	060241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
						zx63h06.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains
		8.9	2.0E-09	2.0E-09 AA461430.1	EST_HUMAN	Alu repetitive element
		1.37	2.0E-09	2.0E-09 AJ271735.1	۲	Homo sapiens Xq pseudoautosomal region; segment 1/2
	7 28726	2.11	2.0E-09	2.0E-09 AL163248.2	L	Homo sapiens chromosome 21 segment HS21C048
9576 10724	4	11.53	2.0E-09	2.0E-09 X16674.1	LN	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyftransferase
						nc11c02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Altrenatitive
- 1		1.62	2.0E-09	AA226070.1	T HUMAN	element;
		2.48	1.0E-09	5031624 NT		Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
- (9 20851	2.48	1.0E-09	5031624 NT		Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1616 11520	0	0.95	1.0E-09	1.0E-09 AJ229041.1	IN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22. seament 1/3

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Table 4
Single Exon Probes Expressed in Heart

						יייי ייייייי טוני	Onigo canti topos capitosos in todas
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2453	12330		0.94		1.0E-09 AI356086.1	EST_HUMAN	qy64e11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2016812.3' similar to contains MER12.t2 MER12 repetitive element;
2860	12788	22580	1,51	1.0E-09	1.0E-09 U80017.1	L	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2895		22614			1.0E-09 M28699.1	LN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2895	ł	22615			1.0E-09 M28699.1	N	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2949	12876	<u> </u>	1.23		1.0E-09 P11799	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MI.CK) [CONTAINS: TELOKIN]
3002	12930	22722			1.0E-09 BE535440.1	EST_HUMAN	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4692	14578		4.26		1.0E-09 AA719297.1	EST_HUMAN	zh35b03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element;contains element MER22 repetitive element;
5560		25549	1.37	1.0E-09	U07000.1	LN	Human breakpoint cluster region (BCR) gene, complete cds
5736	15644	25749	3.21	1.0E-09	1.0E-09 P26694	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
7911	17761		3.1	1.0E-09	1.0E-09 AL163283.2	LN	Homo sapiens chromosome 21 segment HS21C083
9478	19689	24996	2.14	1.0E-09	11418127 NT	N	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
1287	11195	21048	1.8		9.0E-10 AW867740.1	EST HUMAN	MR0-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2803	12733	22532	6.03		9.0E-10 AI870071.1	EST_HUMAN	we78h03.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE.2347253 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element PTR5 repetitive element ;
6087	16032	26172	4.63		9.0E-10 Al452982.1	EST_HUMAN	lj46b09.x1 Soarec_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to TR:000372 000372 PUTATIVE P150.;
141	10115	19935	9.43		8.0E-10 U63630.2	N	Homo saplens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3300	13222	23022			8.0E-10 BE080748.1	EST HUMAN	QV1-BT0631-150200-071-f01 BT0631 Homo sapiens cDNA
4106	14006	23782			8.0E-10 AA376832.1	EST_HUMAN	EST89564 Small intestine I Homo capiens cDNA 5' end
7725			2:32		8.0E-10 U36308.2	LN⊤	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
9005					AL16328	NT	Homo sapiens chromosome 21 segment HS21C080
989	10619	20444	12.45		7706225 NT	LN⊤	Homo sapiens TPA inducible protein (LOC51586), mRNA
686	10619		12.45		7706225 NT	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1605	11510				7.0E-10 Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
1974	11867		1.01		7.0E-10 P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2512	12386		16.88		7.0E-10 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3049		22768	2.65		7.0E-10 X00856.1	NT	H.sapiens DHFR gene, exon 3
5754					7.0E-10 AA345220.1	EST_HUMAN	EST51247 Gall bladder II Homo sapiens cDNA 5' end
6514	16373		1.39		P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon . SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Dafabase Source	Top Hit Descriptor
895	10821		2.81	6.0E-10	6.0E-10 AJ400877.1	LN	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2644	12511	22402	1.47	6.0E-10	6.0E-10 AI424405.1	EST_HUMAN	tf02d07x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:209502; 3:
4634			2.51	6.0E-10	6.0E-10 AW853719.1	EST_HUMAN	RC3-CT0254-031099-012-912 CT0254 Homo sapiens cDNA
9092			1.79		6.0E-10 AW971923.1	EST_HUMAN	EST384012 MAGE resequences, MAGL Homo sapiens cDNA
9947			3.54		6.0E-10 BE699410.1	EST_HUMAN	RC3-NN0070-110800-014-h07 NN0070 Homo sapiens cDNA
744			4.5		5.0E-10 AL046804.1	EST_HUMAN	DKFZp434N219_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N219 5
3430		23152	1.48		5.0E-10 Q01033	SWISSPROT	
6334	16197		1.82		5.0E-10 BF105159.1	EST_HUMAN	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
7496	17366	27570	1.79		5.0E-10 P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688,8 IN CHROMOSOME III
7496	17366		1.79		P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
, ,							qg09f09.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1759049 3
901	/SOOL		SS.O		4.0E-10 AI221083.1	EST HUMAN	similar to contains LTR8 b2 LTR8 repetitive element;
1951	11846	24732	7		4 OF 40 AWE04700 4	100 100 100 100 100 100 100 100 100 100	hg58g03.x1 NCI_CGAP_GC5 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu
	1				AW 334103.1	NAMPIN TO ST	repende eighen,
2527	12401	22292	60.9		4.0E-10 AL163303.2	N	Homo sapiens chromosome 21 segment HS21C103
6229	16125	26278	19.23		4.0E-10 AF224669.1	FZ	Homo sapiens mannosidase, beta A. Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
							Home earling X linked arbidecific actedormal duralisas avadas avadas (FDA)
8436	18310		7.7	4.0E-10	4.0E-10 AF003528.1	ΝŢ	regions represe vermined anniquement extraction by spiels protein gene (EUA), exon 2 and flanking repeat regions
700	70000					1	yy32f06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains
199		20000				EST HOMAN	L.i.i L.i repetitive element
6761			0.03	3.0E-10		Z	Homo sapiens extracellular giycoprolein lacritin precursor, gene, complete cds
4430	\perp			3.0⊱-10		Ł	Homo sapiens chromosome 21 segment HS21C003
4435	_[.				03.2	LN	Homo sapiens chromosome 21 segment HS21C003
9765	_1				P20350		RHOMBOID PROTEIN (VEINLET PROTEIN)
5833				3.0E-10	3.0E-10 BE302970.1		ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
6562	_ [26599		3.0E-10	3.0E-10 AV743302.1		AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
6562	16420	26600	1.31	3.0E-10	3.0E-10 AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
		_					ys74b12.s1 Soares retina N2b4HR Homo sepiens cDNA clone IMAGE:220511 3' similar to contains MER29
7067				3.0E-10	3.0E-10 H87208.1	EST HUMAN	repetitive element;
7233		27302		3.0E-10	-	EST_HUMAN	II.3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
7233				3.0E-10	31.1	EST HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
7979	17829		2.56	3.0E-10	3.0E-10 T65891.1	EST_HUMAN	yc11e12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMACE:80398 5'

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Table 4

Single Exon Probes Expressed

								l leg			1		1		T o		$\overline{}$					$\neg \top$		\Box	_
Single Exon Probes Expressed in Heart	Top Hit Descriptor	THE STAND COME CONTRACTOR	III 2 I TOSA 11 NO. LUGAR GCB1 Home sapiens cDNA clone IMAGE:1289908 3'	MA IOD CENTED MEDICAL SECTION AND SapienS CDNA	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)	Her social tensoribition factor 2 p44 (bt/2p44) gene, partial cds, neuronal apoptosis inhibitory	Protein (naty) and survival motor neuron protein (smn) genes, complete cds (HPRG)	Homo sepiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds, cytochrome P450 polypeptide re(CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds, and cytochrome P450	Polypepude 3 (CTP3A3) gene, partial cds	WEN CANOGE 20020 ACC. / Homo sapiens cDNA clone IMAGE:3940824 5	AVR52123 C. Dumo control SN0038 Homo sapiens cDNA	OVA CT0325 184400 SEP CON CIONE GLOCXA11 3'	OV2.TT0003.464400.042.40.TT0025.1	DKF20434N1317 1 434 (2000) 110003 Homo sapiens cDNA	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete eds	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), advancion local, exercised and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and contained and	Homo saplens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RP1 18a).	CDM protein (CDM) adrange (Annual CDM) adrange (Annual CDM), creatine transporter (CRTR),	Homo sapiens PCCX1 mBNA for material	Human pregnancy-specific olyconologia hate 1 (SPA) Paris	H septiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes	777340R 74 Chrahaman 11.1.1.	ov85h03 x1 Scares fetal live, calcon Avier 6	H.sapiens DMA, DMB, H.A-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14	286b10.r1 Soares testis NHT Homo saniens c/DNA close (AAAOE, Zoosa, E.
gle Exon Pro	Top Hit Database Source	EST HIMAN	TOT LINKS	SWISSPENT	SWISSPROT	LN FN	SWISSPROT	5	TOT LI MANN	EST HIMAN	EST HUMAN	FST HIMAN		EST HUMAN	N IN	\ \ \		N	LN	L	ŢN	NAMI H. T.S.	EST HUMAN		T HUMAN
Sin	Top Hit Acession No.	3.0E-10 AA769294 1	3.0F-10 BF179517 1	P48988	2.0E-10 P48988	U80017 1	2.0E-10 Q28640						T		1.0E-10 AF213884.1	1.0E-10 U52111.2		1.0E-10 U52111.2	1.1	1.0E-10 M30629.1		1.0E-10 AA081868.1			5.1
	Most Similar (Top) Hit BLAST E Value	3.0E-10	3.0F-10	2.0E-10	2.0E-10	2.0E-10	2.0E-10	2.0E-10	2.0E-10	1.0E-10	1.0E-10	1.0E-10	1.0E-10	1.0E-10	1.0E-10	1.0E-10		1.0E-10	1.0E-10	1.0E-10	1.0E-10 X87344.1	1.0E-10	1.0E-10 AI038280	1.0E-10 X87344.1	1.0E-10 A
	Expression Signal	1.54	2.03	1.43	1.43	5.91	2.41	1.71	5.79	3.56	3.14	2.4	0.89	0.91	5.44	4.51		4.51	2.25	2.06	0.93	4.59	3.4	1.43	1.3
	ORF SEQ ID NO:		25227	19814	19815			25801	26389		21353		23178			23716		23717	23724				28408		
	Exon SEQ ID NO:	17876	19271	10019	10019	11751	15463	15693	16230	11397	11493	12411	13372	13411	13842	13939		13939	13945	13981	15012	17709	18165	15012	18859
	Probe SEQ ID NO:	8026	9737	32	32	1855	5547	5787	6367	1492	1589	2537	3456	3770	3933	4036		4036	4042	40/9	5145	7859	8286		9084

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Table 4
Single Exon Probes Expressed in Heart

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ressed in Heart	Top Hit Descriptor	Homo sapiens SH3-domain binding protein 1 (SH3RP1) mRNA	Mus musculus expressed in non-metastatic cells 2 protein (NN/232) (Nm.2) mpN /	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5; and	qf36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.t3 MER10 repetitive element:	yg43e12.r1 Soares infant brain 1NIB Homo saciens CONA clone IMAGE 25144 F.	1943e12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35144 5	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3 beta (COR3 beta) genes, complete cds	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor like protein COR3 beta (COR3 beta) genes, complete cds	qc51c10.x1 Soares, pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR at DHA (unimana)	tive element;	Human endogenous retrovirus HERV-P-T47D	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)	tm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'	Homo sablens FRA3R common frantle radion diadenacina trickonatada ta	Homo sapiens chromosome 21 segment HS210n77	QV2-BT0258-261099-014-801 BT0258 Homo saniens CDNA	EST178226 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to alpha-2-macroglobulin	nc83h05.r1 NCL_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR16_YEAST P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16.	Jians chromosoma O dunlication of the T and	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR) IKE BROTTEN OF 23	2k27g02.s1 Soares pregnant uterus NhHPII Homo sanlens CONA clara 14ACE 1323 21	2K27g02.s1 Soares pregnant uterus NhHPII Homo sanians conta chara 144 CE 47 1794 3	277e03.s1 Soures fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone IMA CE - 4 ano 24 3	RCO-CN0027-210100-011-c01 CN0027 Homo saciens cDNA	
d in Heart	. Top Hit Descriptor	SH3-domain binding protein 1 (SH3RP1) mRNA	expressed in non-metastatic cells 2 protein (NM23B) (Nm23)	er, hepatocellular carcinoma Homo sapiens cDNA 5' end	res_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 re element:	res infant brain 1NIB Homo saciens CONA clone IMA GE 351	res infant brain 1NIB Homo sapiens cDNA clone IMAGE 351	o-globin, beta-H globin, beta-A globin, epsilon-globin, and olfan R3 beta) genes, complete cds	o-globin, beta-H globin, beta-A globin, epsilon-globin, and olfar N3'beta) genes, complete cds	ires_pregnant_uterus_NbHPU Homo sapiens cDNA clone IM. OXISOME PROLIFERATOR ACTIVATED RECEPTOR ALE	ment;	nous retrovirus HERV-P-T47D	RELATED GAG POLYPROTEIN (VERSION 1)	CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936	RA38 common fracile region diadenceine trinkenskus ta	hromosome 21 segment HS21Cn27	31099-014-801 BT0258 Homo saniens cDNA	on carcinoma (HCC) cell line Homo sapiens cDNA 5' end simi	CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5's RNA SPLICING FACTOR RNA HELICASE PRP16.	promosome O di infination of the T and	ECEPTOR 511 (OI FACTORY RECEPTOR 1 KE DECITED.	res pregnant uterus NhHPI/ Homo saplens CDNA clone IV	res pregnant uterus NbHPII Homo sapiens cDNA clone IMA	es fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone	10100-011-c01 CN0027 Homo saplens CDNA	CM2_TN0140 070000 272 201 TN0440 11
Siligle Exon Probes Expressed in Hear	Top Hit Database Source	Homo sapiens S	Mus musculus e	HUMAN EST180120 Live	qf36c04.x1 Soar	Т	Г	Gallus gallus rho COR3'beta (COR	Gallus gallus rho	qc51c10.x1 Soar gb:L02932 PER(Human endogen			Homo saplens FF	Homo sapiens ch	HUMAN QV2-BT0258-26			Homo sabiens ch		T	Τ		Г	Т
XII alibilic	Top Hit Acossion Date	11545732 NT	TN 7706799	3.0E-11 AA309248.1 EST_H			2.0E-11 R24807.1 EST_HUMAN	L17432.1 NT	-17432.1 NT		2.0E-11 A1126371.1 EST_HUMAN	2.0E-11 AF087913.1 NT	910263 SWISSPROT	2.0E-11 AI478617.1 EST_HUMAN	2.0E-11 AF020503.1 NT		EST	2.0E-11 AA307331.1 EST HUMAN	2.0E-11 AA581028.1 EST_HUMAN	2.0E-11 AF029308.1 NT		2.0E-11 AA035369.1 EST HUMAN	2.0E-11 AA035369.1 EST HUMAN		2.0E-11 AW842143.1 EST_HUMAN	2 OF 44 DEPOTOR 4
	Most Similar (Top) Hit BLAST E Value	4.0E-11			2.0E-11	2.0E-11	2.0E-11	2.0E-11 L17432.1	2.0E-11 L17432.1		2.0E-11 /	2.0E-11	2.0E-11	2.0E-11/	2.0E-11	2.0E-11	2.0E-11	2.0E-11	2.0E-11 A	2.0E-11	2.0E-11 Q13606	2.0E-11	2.0E-11	2.0E-11	2.0E-11 A	0 00 44 10
	Expression Signal	1.93	2.15	1.45	1.58	3.64	3.64	3.91	3.91		1.04	1.11	4.23	0.87	0.95	76.0	5.46	1.32	1.83	1.43	4.61	2.07	2.07	1.29	2.25	1 08
	ORF SEQ ID NO:	25252				20926	20927	21359	21360	_				23005				24604	25828		27989	28591	28292			25356
	Exan SEQ ID NO:	19190	11381	14079			11080	11500	11500					13205	13368	14395	14732	14836	15715	17194	17750	18330	18330	19679	18927	18943
	Probe SEQ ID NO:	9611	1476	4179	944	1168	1168	1596	1596		1600	2737	3160	3284	3452	4501	4851	4961	5810	7318	7900	8457	8457	9160	9192	9216

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1		\neg		_	_	_	_	Т	_	Τ-	_		_	_	-	_	_	_	_			_			_	_			_	_	_	-,	_		
	Top Hit Descriptor	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA	Homo saplens SCL gene locus	Homo sapiens chromosome 21 segment HS21C079	Homo sapiens PRO3078 mRNA, complete cds	Homo saplens homogentisate 1,2-dioxygenase gene, complete cds	CM0-BN0105-170300-292-412 BN0105 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C047	Homo sapiens PHD finger protein 2 (PHF2) mRNA	y/73d08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28166 5	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA	602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA	PREGNANCY ZONE PROTEIN PRECURSOR	Homo sapiens chromosome 21 segment HS21C100	Homo sapiens chromosomo 21 segment HS21C100	Homo saplens Xq pseudoautosomal region; segment 2/2	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)	223g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4511523'	AV730554 HTF Homo sapiens cDNA done HTFAW F06 5'	nz88f11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu	repetitive element;	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds	od10g11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29.12	WENZE (epolitive element)	ES 104462 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDV33	1242b05.y1 NCI_CGAP_Brn52 Homo saplens cDNA clone IMAGE:2291217 5	Homo sapiens Xq pseudoautosomal region; segment 2/2	nw24b11.s1 NCI_CGAP_GCB0 Horno sapiens cDNA clone IMAGE:1241373 3'	Homo sapiens chromosome 21 segment HS21C078	Homo sapiens chromosome 21 segment HS21C078	EST386850 MAGE resequences, MAGN Hamo sapiens cDNA	Homo sapiens Xq pseudoautosomal region; segment 1/2
פון בייסיון	Top Hit Database Source	SWISSPROT	LN	NT	LN	N	NT	EST_HUMAN	N	LN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	NT	N	NT	SWISSPROT	EST_HUMAN	EST HUMAN		EST HUMAN	LN	HOL	TO L LOWAIN	- 11	EST_HUMAN	LN	EST HUMAN	LN	NT	EST HUMAN	NT
	Top Hit Acession No.	P08547	11417966 NT	1.0E-11 AJ131016.1	1.0E-11 AL163279.2	1.0E-11 AF119914.1	1	1.0E-11 BE004315.1	1.0E-11 AL163247.2	4885546 NT	1.0E-11 R13174.1	1.0E-11 BF365119.1	1.0E-11 BF365119.1	8.1	1.0E-11 Z20377.1	P20742	9.0E-12 AL163300.2	9.0E-12 AL163300.2	36.1	Q05904	7.0E-12 AA704735.1	AV730554.1			6.0E-12 AF003249.1		0.0E-12 AA847890.1			1	1	5	5	1.	5.0E-12 AJ271735.1
	Most Similar (Top) Hit BLAST E Value	2.0E-11	20E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	1.0E-11	9.0E-12 P20742	9.0E-12	9.0E-12	8.0E-12	7.0E-12 Q05904	7.0E-12	6.0E-12	1	5.0E-12	6.0E-12	n .	0.0E-12	3.0E-12	5.0E-12	5.0E-12	5.0E-12	5.0E-12	5.0E-12	5.0E-12	5.0E-12
	Expression Signal	2.38	2.38	1.24	2.58	1.94	3.12	1.32	14.34	3.25	5.41	1.32	1.32	1.9	1.29	0.82	1.22	1.22	3.57	2.75	11.23	0.92	i C	(S.)	1.19	90 7	200	7.88	1.18	5.93	0.84	4.75	4.75	9.12	2.15
	ORF SEQ ID NO:			20412	20954		21862		24966			27300	27301	28747		22649	27712	27713		24241	28828			62862	27.203		20200	707.30	23070	23367		25676	25677	25940	27339
	Exon SEQ ID NO:	19201	19401	10594	11109	11388	11969	13370	15191	16652	16866	17109	17109	18474	19483	12849	17491	17491	18974	14454	18545	13417	4	16141	2/2/2	17262	4004	100	13264	13580	15037	15578	15578	15815	17145
	Probe SEQ ID NO:	9627	9930	099	1199	1483	2079	3454	5269	6773	6869	7232	7232	8607	9702	2922	7641	7641	9270	4562	8656	3200	7	7074	107/	7453	1027	1021	3344	3666	5171	2995	2995	2909	7268

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Source Top Hit Acession Top Hit Acession Database Source Source	5.0E-12 AL183303.2 NT Hono sapiens chromosome 21 segment HS21C103	4.0E-12 AA700326.1 EST_HUMAN 47/4g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676.3	4.0E-12 AA700326.1 EST_HUMAN 7/74914.51 Socres_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMACE:460676.3	4.0E-12 Al689984.1 EST_HUMAN MARINER TRANSPOSASE	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genet, complete cds; and S171 gene, 4.0E-12 AF109907.1 NT partial cds	4.0E-12 AJ229043.1 NT Homo saplens 959 kb contig between AMI.1 and CBR1 on chromosome 21q22, segment 3/3	Ł	3.0E-12 AW341683.1 EST_HUMAN 014517 SMRP.	3.0E-12 AW341683.1 EST HUMAN 014517 SMRP.	3.0E-12 U37672.1 NT Human prostate specific antigen gene, 5 flanking region	3.0E-12 U37672.1 NT Human prostate specific antigen gene, 5' flanking region	3754495 NT	2.0E-12 J01884.1 NT Rat U3A small nuclear RNA	NT	19.1 EST_HUMAN		2.0E-12 070306 SWISSPROT TBX15 PROTEIN (T-BOX PROTEIN 15)	77.1 EST_HUMAN	2.0E-12 T08169.1 EST_HUMAN EST06060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA73 5' end	2.0E-12 11422229 NT Homo sapiens Ac-like transposable element (ALTE); mRNA	2.0E-12 AF196864.1 NT Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds	1 EST_HUMAN	2.0E-12 AL 163283.2 NT Homo sapiens chromosome 21 segment HS21 C083	2.0E-12 11418248 NT Homo sapiens sulfotransferaso-related protein (SULTX3), mRNA	hh90a09.x1 NCI_CGAP_GU1 Homo saplens cDNA clone IMAGE:2970040 3' similar to contains MER18.t1	ES TOWAIN	1.0E-12/AI871726.1 EST_HUMAN repetitive element;	_
Most Similar (Top) Hit BLAST E Value	5.0E-12 A	4.0E-12 A	4.0E-12 A	4.0E-12	4.0E-12 A	4.0E-12 A	4.0E-12 U	3.0E-12 A	3.0E-12 A	3.0E-12 U	3.0E-12 U	20E-12	2.0E-12 J	2.0E-12 JG	2.0E-12 B	20E-120	2.0E-12.0	2.0E-12 A	2.0E-12 T	2.0E-12	2.0E-12 A	2.0E-12B	2.0E-12 A	2.0E-12	2 2 4	1.VE-14.0	1.0E-12 A	1.0E-12 A
Expression Signal	4.67	3.42	3.55	0.85	2.89	3.51	1.9	3.81	3.81	3.08	3.08	1.03	1.04	1.04	1.8	0.78	0.78	2.22	3.34	2.07	1.68	8.13	1.71	1.52	1 03	70.	2.03	1.16
ORF SEQ ID NO:		20027	20027	24198		28561		20345	20346	28187	28188	23143	23704				24474			26552					7,007	1		22752
Exen SEQ ID NO:	17745	10211	10211	14413	16676	18305	19131	10536	10536	17938	17938	13338			14221	14688		15804		_1	17345		18916	19041	10005	1_		12960
Probe SEQ ID NO:	2882	244	245	4520	6797	8431	9520	909	200	8047	8047	3421	4025	4025	4324	4804	4804	5898	6258	6516	7367	7737	9175	9377	17		1944	3032

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Single Exon Prohes Expressed in User

Single Exon Probes Expressed in Heart	Top Hit Descriptor		nomo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds	AU132248 N I 2RP3 Homo sapiens cDNA clone NT2RP3004070 5	AU 132248 N 12RP3 Homo sapiens cDNA clone NT2RP3004070 5	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds	Hama society I'm FEI PROTEIN KIAA0961	quedators septents putative BPES syndrome breakpoint region protein gene, complete cds qh66a04.x1 Soares_feta_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614.3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN):contains MFR10.41 MED10.	qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Home sapiens cDNA clone IMAGE:1849614.3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMO OC # 100000000000000000000000000000000000	repetitive element;	ac26d05.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMA GE 857577 31	EST374237 MAGE resequences, MAGG Homo sapiens CDNA	PROBABLE TONB-DEPENDENT RECEPTOR HIG712 PRECURSOR	M.setulosus mitochondrial 12S rRNA gene	Homo sapiens Xq pseudoautosomal region; segment 1/2	Infomo saplens CST gene for cerebroside sulfotransferase, expn 1, 2, 3, 4, 5	22/2006.\$1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE 2936513	Home septients prior protein (PrP) gene, complete cds	Homo sapiens priori protein (PrP) gene, complete cds. Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhihitory.	Homo sapiens Button's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosemal proteins.	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S6A3N2T, TCRBV13S6A2T, TCRBV5S6A3N1T, TCRBV5S6A3T, TCRBV5S6A3T, TCRBV5S6A3T, TCRBV5SA3N1T, TCRBV5SA3N1T, TCRBV5SA3N1T, TCRBV5SA3N1T, TCRBV5SA	TCRRV29C142T TOBE 12-P. I CRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1	601463285F1 NIH MGC 67 Homo conjust - DNA	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP-GALACTOSAMINYLTRANSFERASE) (UDP-GALACTOSAMINYLTRANSFERASE)	ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1) Hono septens chromosome 21 comments (GALNAC-T1)	From on one of the FT segment RSZ1C007
gle Exon Pro	Top Hit Database Source	TI		EST LINKS	NAMOR I ST	N	DY ISSUED IN	EST HIMAN		EST HUMAN	EST HUMAN	HOMAN	SWISSPROT	2 2	1 N	1,	NA TOWAIN	LN	 	L		ΙN	HUMAN		ISSEROT	-
Sin	Most Similar (Top) Hit Acession BLAST E No.	1.0E-12 AF000991 1	1 0F-12 AI 1132248 4	1.0E-12 AU132248 1	1 0F-12 182820 4	1.0E-12 09Y2G7	1.0E-12 AF196864 1	1.0E-12 Al248533.1			1.0E-12/AA/82323.1	1		-				T		8.0E-13 U78027.1			7.0E-13 BE778223.1 E	7 0E.43 040473	7.2	
	Expression (Signal E	1.16	27.7	27.7	1.73	1.82	1.72	9.11	7	1 34	3.36	2.2	2.72	1.13	1.16	2.37	5.05	5.05	1.36	2.13			10.33	1.33		
	ORF SEQ ID NO:	22753	23496	23497			26240	26256	26257	27119	29118				23570		20458	20459	21570			29079	+		21840	
	Exon SEQ ID NO:		13710	13710	15544	1 1	16090	16106	16106	16928	18860	19728	19426	13489	13776	17388	10633	10633	11694	17688	0	8/8	19149	19287	11944	
	Probe SEQ ID NO:	3032	3798	3798	5630	5682	6224	6240	6240	7051	9085	9605	9963	3575	3865	7537	200	8	1796	7838	000	080	OCCE	8926	2054	

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Single Exon Probes Expressed in Heart	Top Hit Database Source	EST_HUMAN V82f04.r1 Soares placenta Nb2HP Home saniens CONA class MASE Assess	ZI77a12.s1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:729350 3' similar to contains Alu		Т	7	T HUMAN		19933905.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32995 EST HUMAN A32995 t complex sterility modeling models.	qn32d05x1 NCL CGAP Kid5 Homo sapiens CDNA clone IMAGE:1899345 3' similar to contains Air	1	Т	Caro	III INVANI	Т		T HI INAANI	T		\dashv	Т	LIOMAN					EST_HUMAN hab76f05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Hrmo sarians_CDMA_1
Sing	Top Hit Acession No.	5.0E-13 R78338.1 E	73.1	-	514.1					4.0E-13 A 289831 1		T	, a	-	61			\int			3 0F-13 REDESEND 4		L103246.2 N1	52111.2 NT			
	Most Similar (Top) Hit BLAST E Value	5.0E-13	5.0E-13 AA4357	5.0E-13 P07313	4.0E-13	4.0E-13	4.0E-13	4.0E-13	4.0E-13 N44291	4.0E-13	4.0E-13	4.0E-13 AA4358	3.0E-13	3.0E-13 AA4303	3.0E-13	3.0E-13	3.0E-13 B	3.0E-13.A	L	3.0E-13.052111.2	3.0F-13.R	3 OF 13 A	2000	2.0E-13 U52111.2	2.0E-13 U23839.1	2 0F-13 AF230740 4	2.0E-13 BF431899.1
	Expression Signal	1.05	1.45	2.75	296	1.58	4.86	1.92	1.52	4.57	1.83	1.83	3.8	1.37	1.25	2.63	4.23	2.86	, C	4 03	3,66	26		2.77	1.31	4.71	1.08
	ORF SEQ ID NO:			28367			25404	26298		27831	28645	28646		_	22099		22387		26660	3	28531	28980		19938	20024	21005	22966
	Exon SEQ ID NO:	13201			1 1			16142	16400	17607	18379	18379	10144	10774	12200	12306	12497	13075	16481	17955	18279	18688	-	10118	10207	11156	13167
	Probe SEQ ID NO:	. 3280	3351	8234	1824	2411	5430	6278	6542	7757	8507	8507	173	847	2319	2429	2629	3150	6601	8064	8403	9376		144	82	1249	3244

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4019	13923		1.72		2.0E-13 AL163278.2	N.	Homo sapiens chromosome 21 segment HS21C078
5722	15670	. 25730	3.87	2 OF 13	2 DE-13 OUE852	TOGGSSIMS	OELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN
807.8	16064				0 0E 49 V46040 4	EN LONG	Il man DEKI nano for liter, tree & photospherical discount (FO D 74 41)
1 2 2	1000]	 		1718017	1	initial FTAL gette to the type of prosphorocovinase (EC.2.7.1.17) exon 2
9/6/	1/870	78067	3.97	2.0E-13	5031896 N	. 1	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
9251	18861			2.0E-13	2.0E-13 AW892155.1	EST HUMAN	CM0-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
288	10252	20072	1.37	1.0E-13	1.0E-13 S74129.1	LN	FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
870	10796		4.39		1.0E-13 AJ007973.1	NT	Homo sapiens LGMD2B gene
1314	11220	21077	1.27	1.0E-13	1 0E-13 X87344 1	FV	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 denes
T							WOOTING COAP GORN Homo seniene COMA Close IMACE 4244199 61 circular 11 11 11 12
1976	11869		2.16		1.0E-13 AA720574.1	EST HUMAN	THR repetitive element;
4488	14382	24169			1.0E-13 BF340987.1	EST_HUMAN	602038009F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185866 5
8684	18572	28855	13.83	1 OF 13	1 OF 13 BF108755 1	HAT HIMAN	745e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443.3' similar to
9076	18853			1.0E-13	1.0E-13 AV715377.1	EST HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIF03 5:
9714	19255		1.6		1.0E-13 AJ271735.1	LN	Homo sapiens. Xo oseudosi rhosoma I region: segment 1/2
330	10289	20105	8		9.0E-14 AA781159.1	EST HUMAN	aj24c01.s1 Scares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
-							aj24c01.s1 Scares_testis_NHT Homo sapiens cDNA clone 13912323' similar to contains MER19.t1 MER19
331	10290	20106			9.0E-14 AA781159.1	EST HUMAN	repetitive element;
2451	12328		4.04		9.0E-14 AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2725	12587		4.62		9.0E-14 AB038162.1	N-	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3073	13000	22790	3.74	9.0E-14	9.0E-14 AW513296.1	EST HUMAN	xo54h05.x1 NCI_CGAP_Utf Homo sapiens cDNA clone IMAGE:2707833 3'
							aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER 19.11 MER 19
3200	10289				9.0E-14 AA781159.1	EST_HUMAN	repetitive element ;
3728	13640			9.0E-14	9.0E-14 D14547.1	NT	Human DNA, SINE repetitive element
4650	14536				9.0E-14 AJ002153.1	LN	Saguinus œdipus gene for seminal vesicle secreted protein semenogelin i
3453	13369		1.57		8.0E-14 BE468263.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
3872	13783		2.77	8.0E-14	8.0E-14 R76269.1	EST_HUMAN	y72e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
7434	16447		69.09	8.0E-14	8.0E-14 X89211.1	. TN	H.sapiens DNA for endogenous retroviral like element
7515	17303	27510	3.49	8.0E-14	8.0E-14 AA219316.1		zq17c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629970 3'
8732	18588		4.39	8.0E-14	8.0E-14 BE062558.1	EST HUMAN	QV2-BT0258-261099-014-a01 BT0258 Homo sapiens cDNA

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Single Exon Probes Expressed in

			T	í	Т	\top	T		T			_	-										_	
Single Exon Probes Expressed in Heart	Top Hit Descriptor	xf67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element;	Homo sapiens FRA3B common framile region, direction direction that the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfer of the transfe	Homo sapiens hypothetical protein F1 120585 /F1 120585 / TDNA	Homo saplens hypothetical protein FLJ20585 (FLJ20585) mRNA	Homo sapiens FRA3B common fragile region, diadenosine trinkosnhato hvirologo (FLUIT)	Homo sapiens FRA3B common fracile region disdensation trickes.	CANALICULAR MULTISPECIFIC ORANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE—ASSOCIATED PROTEIN 2) (CANALICI AD MILITARION TRANSPORTER 1 (MULTIDRUG RESISTANCE—ASSOCIATED PROTEIN 2) (CANALICI AD MILITARION TRANSPORTER 1 (MULTIDRUG RESISTANCE—	xb03b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.t2 L1	INE-1 REVERSE TRANSCRIPT ACTIONS OF	SANTIGEN PROTEIN PRECIDENCE	Homo saciens I GMD/8 nene	2k67a06.r1 Soares pregnant uterus NhHPI Homo saviens cONA clear MACE 2020	W73c12.s1 Soares_multiple_sclerosis_2NbHMSP Homo sepiens cDNA clone IMAGE 279190 3' similar to	wm08c03.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE.2435332 3' similar to contains Alu	R.norvegicus mRNA for CPG2 protein	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Atu	Homo sapiens a dishlednin and metallonoteinase domain 30 (ADA Marx)	hx94f11.xf NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3195501 3' similar to contains MER4.b2	MER4 rependive element;	xp45f12x1 NCI_CGAP_HV11 Home spiens cDNA clone IMAGE:2743343 3' similar to contains Alu	Homo sabiens Xr oserudos trecimal regions against 1	Homo sapiens Xa pseudoautosomal region; segment 2/2	Homo sapiens chromosome 21 segment HS21C103
gle Exon Pro	Top Hit Database Source	EST_HUMAN	Z	LN	NT	IN	Ν	SWISSPROT	EST HUMAN	SWISSPROT	SWISSPROT	N	EST HUMAN	EST HUMAN	EST HIMAN	NT	EST HUMAN	.'1	LOT III III AND	7		Ţ		LN
Sinc	Top Hit Acession No.	7.0E-14 AW151673.1	6.0E-14 AF020503.1	8923548	8923548 NT	6.0E-14 AF020503.1	6.0E-14 AF020503.1		5.0E-14 AW073791.1			73.1	-				3.0E-14 AW265354.1	56864	3 0E-14 BE468373 4		354.1			П
	Most Similar (Top) Hit BLAST E Value	7.0E-14	6.0E-14	6.0E-14	6.0E-14	6.0E-14	6.0E-14	5.0E-14 Q63120	5.0E-14	5.0E-14 P08547	4.0E-14 P04928	4.0E-14	4.0E-14 /	4.0E-14 N46328.1	4.0E-14 AI886224	3.0E-14 X95466.1	3.0E-14	3.0E-14	3.05-14.8	3.0E-14 P02894	3.0E-14/A	2.0E-14 AJ271736.1	2.0E-14 A	2.0E-14 A
	Expression Signal	3.07	10.2	1.02	1.02	2.56	2.56	3.92	1.09	5.12	1.77	6.5	0.94	-	2.31	2.13	0.82	1.1	1.23	1.5	7.59	3.98	3.98	6.35
	ORF SEQ ID NO:		20140	24756	24757	27725	27726	20348	24628	25363		21608		23873		20705	24505	24507		24791	24505	20154	20155	20428
	Exon SEQ ID NO:	12699	10319	14982	14982	17502	17502	10538	14860	15316	12685	11732	13607	14094	19760	10859	14722	14725	14972	15024	14722	10331	10331	12673
	Probe SEQ ID NO:	1611	363	5114	5114	7652	7652	602	4985	5397	1107	1835	3693	4194	5777	934	4841	4844	5104	5157	8563	384	384	675

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Single Exon Probes Expressed in Heart

[\top		T	Т	Т	Т	\top	Т	Т	T	Т	Τ	Т	\top		Г	Т	Τ	Т	Т	_	\top	Т	_	T	Т	T	T			$\overline{}$	_	Τ-
	Top Hit Descriptor	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA	Homo saplens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA	Homo sapiens chromosome 21 segment HS21C009	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	Human beta globin region on chromosome 11	RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA	L2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA	UI-H-BI1-adw-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'	Human beta globin region on chromosome 11	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C068	Homo sapiens chromosome 21 segment HS21C068	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase	(SbPL) gene, complete cds s	Homo sapiens chromosome 21 segment HS21C103	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA	ae89c12.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:97(350.3'	xq38h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, ruclear mRNA encoding	mitochondrial protein, complete cds	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein	JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes.	complete cds; and L-type calcium channel a>	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]	601677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
2.6	Top Hit Database Source	EST HUMAN	N	LV.	SWISSPROT	LZ	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	FZ	NT	L	L _Z	Ŀ	Z	LN.	N	SWISSPROT	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	!	Z	L	L	LN			LN	SWISSPROT	EST HUMAN	EST_HUMAN
	Top Hit Acessian No.	2.0E-14 AW372868.1 EST	7657529	2.0E-14 AL163209.2	P08548	2.0E-14 U01317.1	2.0E-14 BE000550.1	2.0E-14 BE158761.1			2.0E-14 U01317.1		4L163268.2	1.0E-14 AL163268.2	7 07 77	44140.1	1.0E-14 AL163303.2	1.0E-14 AF001689.1	205227	1.0E-14 BF335227.1	1.0E-14 BF335227.1		1.0E-14 AW275852.1	1	1.0E-14 AF126145.1	11437150 NT	11437150 NT	7427522 NT			9.0E-15 AF196779.1	21416	9.0E-15 BE903559.1	8.0E-15 BE261482.1
	Most Similar (Top) Hit BLAST E Value	2.0E-14	2.0E-14	2.0E-14	2.0E-14 P08548	2.0E-14	2.0E-14	2.0E-14	2.0E-14	2.0E-14	2.0E-14	1.0E-14	1.0E-14	1.0E-14	7 7 7	1.0E-14 L44140.1	1.0E-14/	1.0E-14 /	1.0E-14 P05227	1.0E-14	1.0E-14	1.0E-14 /	1.0E-14 /	1	1.0E-14/	1.0E-14	1.0E-14	9.0E-15			9.0E-15/	9.0E-15 P21416	9.0E-15	8.0E-15
	Expression Signal	1.36	1.09	1.24	0.95	2.96	2.18	19.91	19.91	4.76	1.81	1.31	7.67	7.67	7	42.12	6.17	6.43	1.38	4.67	4.67	2	1.74		1.97	10.41	10.41	2.85			1.64	4.28	1.53	1
	ORF SEQ ID NO:			22246		25485		26454	26455	28300	25485	20810	21143	21144	24.420	21738	21921	22134	22641	22854	22855	23512	24051	i	25530	26045	26046	21320	-			26449	26748	
	Exon SEQ ID NO:	12219	12293	12355	12507	15423	16008	16293	16293	18048	15423	10968	11289	11289	71057	1	12025	12238	12841	13055	13055	13723	14270	0	13400	19457	19457	11463			12014	16288	16553	10415
	Probe SEQ ID NO:	2339	2416	2479	2640	5505	6114	6432	6432	8160	8791	1051	1384	1384	3000	000	2137	2358	2914	3130	3130	3811	4374	i L	2000	6012	6012	1558			2126	6427	6673	2780

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Single Exon Probes Expressed in Heart

Probe SEO ID							
NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7963	17813		2.83		7.0E-15 AW241958.1	EST_HUMAN	xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR.t2 THR repetitive element;
978	10901	20748	6.12		6.0E-15 AJ271736.1	LN	Homo sapiens Xq pseudoautosomal region; segment 2/2
8622	19770		1.86		6.0E-15 AW836843.1	EST HUMAN	QV1-LT0036-150200-070-c10 LT0036 Homo sapiens cDNA
9948	19415		1.57	6.0E-15	6.0E-15 BF432200.1	EST HUMAN	nab81c12x1 Soares NSF F8 9W OT PA P S1 Homo sapiens cDNA clone IMAGF 3
404	10350	20177	5.79		5.0E-15 AL163208.2	TN	Homo sapiens chromosome 21 segment HS21C008
2733	12595	22490	1.38		5.0E-15 U91328.1	\ Z	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA+I) gene, RoRet gene, and sodium phosphale transmorter (NPT3) name commists and
3423	13340		٢	5.0E-15	5.0E-15 AW296817.1	EST HUMAN	UI-H-BW0-aib-q-10-0-UI-s1 NCI CGAP Sub6 Home sanjens of the close IMAGE: 27342403:
8063	17954		2.22		5.0E-15 AV730056.1	11	AV730056 HTF Homo sapiens cDNA clone HTFAVF06 5
421	8866	19779	2.6		4.0E-15 AL163303.2		Homo saplens chromosome 21 segment HS21C103
4039	13942	23720	0.78		4.0E-15 AL118596.1	EST HUMAN	DKFZp761C0810_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761C0840 s
8414	16438	26623	2.38		4.0E-15 AJ130894.1	N	Homo sapiens mRNA for transcription factor
8414	16438	26624	2.38		4.0E-15 AJ130894.1	N	Homo sapiens mRNA for transcription factor
4123	14023		5.93	3.0E-15	3.0E-15 N89452.1	EST HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
4843	14724		1.41	3.0E-15	3.0E-15 P92485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
4955	14832	24599	0.88	3.0E-15	3.0E-15 AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
4955	14832	24600	0.88	3.0E-15	3.0E-15 AA078097.1	EST HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6314	16177	26335	2.86		3.0E-15 M27685.1	L	Mus musculus ultra high sulfur keratin gene, complete cds
6314	16177	26336	2.86	3.0E-15	3.0E-15 M27685.1	LN	Mus musculus ultra high sulfur keratin gene, complete cds
7709	17559		1.87	3.0E-15	3.0E-15 AA807128.1	EST HUMAN	oc36a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.t1 MER19 repetitive element:
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (D) EC1 ORCT13 ORCT14 general
8173	18061	28311	2.71	3.0E-15	3.0E-15 AB026898.1	NT	complete cds)
250	10216	20033	3.29	2.0E-15	2.0E-15 AF223391.1	LZ	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
364	10320	20141	3.23	2.0E-15	2.0E-15 AF223391.1	LN	Homo saplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
364	10320	20142	3.23	2.0E-15	2.0E-15 AF223391.1	LN	Homo saplens calclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1512	11417		1.14	2.0E-15	8923201 NT	L'Z	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA

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Table 4
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				NIEIN	on 5				contains							054849		4	2			(PROTEIN				MER28.12	FR.12 OFR
Single Exon Probes Expressed in Heart	Top H.t Descriptor	Homo sapiens TSX (TSX) pseudogene, exon 5	ZONADHESIN PRECURSOR	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon	Human BXP20 gene	AV661393 GLC Homo sapiens cDNA clone GLCGSA01 3'	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions	am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element;	602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds	Homo sapiens chromosome 21 segment HS21C079	af06d04.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'	Human SSAV-related endogenous retroviral LTR-like element	H.sapiens DNA for endogenous retroviral like element	nz47f06 x5 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849 HYPOTHETICAL 42 o KD PROTEIN 121 TB-ORBORS contains MED 7 at MED 7	Homo sepiens bituitary tumor transforming age brotein (PTTG) gene, complete cds	Jaf39or11 S1 Spares total fetus Nb2HF8 9w Home sapiens CDNA clone IMAGE 1034084 3' similar to	contains OFR.t2 OFR repetitive element;	QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MAT)	Homo sapiens CCR8 chemokine recentor (CMKBR8) gene complete cds	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA	CM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA	lg22c11.x1 NCI_CGAP_CL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.t2 MER28 repetitive element:	xg49g12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.t2 OFR repetitive element;
le Exon Prob	Top Hit Database Source	NT	SWISSPROT	SWISSPROT	N	NT	EST_HUMAN	NT	EST HUMAN	EST HUMAN	NT	LZ	EST_HUMAN	NT	NT	INWIN TSE	LS TOWN		EST_HUMAN	EST_HUMAN	NT	TOGGOOMO	LN SOLIES	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN
SILC	Top Hit Acession No.	3.0E-16 AF135446.1	228983	203200	3.0E-16 AF020503.1	3.0E-16 U03887.1	-	3.0E-16 AF003529.1	3.0E-16 Al002836.1	3.0E-16 BF690617.1		2.0E-16 AL163279.2	2.0E-16 AA621761.1	103061.1	K89211.1	0 05 48 41723837 4	1.0F-16/AF200719.1		1.0E-16 AA628592.1	1.0E-16 BF327942.1	1.0E-16 U45983.1	02720	1459B3.1	1.0E-16 AW875651.1		9.0E-17.A(392964.1	9.0E-17 AW150257.1
	Most Similar (Top) Hit BLAST E Value	3.0E-16	3.0E-16 Q28983	3.0E-16 P03200	3.0E-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16	3.0E-16 L78810.1	2.0E-16	2.0E-16	2.0E-16 J03061.1	2.0E-16 X89211.1	200	1.0E-16/		1.0E-16	1.0E-16	1.0E-16	1 05 16 000770	1.0F-16 (145983.1	1.0E-16	9.0E-17	9.0E-17	9.0E-17
į	Expression Signal	1.6	2.01	4.05	8.18	66.0	1.01	1.41	4.72	1.27	3.08	1.18	96.0	1.71	1.33	4	2.55		22.41	2.44	23.72		6.59	1.31	2.54	2.02	4.87
	ORF SEQ ID NO:		21207	22670			24521	25431	27098		27922				23764	26720	19963			21704		70030	10007	27416	23379		
	Exon SEQ ID NO:	10410	11341	12873	13785	13786	14741	15373	16908	17541	17678	10880	12217	12524	13987	46506	10149		10361	11823	15783	150GE	15783	17217	13593	15938	16600
	Probe SEQ ID NO:	467	1436	2946	3874	3875	4861	5452	7031	7691	7828	926	2337	2657	4087	6646	178		377	1928	5877	5060	6458	7349	3679	6035	6720

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	Top Hit Descriptor	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds	QV0-OT0032-080300-155-d01 OT0032 Homo saplens cDNA	Homo sapiens chromosome 21 segment HS21C080	MR0-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA	AV730759 HTF Homo saplens cDNA clone HTFAQB07 5'	Mus musculus apolipoprotein B editing complex 2 (Apobec2), mRNA	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane	conductance regulator (CFTR) genes, section 1 of 2 of the complete cds, and unknown gene	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA	hi81d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE::2978695 3' similar to contains L1.t2 L1 repetitive element ;	vc05h08.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE.79839 5'	yd26b04.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:109327 5'	Homo sapiens chromosome 21 segment HS21C047	August of Spares tests. NHT Homo saniens CDNA clone IMAGE: 1640286 3' similar to TR: 0.16530	Q16530 PMS3 MRNA ;contains MER10.t2 MER10 repetitive element;	xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3/	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'	Homo saplens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA	AV720204 GLC Homo sapiens cDNA clone GLCDIF08 5'	qt63a06.x1 NCI_CGAP_Eso2 Home sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu	repetitive element;	qt63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu	repetitive element;	zg81d04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:399751 3	ZONADHESIN PRECURSOR	ZONADHESIN PRECURSOR
	Top Hit Database Source		EST HUMAN Q		EST_HUMAN N	EST HUMAN A		NT H			EST_HUMAN F	HEST HUMAN	Τ	Τ	Π			EST_HUMAN x	SWISSPROT	EST_HUMAN	EST_HUMAN I		NT		THUMAN		EST_HUMAN r		\neg	EST HUMAN	\neg	SWISSPROT
8110	Top Hit Acession No.	9.0E-17 AF200719.1	8.0E-17 AW880701.1	8.0E-17 AL163280.2	8.0E-17 BE172081.1	8.0E-17 AV730759.1	6753097 NT	7.0E-17 AF216850.1		7.0E-17 AF229843.1	6.0E-17 AW983880.1	6 DE-17 AWG62772 1		5.0E-17 T81043 1	4 0E-17 AI 163247 2		4.0E-17 AI073546.1	3.0E-17 AW119123.1	3.0E-17 P35410	3.0E-17 BE326522.1	3.0E-17 BE326522.1		3.0E-17 AB026898.1	11417966 NT	3.0E-17 AV720204.1		2.0E-17 AI270080.1		2.0E-17 AI270080.1	2.0E-17 AA722932.1	2.0E-17 Q28983	2.0E-17 Q28983
	Most Similar (Top) Hit BLAST E Value	9.0E-17	8.0E-17	8.0E-17	8.0E-17	8.0E-17	7.0E-17	7.0E-17		7.0E-17	6.0E-17	R 0E-17	5 OF 17	5.0E-17	A 0E-17	1	4.0E-17	3.0E-17	3.0E-17	3.0E-17	3.0E-17		3.0E-17	3.0E-17	3.0E-17		2.0E-17		2.0E-17	2.0E-17	2.0E-17	2.0E-17
	Expression Signal	2.18	1.7	0.87	3.56	1.36	3.18	3.05		6.83	4.78	7	234	207	2 42	7	1.98	1.35	1.31	1.14	1.14		4.72	3.16	15.82		2.81		2	1.27	2.6	2.6
	ORF SEQ ID NO:				25402			-		26052	19986	25830			20002			21836			23294		27660				20127		20127			22171
	Exon SEQ ID NO:	17720	10919	13729	19444	15174	11347	15184		15921	10168	Í	1	Ľ	L	1	18914	11941	13082	13504	L	_	17445		1_	L	10309	Ŀ	10309	10896	12275	12275
	Probe SEQ ID NO:	7870	1001	3817	5427	6311	1442	5262		6017	196	2 6	7100	C14	0 0	0,00	9171	2051	3157	3590	3590		7594	9134	6066		350		351	972	2397	2397

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Table 4
Single Exon Probes Expressed in Heart

		UROFILAMENT								acting						inzyme E2D 3			ontains Alu							389 3'	A	L20868 60S	L20868 60S	contains L1
oligie Lyones Lybresseu III lealt	Top Hit Descriptor	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)	Mus musculus ultra high sulfur keratin gene, complete cds	Mus musculus ultra high sulfur keratin gene, complete cds	Homo sapiens MHC class 1 region	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin	Homo sapiens chromosome 21 segment HS21C047	Homo sapiens chromosome 21 segment HS21C047	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting	uanscripuonal regulatory elements)	MULIIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)	Homo sapiens chromosome 21 segment HS21C007	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR	Homo sapiens thrombospandin 2 (THBS2) gene, promoter region and exons 1A and 1B	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3	(UBE2D3) genes, complete cds	y/30e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE.128388 5'	he38e05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921312.3' similar to contains Alu	repetitive element; contains LTR8.t1 LTR8 repetitive element;	qe65b05.x1 Soares fetal lung NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3*	qe65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3*	URIDINE PHOSPHORYLASE (UDRPASE)	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]	zp18g12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609862.3°	ij86d03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN):	xx10b04.x1 NCI_CGAP_Part Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);	ya49c07.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53285 3' similar to contains L1 repetitive element;
ב דעמון ו ומחבי	Top Hit Database Source	SWISSPROT HE	NT			SWISSPROT OF	EST_HUMAN ES					ISSPROT		ISSPROT				EST_HUMAN yts			HUMAN			SWISSPROT MY	EST_HUMAN Zp	EST HUMAN 198		EST HUMAN RIE		ya EST_HUMAN rep
6.16	Top Hit Acession No.			127685.1 NT	F055066.1		1	L163247.2 NT	L163247.2 NT			,	7		79410.1 NT		F224669.1 NT			-		-			1		4758977 NT	7.0E-18 AW316976.1 E		
	Most Similar (Top) Hit BLAST E Value	2.0E-17 P12036	2.0E-17 M27685.1	2.0E-17 M27685.1	2.0E-17 AF055066	2.0E-17 Q95156	2.0E-17 AA300640.	20E-17 AL163247.	2.0E-17 AL163247.	7 7 10 0	Z.UE-17 D13391.1	1.0E-17 P08183	1.0E-1/ AL16320/	1.0E-17 P02461	1.0E-17 U79410.1		1.0E-17 AF224669.	1.0E-17 R09942.1	<u>-</u> -	1.0E-17 A	1.0E-17 AI185642.1	1.0E-17 AI185642.1	1.0E-17 Q16831	1.0E-17 Q28824	9.0E-18 AA174078.	9.0E-18 AI472167.1	8.0E-18	7.0E-18	7.0E-18 AW316976.	7.0E-18 R16220.1
	Expression Signal	5.62	1.95	1.95	2.07	1.44	1.38	2.72	2.72	, u	5.0	3.37	2.45	1.68	1.46		1.01	7.17		4.7	1.44	1.44	1.32	2.01	0.96	3.26	1.75	8.39	8.39	0.85
	ORF SEQ ID NO:	22621	25017	25018		26779	26997	27772	27773	72084	106/2	24450	21499	21853	22067						26037	26038	26232	28821	22196		23415	20121	20122	24774
	Exon SEQ ID NO:	12826	15216	15216	15696	16591	16803	17549	17549	17777	1000	10003	1000	11959	12170		13435	13947		15792	15911	15911	16082	18536	12299	17328	13630	10305	10305	15003
	Probe SEQ ID NO:	2899	5295	5295	5790	6711	6925	2697	7699	7887	200	25/	67/1	2069	2287		3519	4045		5885	9009	9009	6216	8719	2422	7468	3718	346	346	5136

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9638	10305	20121	5.73		7.0E-18 AW316976.1	EST_HUMAN	xt0b04.xt NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
9638	10305	20122	5.73	7.0E-18	7.0E-18 AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
3255	13178	22976	1.16		6.0E-18 X71791.2	NT	Rattus norvegicus partial Gdn/Pn-1 gene for glia-derived nexin/protease nexin I, enhancer region
4641	14529		3.37	6.0E-18 P52181	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINĀSE) (TGASE C) (TGC)
						!	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446),
6799	16678		2.69		6.0E-18 11428155 NT	F F	MKNA Homo carions chromosoma 21 scamost US210048
0410	1	1 1007			AL 103240.2		Hearless MA DAR HIA.71 IPP3 I MP2 TAP1 I MP7 TAP2 DOB DOB3 and BINGS O 13 and 11
8642	18506	28784	1.78		6.0E-18 X87344.1	LN.	genes
9394	19052	25308	3.66	6.0E-18	6.0E-18 U87929.1	NT	Human aconitate hydratase (ACO2) gene, exon 4
1130	11044	20886	14.74		5.0E-18 AI280214.1	EST HUMAN	qm65g11.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element;
4217	14115	23893	. 0.92		10946665 NT	NT	Mus musculus gasdermin (Gsdm), mRNA
5058	14928	24700	1.76		5.0E-18 D61517.1	EST_HUMAN	HUM411F05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-411F05 5'
5224	15147	24914	1.38		5.0E-18 AF087913.1	LN	Human endogenous retrovirus HERV-P-T47D
7061	16938	27128	4.26		5.0E-18 BE143312.1	EST_HUMAN	MR0-HT0161-221099-002-c06 HT0161 Homo sapiens cDNA
8346	18223	28474	4.33	5.0E-18	10242378 NT	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
8346	18223	28475	4.33	5.0E-18	10242378 NT	LN	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
9512	19125		5.3		5.0E-18 AW867182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
9837	19336		13		5.0E-18 AV650547.1	EST_HUMAN	AV050547 GLC Homo sapiens cDNA clone GLCCGA02 3'
119	10096	19915	1.36		4.0E-18 BE044076.1	EST HUMAN	ho36h04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
119	10096	19916	1.36		4.0E-18 BE044076.1	EST HUMAN	hos6h04.x1 NCL CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511.3' similar to contains MER29.b3 MER29 repetitive element:
1846					4.0E-18 AI738592.1	EST HUMAN	wi33h08.x1 NC CGAP Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
2154	12042	21940	0.98		4.0E-18 Q06430	SWISSPROT	N-ACETYLLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYI.TRANSFERASE (N- ACETYLGLUCOSAMINYI.TRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
2154	12042	21941			4.0E-18 Q06430	SWISSPROT	N-ACETYLLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N- ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
5293	15214	25014	2.55		4.0E-18 AI017565.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'

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	Top Hit Descriptor	ou23e06.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'	EST63633 Pituitary gland, subtracted (prolactin/growth hormone) Il Homo sapiens cDNA 5' end similar to EST containing O family repeat	ob23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN	P46782 40S RIBOSOMAL PROTEIN S5.;	CM0-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C047	PM0-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE∷485125 5	QV1-LT0036-150200-070-e07 LT0036 Homo sapiens cUNA	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5	ak53a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3` similar to TK:01457/ 014577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE.;	Himan DNA SINF repetitive element	Himan DNA SINE renetitive element	SCORPAGE AND COAP Brief Home canions cDNA clans IMAGE 4156670 5	00.001 104FT NOT CORP. Divisor september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a september of a septe	htg4g01.x1 scares_NFL_1_GBC_S1 Homo sapiens cD1vA cione iwAGE_297.9904 5 strilled to contents. MER19.t2 MER19 repetitive element;	x67e10.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2	MER10 repetitive element ;	xf67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2	MER10 repetitive element;	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:28/5499 3 similar to contains THK D3	THR repetitive element ;	xg47e09,x1 NCL_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2	MER8 repetitive element ;	601114352F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE.3355044 5'	ye43g05,r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains	L1 repetitive element ;	AV653405 GLC Homo sapiens cDNA clone GLCDKE11 3'	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds	Homo sapiens chromosome 21 segment HS21C080
	Top Hit Database Source	EST_HUMAN	EST HUMAN		EST_HUMAN	HUMAN			٦	EST_HUMAN		ECT LIBAAN	NICIAI)		h	ESI HUMAN	EST HUMAN		EST_HUMAN		EST_HUMAN		EST HUMAN		EST HUMAN	EST_HUMAN		EST_HUMAN	EST HUMAN	Z	NT	NT
	Top Hit Acession No.	4.0E-18 AI017565.1			3.0E-18 AA814196.1			3.0E-18 BE001671.1	3.0E-18 AW022015.1	2.0E-18 AW836820.1	2.0E-18 BE256097.1	A 0.0000 A	Z.UE-18 AA8888 IV. I	Z.UE-10[D14547.1	Z.UE-18 D14547.1	2.0E-18 BF347229.1	2 0F18 AW665853.1		2.0E-18 AW151673.1		2.0E-18 AW151673.1		2.0E-18 AW470791.1		AW151299.1	2.0E-18 BE256097.1		1.0E-18 T95406.1	1.0E-18 AV653405.1	1.0E-18 D00099.1	1.0E-18 D00099.1	1.0E-18 AL163280.2
Most Similar		4.0E-18	1 A D E 1 A D	201	3.0E-18	3.0E-18	3.0E-18	3.0E-18	3.0E-18	2.0E-18	2.0E-18	, C	Z.UE-10	Z.UE-101	Z.UE18	2.0E-18	2 OF-18		2.0E-18		2.0E-18		2.0E-18		2.0E-18					L		
	Expression Signal	2.55	7 42	71.	2.38	241	1.19	5.2	4.92	2.83	47.22		3.2	3.04	3.04	1.67	2 53	3	1.53		1.53		5.32		4.44			1.02	2.38	1.97	1.97	1.32
	ORF SEQ ID NO:	25015	00,00	20499	20609		23571			20034					25150		75937		27861		27862		28469		29065				24985			Ш
	Exon SEQ ID NO:	15214	1	1824/	10758	10838	13778	16029	19210	10217	11049	1	15242		5380 15299	5585 15500	1	13/20	0777		17629		18217		8968 18774	1_	1.	4318 14215	1_	1	1_	
- 1	07												5322	2380				8			7779		8340								10	5883

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Exon ORF SEQ NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:	Expression	Ssion Top Hit Database Source
xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx	ORF SEC	Most Similar (Top) Hit BLAST E Value
27769 4.4 1.0E-18 Hon328.1 NT 25324 2.53 1.0E-18 AF003529.1 NT 20289 4.28 9.0E-19 AA281961.1 EST_HUMAN 20289 3.19 9.0E-19 AA281961.1 EST_HUMAN 27110 2.46 9.0E-19 AA281961.1 EST_HUMAN 27111 2.46 9.0E-19 AA281961.1 EST_HUMAN 20289 8.69 9.0E-19 AA281961.1 EST_HUMAN 20289 8.69 9.0E-19 AA281961.1 EST_HUMAN 21987 1.58 7.0E-19 AA281961.1 EST_HUMAN 25913 2.15 7.0E-19 AA281961.1 EST_HUMAN 24041 1.58 7.0E-19 AA281961.1 EST_HUMAN 24042 1.58 7.0E-19 AA085230.1 EST_HUMAN 24041 1.36 6.0E-19 AW852330.1 EST_HUMAN 24595 1.09 6.0E-19 P34986 SWISSPROT 25562 5.24 5.0E-19 AU120817.1 EST_HUMAN 28921 7.19 6.0E-19 AV183725.1 EST_HUMAN 28922	Source	-

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	Top Hit Descriptor	BETA-2 ADRENERGIC RECEPTOR	BETA-2 ADRENERGIC RECEPTOR	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sabiens)	(LOC63222), mRNA	M.musculus mRNA for TPCR33 protein	Homo sapiens phorbolin I protein (PBI) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C001	ze34c09,r1 Scares retina N2b4HK Homo sapiens curva cione invace: 50ccoc 5	601304125F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE: 3030310 3	yo79g07.r1 Scares adult brain N2b4HB55Y Homo sapiens cUNA cione II/ARCE: 104 106 3 Stituta to contains.	MER to repetitive delirent,	Human gene for An-receptor, exon 7-9	Homo sapiens protein tyrosine phosphatase, non-tecepion type substant of the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphatase and the phosphata	aj49b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1383631 3 similar to contains MEN37.17	MER37 repetitive element;	Oryctolagus cuniculus sodium/dicarboxylate cotransporter film/NA, per ital cus	Rabbit phosphorylase kinase beta subunit mkn/i, complete cas	ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5 similar to contains	UFIX repetutive element	RCU-STUT/4-191099-031-1903 STUT/4-100110 Saprans CONA Clone IMACE -272872 5	(31609.F1 Soares melanicyle Zivo in 10110 sapidais cours de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la 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htbr1) Homo sapiens ound clone UNFZp547D092_s	hI46c04.s1 NCL_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2	Mill to openior control of the control of the IMAGE 1042748 circles of MFR29 h2	nl46cV4.s1 NCL_CGAP_F14 Homo sapiens cDNA clone innacE. 1543/16 similar to contains included. MER29 repetitive element;	Homo sapiens ribosomal protein L13a (RPL13A), mRNA	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
	Top Hit Database Source	SWISSPROT B	SWISSPROT B	EST HUMAN A			NT TA	±		EST_HUMAN z	EST HUMAN 6		HOMAN				T_HUMAN	LN	LN		Т	HUMAN	THOMAN				\neg		EST HUMAN		אואואוסר ביים	EST_HUMAN		SWISSPROT
6	Top Hit Acession No.			36.1		11432214 NT			2.0E-19 AL163201.2	2.0E-19 AA012854.1	1.0E-19 BE408611.1			l	4758977 NT		7.1		1.0E-19 M64657.1		1.0E-19 T99920.1	9.1	1.0E-19 N44631.1	7657286 NT	7657286 NT	8.0E-20 AI221371.1	AI221371.1	7.0E-20 BF326455.1	7.0E-20 AL138120.1		7.0E-20 AA55/657.1	7.0E-20 AA557657.1	6912633 NT	P39188
-	Most Similar (Top) Hit BLAST E Value	3.0E-19 Q28997	3.0E-19 Q28997	3.0E-19		3.0E-19	3.0E-19 X89685.1	3.0E-19 A	2.0E-19	2.0E-19	1.0E-19 E		1.0E-19 H30795.1	1.0E-19 D38044.1	1.0E-19		1.0E-19	1.0E-19 U12186.1	1.0E-19		1.0E-19	1.0E-19	1.0E-19	8.0E-20	8.0E-20	8.0E-20	8.0E-20	7.0E-20	7.0E-20					6.0E-20 P39188
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	ORF SEQ ID NO:	23475	23478	24024	17017	-	26645		22279				21906						L	_		27948	27953	26035	26036	26462					5 27018	27019		1 23227
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	Probe SEQ ID NO:	0770	37.70	3110	4545	6370	7443	9416	2513	6849	473		2118	2685	2817		3355	5701	6919	3	7076	7853	7857	6005	6005	6439	6439	3238	6176	5	6947	6047	8952	3508

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Table 4
Single Exon Probes Expressed in

Single Exon Probes Expressed in Heart	Top Hit Descriptor	001444033 E4 NIII 1 1 2 C C C C L I	AV725123 HTC Home series - ONA Classical MAGE:3916231 5	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element :	zh/8d08.s1 Soares fetal liver spleen 1NFLS_S1 Homo saplens cDNA clone IMAGE:418191 3' similar to	Mis misculus MAMAN a contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the 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IMAGE:2761098 3' similar to SW:RS5_MOUSE	ng69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066	ng69h09.s1 NCI_CGAP_Lip2 Home sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORE? FI INCTION THEN OWN	x24e10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW RS5_MOLISE	P9/461 40S RIBOSOMAL PROTEIN S5.;	ZONADHESIN PRECURSOR	ZUNAUHESIN PRECURSOR	Homo sepiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA	Homo saniene RCH4 gene, retrovirus-like element	oa35b08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306935 3' similar to contains MER4.b2	יייייייייייייייייייייייייייייייייייייי
gle Exon Prob	Top Hit Database Source	EST HIBAAN	\top		EST HIMAN	7		T HIMAN	HIMAN		ISSPROT	T	NAM	Z	SWISSPROT E						SWISSEDOT 7	Т	ISSEROI			T HUMAN	7
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	Most Similar (Top) Hit BLAST E Value	6.0E-20	5.0E-20	5.0E-20	5.0E-20	5.0E-20	5.0E-20	4.0E-20	4.0E-20	3.0E-20	3.0E-20 P23273	3 0E-20	3 0F-20	2.01	3.0E-20 P11369	3.0E-20	2.0E-20	2.0E-20	2.0E-20	2 OE-30	2.0F-20 C28983	2 0F-20 028983	20F-20	2.0E-20 D10083 1	2.0E-20 D10083.1	2.0E-20 AA766755.	
	Expression Signal	2.55	1.17	4.66	4.66	1.44	1.44	6.03	1.17	1.04	1.69	0.86	3.26		2.08	5.37	4.52	2.03	2.03	27.2	4.32	4.32	11.35	2.95	2.95	1.95	
	ORF SEQ ID NO:	23850		26704	26705	27197	27198		28087	21876	23795	24201				25352		20852	20853		24525	24526		27378	27379	29089	
	Exon SEQ ID NO:	14075	14385	16514	16514	17005	17005	16504	17845	11981	14015	14417	17049		17946	18929	10741	11011	11011	10741	14746	14746	14960	17177	17177	18797	
	Probe SEQ ID NO:	4175	4491	6634	6634	7128	7128	6624	7995	2092	4115	4524	7172		8055	9195	813	1095	1095	2786	4866	4866	5090	7301	7301	8993	

Page 181 of 413 Table 4 Single Exon Probes Expressed in Heart

Top Hit Descriptor	oa35b08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306935 3' similar to contains MER4.bZ MER4 repetitive element;	CHR220310 Chromosome 22 exon Homo sapiens CDNA clone UAA CE-391 3	### ### ##############################	hr84b06.x1 NCI_CGAP_Kid11 Homo sapiens cUNA clone IMAGE:3133133 5 Similar to comains Electropage element;	Homo sapiens Autosomal Highly Conserved Protein (Anch.) Illinus 1. Anches Autosomal Highly Conserved Protein (Anch.) Illinus Anches Anches Alexandria (As alternative)	Homo sapiens calcium channel alpha1E subunit (CACNA IE) gene, excus 7-49, and pende cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and cas, and	ne60g08.rl Not Coar FTI notice septets coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare into Coare	AJ003514 Selected chromosome 21 cUNA library Homo sapiens culva cione ivir ipi 12-632.1	RC3-NN0068-090500-021-b03 NN0068 Homo saplens cDNA	bb30a02.y1 NIH_MGC_10 Homo sapiens cDNA cone IMAGE:2984.74 5 similar to SW. NIAM_110MAN_100M5065169 NADH-UBIQUINONE OXIDOREDUCTASE ASHI SUBMIT PRECURSOR:	ob71f06.s1 NCI_CGAP_GCB1 Homo saplens cUNA cione IMAGE: 1330633 3	ATE SYNTHAGE A CHAIN (FROTEING)	LAMININ BELAZ CHARA POPOLOGIA (OLI MININI) (LAMININ CHARA SILININ POPOLOGIA (OLI AMININI) (LAMININI CHARA SILININI POPOLOGIA (OLI AMININI) (LAMININI CHARA SILININI POPOLOGIA (OLI AMININI) (LAMININI CHARA SILININI POPOLOGIA (OLI AMININI) (LAMININI CHARA SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILININI SILINI SILININI SILININI SILINI SILININI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SILINI SI	LAMININ BE LAZ CHAIN PRECONSON (S-Edivinin) (Edivining of the Editor S)	(6/a06,r1 Soares pregnant utenus juunit O Humo Sapienis South State in 1951, 1952)	Homo sapiens dNT-2 gene for mitochondrial 5′(3′)-deoxyribonucleotidase (dNT-2 gene), exons 1-5	Human chromosoma protein HMG1 related gene	zg73d03.s1 Soares_fetal_heart_NbHH19W_Homo sapiens cDNA clone iMAGE:398981 3_Smilar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.t3 OFR	repetitive element;	Homo sapiens PTD013 protein (PTD013), mKNA	601304125F1 NIH MGC 21 Homo sapiens CUNA cione IMAGE: 3036310 3	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (F1FN21), Illinnia.	om23g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cUNA clone tMAGE: 1341505.5 stiffular to TN. Odd. 1002711 PRO-POL-DUTPASE POLYPROTEIN;	601649871F1 NIH MGC 74 Homo saplens cDNA clone IMACE:3833880 3	Homo sapiens melanoma antigen, tamily C, 1 (MAGECT), mห่างค
Top Hit Database Source		EST_HUMAN CI	EST_HUMAN M	T HUMAN		T is		EST HUMAN A	EST_HUMAN R	EST_HUMAN C		T	7		EST HUMAN Z	LN T	-IN	7 0	T HUMAN		T HUMAN		EST_HUMAN	T HUMAN	
Top Hit Acession No.	2.0E-20 AA766755.1		1.0E-20 AA281961.1		18491	1.0E-20 AF223391.1	1.0E-20 AA420453.1		1	8.0E-21 AW674891.1	8.0E-21 AA809411.1	021330	P15800	P15800	7.0E-21 AA046502.1	7.0E-21 AJ277557.1	7.0E-21 D14718.1		7.0E-21 AA723404.1	7706668 NT	BE408611.1	5902031 NT	5.0E-21 AA928194.1	5.0E-21 BE968839.1	4885474 NT
Most Similar (Top) Hit BLAST E Value	2.0E-20 A	2.0E-20 H55371.1	1.0E-20	1.0E-20	1.0E-20	1.0E-20	1.0E-20/	9.0E-21	9.0E-21	8.0E-21	8.0E-21	8.0E-21 O21330	7.0E-21 P15800	7.0E-21 P15800	7.0E-21	7.0E-21	7.0E-21		7.0E-21	7.0E-21	6.0E-21	5.0E-21			5.0E-21
Expression Signal	1.95	1.5	5.25		2.42	2.81	1.84	1,08	2 35	1.74	3.42	4.02	2.07	2.07	4.96	1.43	6.84		2.94	2.37					
ORF SEQ ID NO:	29090	25129	21751	24018	27359	28940					28922		21803			26962			28220						
Exon SEQ ID NO:	18797	19482	12648	14235	17161	L	1001	1.		1		1_	11914	11914	14061	1		İ	17971	1_	L	1_	l		
Probe SEQ ID NO:	8003	9574	1067	4338	7285	8839	0327	2880	2000	7115	8825	9207	2023	2023	4161	6887	7036	3	8080	8590	4014	200	7266	4288	4696

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Table 4
Single Exon Probes Expressed in Heart

	Top Hit Descriptor	Homo sapiens DNA for amyloid precursor protein, complete cds	oo86e08.st NCI_CGAP_Kid5 Home sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530 PMS3 MRNA ;contains OFR.t1 OFR repetitive element:	Raftus norvegicus mRNA for rTIM, complete cds	Homo sapiens chromosome 21 segment HS21C001	Homo sapiens LGMD2B gene	601844465F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE: 4064945 5'	RC1-0T0083-100800-019-g08 OT0083 Homo sapiens cDNA	CM1-NN0063-280400-203-h08 NN0063 Homo saplens cDNA	Homo sapiens chromosome 21 segment HS21C013	QV3-HT0458-170200-090-912 H10458 Homo sapiens cDNA	Homo sapiens mRNA for KIAA0397 protein, partial cds	Homo sapiens mRNA for KIAA0397 protein, partial cds	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA	ZONADHESIN PRECURSOR	ZONADHESIN PRECURSOR	ts30f03.x1 NC]_CGAP_Pan1 Homo sapiens cDNA done IMAGE:2230109 3' similar to TR:Q99864 Q99854 HYPOTHETICAL 51.1 KD PROTEIN	OV0-H10103-091199-050-411 H10103 Homo seriens CONA	AU136779 PLACE1 Homo sapiens cDNA clone PLACE 1005052 5	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3	601680636F1 NIH MGC 83 Homo sapiens cDNA clone IMAGE:3951008 5:	601680636F1 NIH MGC 83 Homo saplens cDNA clone IMAGE:3951008 51	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds	nI46c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 renefitive element:	ar88d12.x1 Barstead colon HPLRB7 Home sabiens cDNA clone IMARE 275243 3	DKFZp43410830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp43410830 5	9947e05x1 Soares_testis_NHT Homo:sapiens cDNA clone IMAGE:1838336 3' similar to gb::M64241 QM PROTEIN (HUMAN):	Homo sepiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	t294a03.x1 NGL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204.3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT;
באסויין ווסעד סופ	Top Hit Database Source	H	est HUMAN P	Π	NT	IN IN	EST HUMAN 6	EST_HUMAN R	EST_HUMAN C	H	HUMAN			T HUMAN	SWISSPROT	SWISSPROT	EST HUMAN H	Т	HUMAN		EST HUMAN 60	П	TN TN	EST HIMAN M	\top	HUMAN	EST HUMAN PI		EST_HUMAN N
	Top Hit Acession No.	5.0E-21 D87675.1	4.0E-21 AA970713.1	4.0E-21 AB019576.1	3.0E-21 AL163201.2	3.0E-21 AJ007973.1	3.0E-21 BF184739.1	3.0E-21 BF361093.1	3.0E-21 AW897760.1	3.0E-21 AL163213.2	2.0E-21 BE163247.1	2	2	2.0E-21 BE064410.1	Q28983	Q28983	2.0E-21 Al624582,1	2.0E-21 BE141785.1	2.0E-21 AU136779.1	2 0E-24 RE350127 4			2.0E-21 AF176815.1	1 0E-21 AA557657 1	-	-	1.0E-21 Al223104.1	5730038 NT	9.0E-22 AI702438.1
	Most Similar (Top) Hit BLAST E Value	5.0E-21	4.0E-21	4.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	3.0E-21	2.0E-21	2.0E-21	2.0E-21	2.0E-21	2.0E-21 Q28983	2.0E-21	2.0E-21	2.0E-21	2.0E-21	20E-24	2.0E-21	2.0E-21	20E-21	1 0F-21	1.0E-21	1.0E-21	1.0E-21	1.0E-21	9.0E-22
	Expression Signal	0.95	1.24	3.06	1.06	4.04	1.72	4.79	1.55	1.32	14.75	0.85	0.85	2.09	2.89	2.89	1,77	4.66	3.43	1 98	1.92	1.92	5.13	168	2.46	2.43	4.43	1.46	2.55
	ORF SEQ ID NO:		21473	26138	22015	22762		26100	27656	24992		20688	20689		22361	22362	25126	26944	27190		28776	28777		20994			26289		23993
	Exon SEQ ID NO:	14977	11602	16000		12968	15657	15966	17440	19672	10114	10843	10843	11106	12468	12468	15290	16749	16999	18287	18501	18501	19072	11142	11286	15813	16134	17871	14209
	Probe SEQ ID NO:	5109	1701	6106	2228	3041	5749	6206	7589	9684	140	919	919	1196	2599	2599	5370	6870	7122	8412	8636	8636	9425	1235	1381	2807	6269	8021	4312

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Single Exon Probes Expressed in Heart

1		- T		_I	$-\Gamma$	-1	-,			- 1	-1			т	-7					_														
	, Top l·lit Descriptor	Homo sapiens chromosome 21 segment HS210001	Homo sapiens chromosome 21 segment HS21C001	AV761874 MDS Homo sapiens cDNA clone MDSCCCOR s'	AU140358 PLACE2 Homo sapiens cDNA clone PI ACE2000367	Mus musculus TF-1 cell apontosis related protein-15 (Trans) mRN4	CM0-HT0179-281099-076-h05 HT0179 Homo sapiens cDNA	zk67a06.r1 Soares pregnant uterus NbHPU Homo sanions CNIA clare MACE 1970E 6	Homo sapiens chromosome 21 segment HS210046	ALPHA-2-MACROGLOBULIN PRECIRSOR (ALPHA-24A)	Homo sapiens gene for activin receptor fore IIR complete ods	Homo sapiens HSPC220 mRNA, complete cds	EST00738 Feta Ingin Stratagene (restronge) Home context COMA size Higher	Homo sapiens T cell recentor hata locus TORN/723/3 to TOBN/4203	WX05q07.X1 NCI CGAP Gas4 Home saniens cDN4 Acres 1844 CE 2543645 21	Homo sapiens chromosome 21 segment HS21C403	Human destronhin (DMD) nane avone 7 8 and 0 and ended 23	nea27b06.x1 NCI_CGAP_Pr28 Horno sapiens cDNA clone IMAGE:3255898 3' similar to contains 41.	repetitive element;	Homo saplens Xq pseudoautosomai region: serment 1/2	Homo sapiens chromosome 21 segment HS21C002	1801882813F1 NIH MGC 57 Horn Saniens CONA close IMA CE 4006424 61	Homo sabiens chromosome 21 segment HS21C000	tm14h10x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to qb:L19593 HIGH	AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN), contains L1.t1 L1 repetitive element	WIG6b04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTFIN L21_HUMAN	Human chromosomal protein HMG1 related gene	db28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to	contains MER12.t2 MER12 repetitive element;	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA	x/3d05.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clune IMAGE 287380 3/	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR	Homo sapiens protein kinase. AMP-activated gamma 3 non-catalytic substant (DDL/AC2)	PM1-ST0262-261199-001-d12 ST0262 Homo sapiens cDNA
, -	Top Hit Database Source	LN	LN	EST HUMAN	EST HUMAN	NT	EST HUMAN	EST HUMAN	LN	SWISSPROT	LN	\ L	EST HUMAN		EST HUMAN	LN	Į.		EST_HUMAN	TN	TN	EST HUMAN	IN		EST_HUMAN	EST HUMAN	NT		ESI_HUMAN	EST HUMAN	EST_HUMAN	SWISSPROT	TN	EST_HUMAN
	Top Hit Acession No.	9.0E-22 AL163201.2	9.0E-22 AL163201.2	9.0E-22 AV761874.1	9.0E-22 AU140358.1	9790256 NT	8.0E-22 BE144748.1	8.0E-22 AA046502.1	7.0E-22 AL 163246.2	Q61838	7.0E-22 AB008681.1	7.0E-22 AF151054.1	7.0E-22 M78590.1	7.0E-22 AF009660.1	6.0E-22 AW029123.1	5.0E-22 AL163303.2	5.0E-22 U60822,1		5.0E-22 BF476511.1	4.0E-22 AJ271735.1	4.0E-22 AL163202.2	4.0E-22 BF218030.1	4.0E-22 AL163209.2		3.0E-22 A1469679.1	3.0E-22 A1859038.1	014718.1		41090125.1	-	-1		8394043 NT	2.0E-22 AW817794.1
	Most Similar (Top) Hit BLAST E Value	9.0E-22	9.0E-22	9.0E-22	9.0E-22	9.0E-22	8.0E-22	8.0E-22	7.0E-22	7.0E-22 Q61838	7.0E-22	7.0E-22	7.0E-22	7.0E-22	6.0E-22	5.0E-22	5.0E-22		5.0E-22	4.0E-22	4.0E-22	4.0E-22	4.0E-22	1000	3.0E-22,	3.0E-22	3.0E-22 D14718.1	100	3.0E-22 AIU90125	3.05-22	2.0E-22 N24942.1	2.0E-22 P24916	2.0E-22	2.0E-22 /
	Expression Signal	1.26	1.26	3.65	2:92	2.39	4.55	3.8	4.23	2.32	1.18	1.34	2.63	1.86	1.82	2.53	3.97		2.03	0.85	2.7	2.97	1.51		7:1	1.86	1.49	0.4.0	2.12	2.73	2.86	1.33	4.06	1.26
	ORF SEQ ID NO:	27070	27071	28309	29048				20401	23861	24613		27196	27599		25955	28001					28244				22288		24374	12000	70007		22244	23091	23808
	Exon SEQ ID NO:	16879				18800			10585	14086	14844	16921	17004	17389	16675	15832	17762		19213	13498	19767	17995	19315	10868	0000	12397	13534	145B1	16677	7/001	11805	12352	13292	14033
	Probe SEQ ID NO:	7002	7002	8171	8945	7668	933	6099	649	4186	4969	7044	7127	7538	9629	5927	7912	1,000	9045	3584	6902	8105	9803	043	5	2523	3920	4695	6703	20,00	DI.B.	2476	3373	4133

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Single Exon Probes Expressed in Heart

Original Lybressed III Heart	Top Hit Database Source	zo20f01.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE 322873 6' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTFIN 3 PRFCI IRSOR (Hi MAAN):	EST_HUMAN RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA	q176h08.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains EST HUMAN MER29.t3 MER29 repetitive element		T	Г	Т	EST HUMAN PM4-SN0020-010400-009-h02 SN0020 Homo sapiens CDNA	Ī	Human DNA, SINE repetitive element	HUMAN MR0-B10659-220200-002-h07 B10659 Homo saniens cDNA	HUMAN IL2-UM0076-070400-061-F11 UM0076 Homo serviens cDNA	Gallus gallus Dach2 protein (Dach2) mRNA complete cds	HUMAN HA2340 Human fetal liver cDNA library Homo saniens cDNA	EST HUMAN HA2340 Human fetal liver cDNA library Homo saniens cDNA	Г		Homo sapiens Not56 (D. melanogaster)-like protein (NOT56) mRNA	Raftus novegicus RIM1B (Rim1B) mRNA. complete cds	Homo saplens chromosome 21 segment HS21C049	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	Homo saplens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	qg59c03.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to SW:MV10, MOUSE P23249 PROTEIN MOV-10.	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (WAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrocenase-like protein (NSDH1) societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its societies and its s	Pongo byamaeus olfactory recentor (PPV146) grave marrial cye	Sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold and the sold
<u></u>	Top Hit Acession No.	20E-22 W39456.1	2.0E-22 BF092116.1	2.0E-22 Al276522.1	2.0E-22 AA715315.1	2.0E-22 AA715315.1	2.0E-22 AW418960.1	2.0E-22 AL163280.2	1.0E-22 AW865517.1	J50871.1	14547.1	1.0E-22 BE084667.1	9.0E-23 AW802801.1	8.0E-23 AF198349.1	8.0E-23 AI133716.1	8.0E-23 AI133716.1	7.0E-23 AV647246.1	10092626 NT	5031952 NT	6.0E-23 AF199333.1	6.0E-23 AL163249.2	6.0E-23 AF224669.1	F224669.1	6.0E-23 AI209130.1	82671.2 NT	5.0E-23 AF179818.1 NT	
	Most Similar (Top) Hit BLAST E Value	20E-22	2.0E-22	2.0E-22	2.0E-22	2.0E-22	2.0E-22	2.0E-22	1.0E-22	1.0E-22 U50871.1	1.0E-22 D14547.1	1.0E-22	9.0E-23	8.0E-23	8.0E-23	8.0E-23	7.0E-23	7.0E-23	7.0E-23	6.0E-23 A	6.0E-23	6.0E-23	6.0E-23 AF224669.	6.0E-23 A	5.0E-23 U82671.2	5.0E-23 A	
	Expression Signal	1.44	3.39	1.49	7.07	7.07	2.04	1.85	1.78	2.65	1.74	1.49	4.71	0.84	1.48	1.48	1.45	1.04	3.51	1.62	3,12	1.99	1.99	2.18	3.51	3.51	
	ORF SEQ ID NO:	25561	25763	27661	27710	27711	29071	25200	21609	22303	23084	26589		23236	24935	24936		24438	28526		23846	25338	25339	25297	25088	25797	
	Exon SEQ ID NO:	19447	15655	17446	17490	17490	18779	19304	11733	12413	13284	16411	19342	13439	15165	15165	13192	14649	18274	13305	14071	18899	18899	19021	15262	19454	
	Probe SEQ (D NO:	5570	5747	7595	7640	7640	8974	6006	1836	2539	3365	6553	9844	3523	5241	5241	3271	4764	8338	3387	4171	9146	9146	9341	5341	5781	

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Table 4
Single Exon Probes Expressed in Heart

Surge Explessed it real	Top Hit Database Source	235g09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to CONTAIN contains MER29.t2 MER29 repetitive element;	NT Human endogenous retroviral element HC2	NT Human endogenous retroviral element HC2	NT Homo saplens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	NT Human matrix Gla protein (MGP) gene, complete cds	SWISSPROT TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)	SWISSPROT TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)	qs73f11x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537 REST HUMAN MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SPOTENCE	П		HUMAN	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide	4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450	NT polypeptide 5 (CYP3A5) gene, partial cds	NT Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1	NT Homo saplens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	EST_HUMAN AU133931 OVARC1 Homo sepiens cDNA clone OVARC1000946 5	NT Homo sapiens chromosome 21 segment HS21C052	NT Homo saplens chromosome 21 segment HS21C010	EST_HUMAN 601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5	zw82c06.r1 Soares_testis_NHT Horno sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.t2 EST HUMAN PTR5 repetitive element:	EST_HUMAN TR:E19822 E19822 CA PROTEIN.	SWISSPROT OLFACTORY RECEPTOR-LIKE PROTEIN 13	SWISSPROT OLFACTORY RECEPTOR-LIKE PROTEIN 13	EST_HUMAN QV0-DT0047-170200-122-e06 DT0047 Home sapiens cDNA	NT Macaca fuscala mRNA for Test s-Specific Protein Y (TSPY), complete cds	$\overline{}$	NT Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3	nn31h05.s1 NCI_CGAP_Gas1 Homo saplens cDNA clone IMAGE:1085529 3' similar to SW.POL_MLVRK EST_HUMAN P31795 POL POLYPROTEIN;
ō	Top Hit Acession No.	3.0E-23 AA130165.1	3.0E-23 Z70664.1	3.0E-23 Z70664.1	2.0E-23 AJ289880.1	2.0E-23 M55270.1	P22105	P22105	2.0E-23 Al201458.1	2.0E-23 BE165980.1	2.0E-23 H59931.1	2.0E-23 H59931.1			2.0E-23 AF280107.1	2.0E-23 M32658.1	2.0E-23 AF009660.1	2.0E-23 AU133931.1	1.0E-23 AL163252.2	1.0E-23 AL163210.2	1.0E-23 BE378471.1	1.0E-23 AA448097.1	9.0E-24 AA663213.1	P23269	P23269	7.0E-24 AW937954.1	6.0E-24 AB001421.1	6.0E-24 AL163249.2	5.0E-24 AJ229043.1	4.0E-24 AA594178.1
	Most Similar (Top) Hit BLAST E Value	3.0E-23	3.0E-23	3.0E-23	2.0E-23	2.0E-23	2.0E-23 P22105	2.0E-23 P22105	2.0E-23	2.0E-23	2.0E-23	2.0E-23			2.0E-23	2.0E-23	2.0E-23	2.0E-23	1.0E-23	1.0E-23	1.0E-23	1.0E-23	9.0E-24	8.0E-24 P23269	8.0E-24 P23269	7.0E-24	6.0E-24	6.0E-24	5.0E-24	4.0E-24
	Expression Signal	3.56	3.61	3.61	4.36	2.77	1.06	1.06	1,46	3.03	2.98	2.98			5.62	2.69	2.47	2.02	1.6	4.49	2.91	4.54	1.88	1.08	1.08	1.31	2.4	10.14	7.18	3.06
	ORF SEQ ID NO:	26653	27435	27436	20402		22519	22520			23589	23590							24110			26937		24225	24226				23585	25609
	Exon SEQ ID NO:	16460	17233	17233	10586	12644	12627	12627	13245	13569	13804	13804			16475	18888	19218	19676	14323	14543	15937	16744	_	14442	14442	13708	10623	10748	13800	15526
	Probe SEQ ID NO:	6580	7329	7329	650	1126	2765	2765	3325	3655	3894	3894			6595	9131	9656	9774	4428	4657	6034	6865	540	4549	4549	3796	069	820	3889	5611

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Top Hit Descriptor	Homo sapiens mRNA for KIAA 1093 protein, partial cds	Homo saplens G-2 and S-phase expressed 1 (G ISE1), mixINA	hh68c08.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967950 3' similar to contains MEK29.b2	MER29 repetitive element;	Homo sapiens chromosome 21 segment HS21CU52	601810449F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053396 5	zp11f09.r1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE∷609161 5	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA	DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DNF2p761L1712.5	Human O family dispersed repeat element	Homo sapiens CGI-127 protein (LOC51646), mRNA	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA	Mus musculus mRNA for HGT keratin, partial cds	Homo sapiens PTEN (PTEN) gene, exon 2	Homo sapiens chromosome 21 segment HS21C103	GM0-NN1010-130300-281-d07 NN1010 Homo sapiens cDNA	ne92e10.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2	MER1 repetitive element;	ne06a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THK.b2 THR. repetitive element;	nf25h06.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST	P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA.;	zh65h07.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5	Mus musculus ctogelin (Otog), mRNA	QV2-LT0051-260300-111-f03 LT0051 Homo sapiens cDNA	EST391217 MAGE resequences, MAGP Homo sapiens cDNA	ye58h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5	PM3-OT0093-280200-001-907 OT0093 Homo sapiens cDNA	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)	Homo sapiens chromosome 21 segment HS21CU10
Top Hit Database Source	NT	NT		EST HUMAN	NT	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	TN	EST_HUMAN	NT	L	LN	EST_HUMAN		EST_HUMAN	EST HUMAN		EST_HUMAN	EST HUMAN	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	IN	NT	SWISSPROT	NT
Top Hit Acesslon No.	4.0E-24 AB029016.1	11418318 NT		3.0E-24 AW614871.1	3.0E-24 AL163252.2	3.0E-24 BF127762.1	2.0E-24 AA167539.1	2.0E-24 AW898189.1	2.0E-24 AL119158.1	2.0E-24 M28877.1	7706340 NT	1.0E-24 AW820194.1	1.0E-24 D86423.1	1.0E-24 AF143313.1		1.0E-24 AW901164.1		7.0E-25 AA483944.1	7 DE-25 AA468646.1		7.0E-25 AA583540.1	6.0E-25 W87623.1	7305360 NT	5.0E-25 AW838171.1	5.0E-25 AW979107.1	4.0E-25 T98107.1	4.0E-25 AW887671.1	4.0E-25 BE170957.1	8923321	8923321	P29622	3.0E-25 AL163210.2
Most Similar (Top) Hit BLAST E Value	4.0E-24	4.0E-24		3.0E-24	3.0E-24	3.0E-24	2.0E-24	2.0E-24	2.0E-24	2.0E-24	1.0E-24	1.0E-24	1.0E-24	1.0E-24	1.0E-24	1.0E-24		7.0E-25	7.0E-25			6.0E-25	6.0E-25	5.0E-25	5.0E-25				3.0E-25	3.0E-25		3.0E-25
Expression Signal	2.12	1.53		3.02	4.12	5.14	2.33	1.01	3.14	6.55	2.18	1.87	0.91	1.63	4.07	1.98		2.32	3,75		7.46	4.32	11.44	0.95		2.08	2.78	3.02	2.66			2.47
ORF SEQ ID NO:	25293				27463				27146		21438		22710		26484			24575			29045	L	26580			21201			22999			
Exon SEQ ID NO:	19121	19309	1_	16784	17258	L	1_		16952	L	1_	L	1_					14805	ļ		18750	15131	16401		L	L	1			1.		16733
Probe SEQ ID NO:	9206	9748		9069	7449	9587	2298	3729	7075	9433	1670	2638	2987	4173	6456	6633		4926	8705	3	8942	6174	6543	5166	8634	1430	3356	4221	3278	3278	4798	6854

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Cingle Lyon Flores Lybressed II Teal	Top Hit Acession Database Top Hit Descriptor Source	E165980.1 EST HUMAN MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA	L038487.1 EST_HUMAN DKFZp566C2146_r1 568 (synonym: hfkd2) Home sapiens cDNA clone (DKFZp566C2146 5	EST_HUMAN	FZ	SWISSPROT	naa03c07.xt NCL_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.tt F445556.1 EST_HUMAN OFR repetitive element:	EST HUMAN	Z NT	7.1 EST_HUMAN	EST HUMAN	3.1 EST HUMAN	SWISSPROT	- NT	1 EST_HUMAN	EST_HUMAN	8.0E-27 AW851519.1 EST_HUMAN CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA	AW 857579.1 EST_HUMAN CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA		7.0E-27 AW629172.1 EST_HUMAN O76040 ORF2: FUNCTION UNKNOWN.	J271735.1 NT Homo sapiens Xq pseudoautosomai region; segment 1/2	1 EST HUMAN	Ŋ	1	T_HUMAN	9910569 NT Mus musculus sperm tall associated protein (Stap), mRNA
Olivigio L	ession	-	+				-	EST	Z.	1.7				-	1 EST		EST	.1.				1 EST		1 EST	1 EST	9910569 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-26 BE165980	1.0E-26 AL038487	1.0E-26 H55093.1	9.0E-27 U93163.1	9.0E-27 P54296	9.0E-27 BF445556	1	8.0E-27	8.0E-27 AW16273	8.0E-27 AW162737	8.0E-27 A	8.0E-27 P12236	8.0E-27 AF181897	8.0E-27 BE926560	8.0E-27 N84970.1	8.0E-27 A	8.0E-27 A	7.0E-27 Z	7.0E-27 A	7.0E-27 AJ271735.	7.0E-27 AV723365	6.0E-27 M26697.1	5.0E-27 BF666614	5.0E-27 B	4.0E-27
	Expression Signal	2.75	3.17	1.84	3.11	3.48	3.97	3.09	4.13	18.87	18.87	0.98	3.31	0.91	3.12	4	1.68	1.68	1.22	2.09	4.22	2.07	6.21	2.92	2.92	1.54
	ORF SEQ ID NO:					28118		19787		21158	21159		22874	23035			27386							27970	27971	26080
	Exon SEQ ID NO:	16034	18146	19737	17342	19470	18812	9666	10486	11300	11300	\mathbb{L}_{-}	13073	13230	15122	15956			10602	14896	18020	19204		17727		15949
	Probe SEQ ID NO:	6809	8266	9493	7364	8027	9013	10	545	1395	1395	2121	3148	3309	6165	6196	7310	7310	899	5023	8132	9631	8109	7877	7877	6046

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Single Exon Probes Expressed

	Top Hit Descriptor	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	channel mKINA, complete cds	like element	a-pinding protein	7844C08 Chromosome 7 Eatel Brein, ChNA Hit.	A LINI 4 HOMO Sapiens CDNA clone 7844C08	is contactioned invace; sabzoac 5:	nk01b10.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN):	hI51h12.XI Soares_NFL_T_GBC_S1 Home sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN N	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, commete cds; and unknown account	BELLEVILLE GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GEN	Raffus nonvenients voltage and adversarial planted docts, clos gene, complete cds, and unknown gene	iannel mkina, complete cds	nh09Hb/st NCL CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.13 L1	1 10000	EST00738 Fefal brain Stratacene (cettables) to mono sapiens cDNA clone HFBCF07	clone MAMMA 4000746 E	nk01b10.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAI_PROTEIN P1 (411 MAN).	1/VIA	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	(20) x (100 x 1) 10 11 11 11 11 11 11 11 11 11 11 11 11	1900-1 (NFT-1), FIKINA	A COUNTY OF THE SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD 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SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD SHOULD	מייים פילטטטטער פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין איניין פין פין פין פין פין פין פין פין פין	parual cas	mo sapiens culvA	DAIA
Single Exon Probes Expressed in Heart		Battis porvedicis or trative four robont in plant in the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the	H saniene DNA for endocessing the	R rathus RVA3 mRNA for a natural licenal control	Τ	Т	Т	Г				Homo sapiens in almerization	Raffus nonequirus voltade acted codi.	Т		T	T	Π		Т	Homo sapiens DNA, DLEC1 to ORCTL4 g	Homo sapiens Refine-derived POI L-domain factor 4 (PDE 4)	Τ	Т	1	T	T	Bos fatture lafrophilin 3 chilon maint 11.
gle Exon Pı	Top Hit Database Source	FZ	L	L N	EST HIMAN	EST HUMAN	EST HUMAN	NT	EST_HUMAN	EST HUMAN	۲	Ę	IN	EST HUMAN		EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	NT	L L	トラ	EST HUMAN	EST HUMAN	TN	EST HUMAN	NT	NT
Sin	Top Hit Acession No.	4.0E-27 AF078779.1	4.0E-27 X89211.1	3.0E-27 X60658.1	3.0E-27 BE071924.1	3.0E-27 AA077705.1			2.0E-27 AA665345.1	2.0E-27 AW629172.1	2.0E-27 AF111167.2	2.0E-27 AF111167.2			5		2.0E-27 M78590.1	2.0E-27 AU121685.1	2.0E-27 AA565345.1	1.0E-27 AL163246.2	1.0E-27 AB026898.1	05855	1.0E-27 F30158.1	1.0E-27 F30158.1	_	7.		1.0E-27 AF111093.1
	Most Similar (Top) Hit BLAST E Value	4.0E-27	4.0E-27	3.0E-27	3.0E-27	3.0E-27	3.0E-27	2.0E-27	2.0E-27	2.0E-27	2.0E-27	2.0E-27	2.0E-27	2.0E-27	2.0E-27	2.0E-27	2.0E-27	2.0E-27	2.0E-27	1.0E-27	1.0E-27	1.0E-27	1.0E-27	1.0E-27	1.0E-27	1.0E-27	1.0E-27	1.0E-27
	Expression Signal	1.23	2.56	5.42	1.27	5.13	2.98	7.96	18.58	10.27	1.43	1.43	1.09	1.5	2.3	1.22	1.22	2.80	20.82	1.56	1.4.1	6.31	2.2	2.2	1.72	1.89	2.68	3.14
	ORF SEQ ID NO:		28985	21782	23849	24976	27549	19820			22916	22917	23627	26780		27847	27848	28450			20749	25972	26136	26137	27075	-	27672	29046
	Exan SEQ ID NO:	16536	18692	11889	14074			10023	11749	12998	13112	13112	13852	16592	17206	17618	17618	18201	11749	10374	10903	15848	15999	15999	16882	17071	17457	18751
	Probe SEQ ID NO:	9599	8880	1995	4174	5278	7365	36	1853	3071	3187	3187	3944	6712	7338	7768	7768	8324	8778	429	086	5943	6105	6105	7005	427	7606	8943

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Single Exon Probes Expressed in Heart	Top Hit Database Source		EST HUMAN AU128280 NT2RP1 Home senions CNN ATTENDED TR. 007280 TR. 007313	T		\top		\top	NICAMOLI	HIMAN	N. Carolina			EST_HUMAN repetitive element contains element PTR5 repetitive element;	EST HUMAN THR repetitive element:	1		\top		EST_HUMAN REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);		Felis catus GAPDH mRNA for oliveraldehene 3 should be in the locus and trypsinogen gene families	qf66f10.x1 Soares_tests.NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1			HOMAN	
Sing	Top Hit Acession No.	9.0E-28 BE348300 4		5.1	7.	29.1	8.0E-28 AW157571 1	Τ	7866	7.0E-28 AV735348.1				0.0E-20 AA304362.1 E	5		4.0F-28 AW105066 1				-029308.1 NT		1-			3588 1 FST	
	Most Similar (Top) Hit BLAST E Value	9.0E-28	9.0E-28	9.0E-28 AI59011	9.0E-28 AI59011	9.0E-28	8.0E-28	7.0E-28	7.0E-28	7.0E-28	6.0E-28	6.0E-28	L	0.05-20	5.0E-28	5.0E-28 R79762.1	4.0E-28	4.0E-28 B	4 OF 30	4.0E-20 A1198941	4.0E-28 AF029308.1	4.0E-28 AB038241.1	4.0E-28 AI198941	3 0F-28 AF4553924	3.0F-28 RF354030 4	3 0F-28 1153588 1	22,22
	Expression Signal	2.32	3.01	1.21	1.21	3.74	1.97	7.54	2.54	1.44	1.27	1.27.	27.0	213	3.08	1.85	1.42	3.39	<u>г</u>		4.29	53.6	2.94	1,89	2.19	1.84	
	ORF SEQ ID NO:		20089	24760	24761			20922	28660		23670	23671				23616	22347	22788	26359			+	26359		27193	28430	
	Exon SEQ ID NO:	10109	10270	14986	14986	18866	19592	11077	18395	18836	13894	13894	19232		10277	13836	12455	12997	16199		18119	18248	16199	11169	17001	18183	
	Probe SEQ (D NO:	136	308	5118	5118	9093	9418	1164	8523	9053	3987	3987	9673		315	392/	2584	3070	6336		8239	1000	8388	1262	7124	8306	

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Single Exon Probes Expresse

				7		_				1	1	т	1			_	_	Τ	7-			_			,	_			_
Single Exon Probes Expressed in Heart	Top Hit Descriptor	wj98f07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu	RC1_BT054_22000 045_26_BT552_1.	Home sapleme ITOB 2000 Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of th	qo35b06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains [1, b2 i 1	februaye element;	EST384394 MAGE resequences: MAGI Homo conjunctions	Homo sapiens mannosidase, beta A. Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3	Hilman gene for A rounder	0/4. BT0824 130000 250 Los BT502. 1	Homo sanians ultimitation TDB	Home capitals any durants In R matti, 1 isotom (UTY) mRNA, alternative transcript 2, complete cds	Homo saciens hypothetical protein L12 (H. sapiens) (LOC63091), mRNA	EST179615 HCC cell line (matastasis to liver in mouse) Il Homo sapiens cDNA 5' end similar to similar to	Jano conjunc	Home septents gantima-glutamytiransferase-like activity 1 (GGTLA1), mRNA	Profit of a spirits gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA	Hams carions of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract o	hi76n06 x1 Spares NET T GPC S4 U.	HYPOTHETICAL GENE 50 PROTEIN	EST378571 MAGE researchman MAGILL	Rattus norvegicus mRNA for 45 kDa secretory profess curdinal	wp69b01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR 015475	RO31/TORS 210000 024 - 05 1/T2222 Contains LTR7.61 LTR7 repetitive element;	602184092F1 NIH MGC 42 U	Homo saniens chromosomo 21	RC3-070091-170300-011-c12 OT0091 Home carriers CRNA	Ch15cn2 v4 Normal Linear T-1-1 addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition to the children addition addition to the children additi	QV1-HT0471-280300-121-a05 HT0471 Home Calls Home sapiens cDNA clone NHTBC_cn15c02 random
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Sin	Top Hit Acession No.	3.0E-28 A(831991 1	-					2.0E-28 AF224669 1		1.3		479885	8922793 NT	1.0E-28 AA308744 1	18434	4758434 NT	1.0E-28 AA054182 1		_		7.0E-29 AW966447.1					5.0E-29 AL163203.2			
	Most Similar (Top) Hit BLAST E Value	3.0E-28	2.0E-28	2.0E-28	2.0E-28	2.0E-28	2.0E-28	2.0E-28	1.0E-28 D38044.1	1.0E-28	1.0E-28	1.0E-28	1.0E-28	1.0E-28	1.0E-28	1.0E-28	1.0E-28 A	1.0E-28 A	9.0E-29 A	8.0E-29 Q00130	7.0E-29 A	7.0E-29 A	6.0E-29 A1936748 1	6.0E-29 BE940436.	6.0E-29 B	5.0E-29 AI	5.0E-29 AW887541.	4.0E-29 AI752367.1	4.0E-29 BE164930.1
	Expression Signal	2.44	6.45	10	2.7	4.28	5.86	2.27	2.42	1.55	1.03	4.48	3.02	2.63	5.15	5.15	3.95	1.43	2.6	2.92	0.91	5.08	6.52	3.88	1.86	0.98	7.61	1.68	6.65
	ORF SEQ ID NO:		19884	20905	22200			28992	21233	21963	22407			27413	27753	27754			24896		21349		20325						
	Exen SEQ ID NO:	19106	10067	11062	12304	15727	17379	18698	11368	12060	12517	16467	16555	17214	17528	17528	18840	19485	19691	19169	11488	19410	10518	19028	19076	14807	16945	13119	15568
	Probe SEQ ID NO:	9489	83	1149	2427	5821	7528	8887	1463	2173	2650	6587	6675	7346	7678	7678	9028	9797	9892	9585	1584	9942	580	9353	9438	4928	7068	3194	5656

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Table 4

Single Exon Probes Expressed in Heart	Top Hit Descriptor		riuman 90 kD heat shock protein gene, complete cds	Indus sapiens PTS gene for 6-pyruvoyttetrahydropterin synthase, complete cds	UV1-B10821-120900-360-b03 BT0821 Homo sapiens cDNA	xv17f03.x1 Soares_NFL_T_GBC_S1 Homo seniens cDNA clara IMA CT_And a CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES AND A CARAGES 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HS210048	Homo sapiens chromosome 21 segment HS21C048	Homo sopiens Chromosome 21 segment HS21C048	OVA OTRACE STORMOSTIC 21 segment HS21 C048	4V0-0 10032-080300-155-d01 OT0032 Homo sapiens cDNA	RC1-HN0003 20000 004 1 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	nz20c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE-17988322 21 in::	MER4 repetitive element;	Homo sapiens zincliron regulated transporter-like (ZIRTL), mRNA	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05	PT2.1 13 B11: fumor2 Homo senions cDNA 5' end similar to EST containing O family repeat	O UNIO CITALINA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA CALLA DE LA 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	Most Similar (Top) Hit BLAST E Value	4.0F-20	3.0F-29 AB0422	3,0E-29	3.0E-29 D38044	L	3.0E-29 AW3033	3 0E_20	3 0F-29 DE3882	2.0E-29 /	2.0E-29	2.0E-29	2 OE 20 V	2.0E-29 A	2.0E-29 A	2 OE 20 A	2.0E-29 A	2.0E-29 AL163248	2.0E-29 A	2.0E-29 A	2.0E-29 A	2.0E-29 AL163227	1.0E-29 A	9 0E-30 AA76124E 4	9 OF 30	8 OF 30 FORER 4	8.0E-30 AA383873	8.0E-30 AI557072.	
	Expression Signal	4.71	1.45	1.31	2.07	7	1.64	2.22	1.51	1.43	1.43	6.12	6.12	2.03	1.43	1.43	2.95	2.95	3.39	3.39	1.96	1.73	5.41	3.04	1.5	8.81	3.37	3.53	
	ORF SEQ ID NO:	27149	23997	24305	27138	27429		28728		20240	20241	21278	21279	23855	25765	25765	27539	27540	27973	27974			27174	25995			26880	27105	
	Exon SEQ ID NO:	16956	14214		16947	17229		18459	18959	10427	10427	11421	11421	14082	15658	15658	17334	17334	17729	17729	18618	18807	16982	15871	18889	15721	16691	16916	
	Probe SEQ ID NO:	7079	4317	4626	7070	7362	7492	8591	9248	484	484	1516	1516	4182	5750	6461	7474	7474	7879	7879	8804	9004	7105	9969	9132	5815		7039	

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Table 4 ·
Single Exon Probes Expressed in Heart

Single Exon Plones Expressed in near	Top Hit Descriptor	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA	Human lambda-immunoglobulin constant region complex (germline)	Human mRNA for integrin alpha subunit, complete cds	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA	Human lambda-immunoglobulin constant region complex (germline)	tg92g03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu	Impounded element.	man acumate nyulatase (NCCZ) gene, aku 1	Homo sapiens chromosome 21 segment HS21C078	Homo saptens chromosome 21 segment HS21C010	Homo sapiens chromosorne 21 segment HS21C010	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA	CM1-ST0181-091199-035-f08 ST0181 Homo sapiens cDNA	qq93c05.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to	contains MER29.b2 MER29 repetitive element	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6	TRANSCRIPTION FACTOR AP-2	CMO-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA	Homo sapiens Y-linked zinc finger protein (ZFV) gene, complete cds	UI-H-BI1-afo-c-12-0-UI.s1 NCI_CGAP_Sub3 Homo saplens cDNA clone IMAGE 2722558 3'	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5	C18939 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-570C01 5'	7e37c12.x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3284562 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE IL/BIOUINONELEI AVOPROTEIN SUBLINIT PRECUIRSOR		7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR;	EST383657 MAGE resequences, MAGL Homo saplens cDNA
e Exoli Piopes	Top Hit Database Source	EST_HUMAN PI	NT H	TN IN	EST_HUMAN Q	H. H.		ESI HUMAN				NT	EST_HUMAN Q	EST_HUMAN Q	EST_HUMAN C		EST_HUMAN cc	NT	SWISSPROT		EST HUMAN H		EST_HUMAN IL	NT H	EST_HUMAN U		EST HUMAN 60		76 PENT HUMAN	7	EST_HUMAN P	
Buic	Top Hit Acession No.	3.1			6.0E-30 BE008026.1								4.0E-30 AW937471.1 E	4.0E-30 AW937471.1	4.0E-30 AW812488.1		.1	3.1		15.1			2.0E-30 BE765232.1	2.0E-30 AF114156.1	31.1	5.1	5.1	1	7.1			2.0E-30 AW971568.1 E
	Most Similar (Top) Hit BLAST E Value	7.0E-30 BE09113	6.0E-30 X51755.1	6.0E-30 D25303.1	8.0E-30	6.0E-30	L	5.0E-30 AI39899Z	3.0E-30.C	5.0E-30 /	5.0E-30 /	5.0E-30 /	4.0E-30	4.0E-30 /	4.0E-30		3.0E-30 AI338551	3.0E-30 AF128893	3.0E-30 P34056	2.0E-30 AW8573	2.0E-30 F08688.1	2.0E-30 BE17587	2.0E-30 E	2.0E-30 /	2.0E-30/	2.0E-30 BE29894	2.0E-30 BE29894	2.0E-30 C18939.	2 0E-30 RE6706	7	2.0E-30 BE67061	2.0E-30
	Expression Signal	1.16	0.95	1.26	2.41	3.15		31.23	(35)	3.55	6.68	6.68	1.64	1.64	1.49		1.71	0.91	2.38	1.18	2:32	5.91	10.97	6.38	. 2.11	1.72	1.72	3.46	بر بر	2	1.55	3.3
	ORF SEQ ID NO:			21505	22878			73620			28632	28633	21880	21881	27231			23395	28675	20411		21234	22438	52609	23419	24346	24347	27036	27085			27814
	Exon SEQ ID NO:	11403	11454	11637	13078	11454		13840	732C61	18141	18368	18368	11985	11985	17039		11048	13611	18410	10593	10984	11369	12548	12816	13633	14554	14554	16844	16896			17593
	Probe SEQ ID NO:	1499	1549	1736	3153	9915		3931	cozc	8261	8495	8495	2096	2096	7162		1134	3697	8538	629	1068	1464	2683	2889	3721	4668	4668	9969	7019		7019	7743

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	Top Hit Descriptor	ha33406.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR b3 THR repetitive element ;	C18939 Human placenta cDNA (TFujlwara) Homo sapiens cDNA clone GEN-570C01 5'	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.8 MER1 MER1 repetitive element;	Homo sapiens chromosome 21 segment HS21C003	ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'	602022560F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157991 5'	Homo sapiens methionine aminopeptidase; elF-2-associated p67 (MNPEP), mRNA	EST186868 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end	601809932F1 NIH_MGC_18 Hamo sapiens cDNA clone IMAGE:4040694 5'	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA	Homo sapiens chromosome 21 segment HS21C008	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE.3182012 3'	Human lambda-immunoglobulin constant region complex (germline)	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sapiens MHC class 1 region	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'	RC5-BT0377-091299-031-D12 BT0377 Homo sepiens cDNA	601433087F1 NIH_MGC_72 Hamo sapiens cDNA clone IMAGE:3918524 5'	Homo sapiens type I DNA topoisomerase gene, exon 8	Homo sapiens type I DNA topoisomerase gene, exon 8	7k08f04.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR.Q13537 Q13537 SIMILAR TO POGO ELEMENT.; contains L1.t1 L1 repetitive element:	Homo sapiens Xq pseudoautosomal region; segment 1/2	POLYPEPTIDE N-ACETALGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GAINAC:T1)	Homo sapiens chromosome 21 segment HS21C080
or Tipy of	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	LZ	EST-HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	N	L Z	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN⊤	N L	EST HUMAN	N	SWISSPROT	LN
5	Top Hit Acession No.	2.0E-30 AW470791.1	1.0E-30 C18939.1	1.0E-30 AW468897.1	1.0E-30 AL163203.2	1.0E-30 AA664377.1	1.0E-30 BF347728.1	5803091 NT	1.0E-30 AA315045.1	1.0E-30 BF183230.1	H55593.1	9.0E-31 Z38293.1	8923389	8.0E-31 AL163208.2	7.0E-31 AA372637.1	BE326517.1	BE326517.1	7.0E-31 X51755.1	6.0E-31 AF223391 1	6.0E-31 AF055066.1	6.0E-31 AU119105.1	6.0E-31 AW372868.1	6.0E-31 BE894488.1	M60694.1	M60694.1	5.0E-31 BF056540.1	4.0E-31 AJ271735.1	010473	30.2
	Most Similar (Top) Hit BLAST E Value	2.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30	1.0E-30 H55593.1	9.0E-31	8.0E-31	8.0E-31	7.0E-31	7.0E-31 BE32651	7.0E-31 BE32651	7.0E-31	6.0F-31	6.0E-31	6.0E-31	6.0E-31	6.0E-31	5.0E-31 M60694.	5.0E-31	5.0E-31	4.0E-31	4.0E-31	4.0E-31
	Expression Signal	4.47	10.22	1.6	2.92	3.24	2.57	1.03	0.93	2:32	5.1	2.04	1.64	5.14	1.72	1.7	1.7	2.56	2.79	3.68	2.11	1.88	1.78	2.85	2.85	1.21	3.78	104	2.59
	ORF SEQ ID NO:	27889	20069	20281		21953	22187	66922	22736	26582			20820			22392		25272				25351		19973	19974			21357	
	Exon SEQ ID NO:	17652	10249	10469	10632	12052	12290	12300	12943	16403	19615	16890	10977	12242	10627	12500	12500	19168	13539	16618	18008	18926	19541	10157	10157	16793	10519	11498	11674
	Probe SEQ ID NO:	7802	284	527	669	2165	2413	2973	3015	6545	9733	7013	1060	2362	694	2633	2633	9583	3625	6239	8120	9191	9319	185	185	6915	581	1594	1775

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Single Exoll Plobes Expressed in near	Top I-fit Descriptor	DKFZp547B235_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547B235 5'	MR3-ST0220-151299-028-a08_1 ST0220 Homo sapiens cDNA	Homo sapiens minisatellite ceb1 repeat region	qf21h03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595 Q16595 FRATAXIN. ;	Human familial Alzheimer's disease (STM2) gene, complete cds	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5	oz15a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384.3'	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)	Human chromosome 22 immunoglobulin V(K)I gene, part. with 5' breakpoint between orphon and neighbouring non-amplified region	tm34a10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159994 3' similar to contains MER29 t3	MEK29 repetitive element;	601511530F1 NIH MGC_71 Home sapiens cDNA clone IMAGE;3913087 5	Homo sapiens PRO1181 mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA	Homo sapiens FLI-1 gene, partial	AV731500 HTF Homo sapiens cDNA clone HTFAKC07 5'	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'	zi95a07.s1 Soares, fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE.448500 3' similar to contains THR.t3 THR repetitive element;	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4	(MLLT4) mRNA	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5	H.sapiens mRNA for myosin	H.sapiens mRNA for myosin
JIE EXOII FIOD	Top Hit Database Source	HUMAN	EST HUMAN	NT	EST HUMAN	Г	EST HUMAN	HUMAN	SWISSPROT	LN.		HUMAN	T HUMAN	NT	NT			NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	Π					T_HUMAN	L	L
Silic	Top Hit Acession No.	1.0E-31 AL134376.1	1.0E-31 AW391679.1	7.1	\l086434.1		6.1	8.0E-32 Al056770.1	52591				3.1		4.0E-32 AL163246.2	11432574 NT	11432574 NT	(17293.1	4V731500.1	4V758634.1	10758634.1	AA777621.1	3E279086.1	5174574 NT		5174574 NT	3E279086.1	3E296613.1	238133.1	238133.1
	Most Similar (Top) Hit BLAST E Value	1.0E-31	1.0E-31	1.0E-31 AF04872	1.0E-31 Al086434	9.0E-32 U50871.1	9.0E-32 AV72397	8.0E-32	7.0E-32 P52591	7.0E-32 X17283.1	1	6.0E-32 AI478104	6.0E-32 BE88801	5.0E-32 AF11662	4.0E-32	4.0E-32	4.0E-32	3.0E-32 Y17293.1	3.0E-32 AV731500	3.0E-32 AV75863	3.0E-32 AV75863	3.0E-32 AA77762	3.0E-32 BE27908	3.0E-32		3.0E-32	3.0E-32 BE27908	2.0E-32 BE29661	2.0E-32 Z38133.1	2.0E-32
	Expression Signal	1.01	3.15	1.87	2.72	66'0	2.34	3.32	1.17	2.77		6.0	1.5	29.57	1.74	2.82	2.82	3.4	79.7	6.73	6.73	8.08	3.04	2.43		2.43	4.94	0.91	19.01	19.01
	ORF SEQ ID NO:	24210	24927	25738	28411		26029	21815	24426			22456		20779		26510	26511	20213	21210	27477	27478	28421		24882		24883		24454	25929	25930
	Exon SEQ ID NO:	14428	15159	15635	18167	12763	15905	11923	14639	18972	Ì			10936	10839		16342	10392	11343	17271	17271	18176	18995	15090		- 1		14667	15806	15806
	Probe SEQ ID NO:	4535	5235	5728	8288	2835	0009	2032	4754	85268		2702	6329	1018	915	6484	6484	448	1438	7404	7404	8297	9294	9655		9655	9802	4783	5900	2900

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	Top Hit Acess No	AA114294.1	AA114294.1	AV736449.1	AV736449.1	BE743299.1	11439,		BE327112.1	AF223391.1	BF347229.1	AL163280.2	50317	50317	A1500115 1	AV730058 1	AV730015.1	AW971307.1	BF347229.1	AW971568.1	AA601416 1	AL163285.2	J04038.1		67556	67556	BF373515.1	111418	45072	45072
	Most Similar (Top) Hit BLAST E Value	2.0E-32	2.0E-32	2.0E-32	2.0E-32		1.0E-32		9.0E-33		9.0E-33	9.0E-33		7.0E-33	7.0F-33	7 0F-33	7.0E-33	7.0E-33	7.0E-33	7.0E-33	7.0F-33	6.0E-33	6.0E-33	6.0E-33	6.0E-33	6.0E-33	5.0E-33	5.0E-33	5.0E-33	5.0E-33
	Expression Signal	3.41	3.41	1.61	1.61	1.06	7.04	5.18	4.98	4.19	1.99	5.89	2.06	2.06	17.6	8.4	1.78	12.85	3.9	2.15	3.43	0.85	13.52	2.57	124	1.24	1.78	1.18	1.37	1.37
	ORF SEQ ID NO:	26884		25175	25176		26090	27065			27172		19850	19851	21902		21439		28338	28709	25322		27059	27117	27822	27823			21626	21627
	Exon SEQ ID NO:	16694		19385			15958	16874	13352	15773	16980	18065	10041	10041	12004	1	11573	13128	18087	18441	18978	13590	16865	16926	17600	17600	11640	11735	11752	11752
	Probe SEQ ID NO:	6815	6815	8066	9908	3055	6198	6997	3435	5867	7103	8177	54	54	2115	2612	2800	3204	8203	8573	9274	3676	6988	7049	7750	7750	1739	1838	1856	1856

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Probe SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ	Exon SEQ ID NO: 121111 11027 11027 11027 14278 16399 14899 1775 17138	21861 22265 24565 24666 24669 24669 24669 24669 25894	Signal Signal Signal Signal 1.62 1.62 1.77 1.77 1.73 1.75 1.63 1.77 1.63 1.77 1.63 1.77 1.77 1.73 1.74 1.74 1.74 1.74 1.74 1.74 1.74 1.74	Most (Top Hit Acession No. No. AL163285.2 AL163207.2 AL163210.2 AN293349.1 AL163210.2 AW293349.1 AL163210.2 AW29339.1 AA053053.1 AV647851.1 AV647851.1 AV647851.1 AV647851.1 AV647851.1 AN60189.1 BE159039.1 A1421332 AI277492.1 AI052256.1 AF003528.1	Top Hit Database Source NT NT NT NT NT EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN NT EST_HUMAN EST_HUMAN NT EST_HUMAN	Homo sapiens chronosome 21 segment HS210085 Homo sapiens chronosome 21 segment HS210085 Homo sapiens chromosome 21 segment HS210085 Homo sapiens chromosome 21 segment HS210085 Homo sapiens chromosome 21 segment HS210007 Homo sapiens chromosome 21 segment HS210007 Homo sapiens chromosome 21 segment HS210007 Homo sapiens chromosome 21 segment HS210010 UIH-BIC-ahl-c-03-0/UIH Colling Sub MER28 repetitive element; Homo sapiens chromosome 21 segment HS210010 UIH-BIC-ahl-c-03-0/UIH Colling Sub Homo sapiens cDNA clone IMAGE: 2127149 3: 217408.17 Stratagene colon (#387204) Homo sapiens cDNA clone IMAGE: 510038 6' similar to abx.12671_inal HETEROGENEOUS NUOLEAR RIBONUCLEOPROTEIN A1 (HUMAN); Homo sapiens killer cell immunoglobulin-like receptor, three domains, long cytopiasmic tail. 1 (KIR3DL1), mRNA HNOSOT XI NCI. CGAP Kild 3 Homo sapiens cDNA clone IMAGE: 3146256 3' similar to contains MER29 repetitive element; Homo sapiens colon (#387204) Homo sapiens cDNA clone IMAGE: 3146256 3' similar to contains MER29 repetitive element; MER29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element; HRR29 repetitive element;
8637	18502	28778	2.02		1.0E-33 AW996818.1	EST_HUMAN	QV3-BN0047-230200-102-b03 BN0047 Homo sepiens cDNA
8921	18729	29024	5.33		1.0E-33 U60822.1		Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
9553	19151		1 92		1.0E-33 AI927191.1	EST HUMAN	wo88c06.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2452410 3
9553	19151		1.92		AI92/191.1	HOLL HOMAIN	WOSSCUD.XT INCLEGAPENIET FROM SAPIENS CLIVA CIONE INVAGE: 2402410 3

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Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	nea33a08.x1 NCI_CGAP_Kid71 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:075912 075912 DIACYLGLYCEROL KINASE IOTA.;	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'	601236468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'	602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300660 3'	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA	ah53h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'	Homo sapiens zinc finger protein 208 (ZNF208), mRNA	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA	Homo sapiens mRNA for KIAA1365 protein, partial cds	H. sapiens immunoglobulin kappa light chain variable region L14	Homo sapiens clk2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and metaxin genes, complete	dds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial	spo	601431984F1 NIH_MGC_72 Homo saplens cDNA clone IMAGE:3917229 5	4g38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN 092539 HYPOTHETICAL PROTEIN KIAAA0240	qg38c05.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE-1837448 3' similar to	SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249.;	zh84f12.r1 Soares_fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015.5	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'	yu98a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains	PTR5 repetitive element;	601300705F1 NIH MGC_Z1 Homo sapiens cDNA clone IMAGE:3635401 5	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3	DIKETAGAI 148 11 434 (eumonum htees) Homo conjune conjune	2011 STATE OF THE WAST BURNEY OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE O	COLLECTION THIS WIGGE HOURS SELIENS CLINA CIONE IMAGE: 3345063.5	Homo sapiens phospholipid scramblase 1 gene, complete cds	MR1-TN0045-130900-010-e01 TN0045 Homo sapiens cDNA	7n25a09.x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2:	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2.;	
gle Exon Pro	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	EST_HUMAN	TN	IN	NT	NT				EST_HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN		EST HUMAN	ESI HUMAN	MANNET TOT	EST HIMAN	EST HIMAN	יייייייייייייייייייייייייייייייייייייי	Z	EST_HUMAN	EST_HUMAN	EST_HUMAN	
	Top Hit Acession No.	8.0E-35 BF589937.1	8.0E-35 BF183195.1	8.0E-35 BE378480.1	8.0E-35 BF569282.1	11425417 NT	6.0E-35 AA757115.1	6005975 NT	6005921 NT	6.0E-35 AB037786.1	X63392.1			5.0E-35 AF023268.1	5.0E-35 BE890992.1	5.0E-35 A 208765.1				4.0E-35 BE257907.1			4.0E-30 BE409102.1	4 OE-35 BE350107 1				-	3.0E-35 BF376402.1	3.0E-35 BF433100.1	3.0E-35 BF433100.1	
	Most Similar (Top) Hit BLAST E Value	8.0E-35	8.0E-35	8.0E-35	8.0E-35	7.0E-35	6.0E-35	6.0E-35	6.0E-35	6.0E-35	5.0E-35 X63392.1	-	l d	5.0E-35	5.0E-35	5.0E-35/		5.0E-35	5.0E-35	4.0E-35	!	4.0E-35 H91193.1	4.UE-30.	4.05.35	4.0E-35/	3 OF 35 F	20.00	3.05-35/	3.0E-35	3.0E-35	3.0E-35	
}	Expression Signal	3.3	3.09	3	3.49	1.52	1.28	1.78	3.6	2.7	2.29	-	(2.2	3.14	2.18		2.18	3.42	14.91	,	5.7	67:	00.7	6.84	9 63	2 40	2.42	1.06	22.73	22.73	
	ORF SEQ ID NO:	21476	24435	28217					26676	27771	21454			23892		26848		26849		21186		72217			27030	21324			24465	24971	24972	
	Exan SEQ ID NO:	11604	14646	17966	18969	15811	11296	11820	16490	17548	11583		0007	14208	16640	16658		16658	18389	11321	L	17077	+ 0+	16144	16835	11466	10167	/0171	14678	15197	15197	
	Probe SEQ ID NO:	1703	4761	8075	9265	5905	1391	1925	6610	7698	1681			154	6/61	6779		6779	8517	1415	110	17.70	21-00	6280	2992	1561	2363	2203	4793	5275	5275	

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Table 4
Single Exon Probes Expressed in Heart

					_		-	_	10	T (0				_		<u> </u>	_	,	_ -			_	11.11		_	10000	Mag 1	<i>.</i>	-20.00	tarie sum
	Top Hit Descriptor	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT	A971F Heart Homo sapiens cDNA clone A971	Homo sapiens mRNA for Gab2, complete cds	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA	Homo sapiens Grb2-associated binder 2 (KIAA0571) mRNA	Homo sapiens mRNA for KIAA0895 protein, partial cds	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project≍TCBA Homo sapiens cDNA clone TCBAP4328	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project∺TCBA Homo sapiens	cDNA clone TCBAP4328	yq19a12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone INAGE 274079 5	QV0-BT0701-210400-199-b04 BT0701 Home sapiens cDNA	H.sapiens PROS-27 mRNA	Homo sapiens Grb2 associated binder 2 (KIAA0571) mRNA	Homo sapiens Grb2-associated binder 2 (KIAA0571) mRNA	601496774F1 NIH MGC 70 Homo sabiens cDNA clone IMAGE: 3808600 F	601496774F1 NIH MGC 70 Home sapiens cDNA clone IMAGE 3898695 5	Homo sapiens chromosome 21 segment HS21C010	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' sImilar to	REPETITIVE ELEMENT	finite16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12.1	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA	IL2-ST0162-131099-006-412 ST0162 Homo sapiens cDNA	yd93a01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to	STATES AT THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE ST	House Septens hypometical protein (LOC31233), mRNA	incept 1x1 NC_CGAP_Ma13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.53 MER29 repetitive element ;	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29 b3 MER29 repetitive element;
910 - 1100 - 018	Top Hit Database Source	F	EST HUMAN	EST HUMAN	NT	NT	N	LN	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	N	NT	NT	EST HUMAN	EST HUMAN	NT		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TOT TOTAL	TOWN		EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	3.0E-35 AF223391.1	2.0E-35 N88965.1	2.0E-35 T11909.1	2.0E-35 AB018413.1	6912459 NT	6912459 NT	2.0E-35 AB020702.1	2.0E-35 BE247575.1		2.0E-35 BE247575.1	2.0E-35 H49239.1	3F332417.1	X59417.1	6912459 NT	6912459 NT	2.0E-35 BE904978.1	2.0E-35 BE904978.1	2.0E-35 AL163210.2		V88965.1	1.0E-35 AA631949.1	1.0E-35 AA631949.1	1.0E-35 AW389473.1	1.0E-35 AW389473.1	87047 1	7705004 NT	∼ I	3E350127.1	3E350127.1
	Most Similar (Top) Hit BLAST E Value	3.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35		2.0E-35	2.0E-35	2.0E-35	2.0E-35 X59417.1	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	I	2.0E-35 N88965.1	1.0E-35/	1.0E-35 /	1.0E-35/	1.0E-35 /	1.0F.35	1 0F-35	33	1.0E-35 BE350127	1.0E-35 BE350127
	Expression Signal	1.81	1.74	1.25	5.2	26.0	76.0	0.88	1.09		1.09	2.55	1.66	3.72	1.36	1.36	1.51	1.51	3.97	!	4.17	4.38	4.38	44.43	44.43	1	234	i	1.11	1.11
	ORF SEQ ID NO:		19902	20928		22991	22992		23539		23540		25401	28312	22991	22892	25354	25355			19902	19828	19829	20500	20501		22262		22496	22497
	Exon SEQ ID NO:	17325	12659	11083	12058	13193	13193	13427	13747	!	13/4/	14462	15347	18063	13193	13193	18936	18936	19264	L	12659	10028	10028	10667	10667	10817	12369		12602	12602
	Probe SEQ ID NO:	7465	103	1171	2171	3272	3272	3511	3835	000	3835	4570	5426	8175	9028	902B	9205	9206	9725	0000	3832	₽	₽	735	735	891	2495		2740	2740
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Table 4
Single Exon Probes Expressed in Heart

		T		T	T	Τ		Τ	T	T	T	\top	Τ	Т	Τ	Τ	Τ	T		T	Ť		z	T	1		T	Τ	Τ	7	T	Ť	T
Ougle Lyons Lybrassed III IRall	Top Hit Descriptor	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA	AV650422 GLC Homo sapiens cDNA clone GLCCEF06 3'	AV650422 GLC Homo sapiens cDNA clone GLCCEF06 3'	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'	AU158595 PLACE3 Hamo sapiens cDNA clone PLACE3000382 3'	promma-7.D01.r bytumor Homo sapiens cDNA 5'	Homo sapiens hypothetical protein (LOC51233), mRNA	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA	601584833F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE 3938985 5	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA	Human carcinoembryonic antigen gene family member 12 (CGM12) gene exons Land I /N	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, expns. Land I /N	Homo sapiens glutathione transferase A4 gene. exon 1	Homo sapiens ninjurin 2 (NINJ2), mRNA	Homo sapiens TCL6 gene, exon 12	UI-H-BW1-anv-c-12-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE 3083542 3'	th93b06.x1 Soares_NSF_F8_9W_OT_PA_F_S1 Homo saplens cDNA clone IMAGE:2126195.3' similar to gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECLISSOR (HIMAN):	hoo6h02.x1 NCL_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN P52292 IMPORTIN ALPHA-2 SUBLINIT	Homo sapiens syncytin precursor, mRNA, complete cds	#95c09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024.3' similar to contains MER9.b2	MER9 repetitive element;	601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5	Homo sapiens Xq pseudoautosomal region; segment 1/2	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens API5-like 1 (API5L1), mRNA	Homo sapiens API5-like 1 (API5L1), mRNA	Homo saplens Xq pseudoautosomal region; segment 1/2
are LAUIT 10	Top Hit Dalabase Source	N	EST HUMAN	EST HUMAN	LN	LN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	FN	LN	EST HUMAN	EST HUMAN	NT	N	LN	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	LN		EST_HUMAN	EST_HUMAN	NT	EST HUMAN	NT	N L	L	NT
5	Top Hit Acession No.	E006030 NT	AV650422.1	1.0E-35 AV650422.1	7656905 NT	7656905 NT	11526236 NT	1.0E-35 AU158595.1	AU158595.1	A1525119.1	7705994 NT	11418110 NT	1.0E-35 BE792832.1	AW857579.1	4557498 NT	J06672.1	J06672.1	AF052051.1	7706622 NT	6.0E-36 AB035346.1	3F515101.1	11435169.1	6.0E-36 AW 780143.1	AF208161.1					5.0E-36 BE388436.1	2	5729729 NT	5729729 NT	
	Most Similar (Top) Hit BLAST E Value	1.0E-35	1.0E-35 AV65042	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35 AU15859	1.0E-35 AI525119	1.0E-35	1.0E-35	1.0E-35	7.0E-36 AW85757	7.0E-36	7.0E-36 U06672.1	7.0E-36 U06672.1	7.0E-36 AF05205	6.0E-36	6.0E-36	6.0E-36 BF515101	6.0E-36 AI435169	6.0E-36	6.0E-36 AF208161		6.0E-36 AI380499	6.0E-36	5.0E-36	5.0E-36	5.0E-36 AL163209	5.0E-36	5.0E-36	5.0E-36 AJ271735.
	Expression Signal	1.07	2.2	2.2	4.7	4.7	1.43	2	2	4.16	1.69	1.37	2.26	0.94	4.03	6.04	6.04	5.23	1.88	6.17	0.91	19.79	3.34	2.21		2.74	1.69	69.9	7.71	1.96	1.42	1.42	2.64
	ORF SEQ ID NO:	22826	22848	22849	24003		25154		57579		22262			22622		26548	26549	25279	21741		23290	24965	26237	27096		28931	25071	19928	22478	23264	24358	24359	19928
	Exon SEQ ID NO:	13030	13051	13051	14222	14222	15301	19469	19469	18782	12369	18971	19198	12827	13007	16371	16371	19071	11854	12247	13501	15190	16087	16904		18646	19580	10107	12584	13475	14564	14564	10107
	Probe SEQ ID NO:	3104	3126	3126	4325	4325	5382	7501	7501	8977	9186	9267	9620	2900	3080	6512	6512	9423	1959	2367	3587	5268	6221	7027	0	8833	9821	133	2722	3561	4678	4678	9026

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Single Exon Probes Expressed in Heart	ORF SEQ Expression (Top) Hit Top Hit Acession (Top) Hit Top Hit Acession Signal BLASTE No. Source Source	25337 2.36 5.0E-36 11417862 NT Homo sapiens calcineutip binding profess 17(k) 8.03283 - 131.4	1.43 4.0E-36 BE010038.1 EST HUMAN	21196 1.54 4.0E-36 P10266 SWISSPROT	21389 1.58 4.0E-36 BE382574.1 EST HUMAN	EST HUMAN	3.21 4.0E-36 BE389299.1 EST HUMAN	3.21 4.0E-36 BE389299.1 EST HUMAN	2.21 4.0E-36 11497041 NT	1.74 4.0E-36 M33320.1 NT		L Z	4.0E-36 AA400370.1 EST HUMAN	11420516 NT	4.0E-36 AV753629.1	3.0E-36 AF099810.1	3.0E-36 7662401 NT	5.15 3.0E-36 10181139 NT	1.78 3.0E-36 RE035307.1 ECT LIMANI	2.7 2.0E-36 BE259267 FST HIMAN	4.62 2.0E-36 AW 880376.1	2.16 2.0E-36 AF267747.1 NT	3.99 2.0E-36 T08756.1 EST HUMAN	11.82 2.0E-36 T69629.1 EST HUMAN	1.9 1.0E-36 BE409310.1 EST_HUMAN	0.86 1.0E-36 BE146523.1 EST HUMAN	0.86 1.0E-36 BE146523.1 EST HUMAN	21942 1.31 1.0E-36 BF673761.1 EST_HUMAN 602136493F1 NIH_MGC 83 Homo sablens cDNA clone IMA GF: 4272888 F		5.94 1.0E-36 AI867714.1 EST HUMAN	2.03 1.0E-36 AA148034.1 [EST_HUMAN	2.03 1.0E-36 AA148034.1 EST_HUMAN	2.84 1.0E-36 AW 103658.1 EST HUMAN	27917 4.06 1.0E-36 BF364169.1 EST_HUMAN QV3-NN1023-010600-199-h01 NN1023 Homo sapiens cDNA
		25337	20961	21196	21389		23036	23037	25704	26547	27050	27051	28481			20437	22033	24081	28584	22857	24534	25127	25556	25989	20643	21884	21885	21942			26711	26712	2/28/	27917
	Exon SEQ ID NO:	19010	11115	11329	11530				_			i		19015	19545	10614	12136		L	13057	14757	15291	15483	15867		- [11987	12043	7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	13000	16520	16520	76071	1/6/4
	Probe SEQ ID NO:	9318	1205	1424	1626	2175	3310	3310	5693	6511	6269	6979	8356	9334	9380	681	2252	4402	8452	3132	4877	5371	5567	2962	867	2098	2098	2155	5750	20.10	0640	2220	7007	1824

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Top Hit Acession De No. S S NW 897636.1 EST NW 807636.1 EST NW 8076313.2 NT NW 226723.1 NT AR009277.1 EST NW 22618.1 EST BESS8077.1 EST BESS8077.1 EST BESS8077.1 EST BESS8077.1 EST BESS8077.1 EST BESS8077.1 EST BESS8077.1 EST BESS8077.1 EST BESS8077.1 EST BESS8077.1 EST BESS8077.1 EST BESS8077.1 EST BESS8077.1 EST	(Top) Hit BLAST E Value Value 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-36 A 1.0E-37 A 1.0E-36 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-37 A 1.0E-3	8 - 4 0 - 0 0 0 0 0 8	Signal Signal 3.44 1.1.2 2.7 1.1.2 2.7 1.1.3 2.7 1.1.3 2.7 1.1.3 3.0 0.2 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0.3 3.0 0		
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	AA307123.1	5.0E-37 AA307123.1	5.0E-37 AA30712	3.37 5.0E-37 AA30712	15615 25716 3.37 5.0E-37 AA30712
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1.0	AW961150	3.0E-37 AW961150	1.7 3.0E-37 AW961150	1.7 3.0E-37 AW961150	12341
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7-1-1	AL042800.1 ES AL042800.1 ES AR307720.1 ES AF202723.1 NT AA307723.1 ES AA307723.1 ES AA307723.1 ES AA307723.1 ES AA307723.1 ES AA307723.1 ES AA4048956.1 ES AU961150.1 ES AW961150.1 ES	AIR 17700 AIR 17700 AIR 17700 AIR 17700 AIR 17700 AR 30712 AR 30712 AR 30712 AR 30712 AR 30712 AR 30712 AR 30712 AR 30712 AR 30712 AR 30712 AR 30712 AR 30712	7.0E-37 AL042800 7.0E-37 AI817700 6.0E-37 AF202723 5.0E-37 AA307122 5.0E-37 AA307122 5.0E-37 AA70279 4.0E-37 AA70279 3.0E-37 AL048956 3.0E-37 AW96116	6.77 7.0E-37 AL042807 4.16 7.0E-37 AL042807 4.16 7.0E-37 AF307720 2.48 6.0E-37 AA507722 3.37 5.0E-37 AA307722 4.17 5.0E-37 AA70279 2.23 4.0E-37 AA70279 2.23 4.0E-37 AA70279 2.28 3.0E-37 AL048956 2.86 3.0E-37 AW96115	18028 28274 6.77 7.0E-37 AL042500 18148 28388 4.16 7.0E-37 Al536702 15615 25716 3.37 5.0E-37 AA30712 15615 25717 3.37 5.0E-37 AA30712 18171 4.17 5.0E-37 AA30712 18931 3.57 5.0E-37 AA30712 15027 2.23 4.0E-37 AA30712 15027 1.11 4.0E-37 AA30712 15027 2.23 4.0E-37 AA30579 11863 21755 2.85 3.0E-37 AL048956 12341 1.7 3.0E-37 AL048956 12341 1.7 3.0E-37 AW96116 12863 3.0E-37 AW96116

Page 206 of 413
Table 4
Single Exon Probes Expressed in Heart

Oligie Lyol Flores Lyplessed III Igan	st Similar Top Hit Acession Database Source Source	.1 EST_HUMAN	2.0E-37 AU131202.1 EST_HUMAN AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5	2	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylasse, cerebrotendinous years) A403240 NT santhomatoris, polygod the mRNA	AA346720.1 EST HUMAN	BF204032.1 EST_HUMAN	LN	2.0E-37 11417972 NT Homo saplens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	1.0E-37 AL163281.2 NT Homo sapiens chromosome 21 segment HS21C081	1.0E-37 AF189011.1 NT Homo sapiens ribonuclease III (RN3) mRNA, complete cds	EST_HUMAN		1.0E-37 AA171406.1 EST_HUMAN contains L1.t2 L1 repetitive element;	1.0E-37 M22878.1 NT Human somatic cytochrome c (HC1) processed pseudogene, complete cas	1.0E-37 BE771814.1 EST_HUMAN CM3-FT0096-140700-243-d07 FT0096 Homo sapiens cDNA	9.0E-38 10048482 NT Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA	1436955 NT	BF346221.1 EST_HUMAN	8.0E-38 11436955 NT Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA	EST_HUMAN	T_HUMAN	11425114 NT	6.0E-38 11425114 NT Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA	5947 NT	6.0E-38 AB002059.1 NT Homo sapiens DNA for Human P2XM, complete cds	5.0E-38 AW971819.1 EST_HUMAN EST383908 MAGE resequences, MAGL Homo sapiens cDNA	5.0E-38 AJ237740.1 NT Homo sapiens RIBIIR gene (partial), exon 8	0.1 EST HUMAN	4.0E-38 Z25466.1 NT B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS	Z25466.1 NT	1435947 NT	3.0E-38 AF003530.1 NT Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
	Most Similar (Top) Hit Top Hii BLAST E Value	2.0E-37 AU131;	2.0E-37 AU131.	2.0E-37 AL1632	2 OE.37	2.0E-37 AA346;	2.0E-37 BF2040	2.0E-37 AF1760	2.0E-37	1.0E-37 AL1632	1.0E-37 AF1890	1.0E-37 BE872.	1.0E-37 BF371;	1.0E-37 AA171	1.0E-37 M2287	1.0E-37 BE771	9.0E-38	8.0E-38	8.0E-38 BF346	8.0E-38	7.0E-38 AW972	6.0E-38 BF0330	6.0E-38	6.0E-38	6.0E-38	6.0E-38 AB002(5.0E-38 AW971	5.0E-38 AJ2377	5.0E-38 BE871	4.0E-38 Z 25466	4.0E-38 Z25466	3.0E-38	3.0E-38 AF003
	Expression Signal	1.94	1.94	1.47	503	3.36	3.23	16.4	3.15	3.61	22.51	96.0	2.13	2.85	20.59	2.46	3.05	1.95	1.44	1.36	1.38	1.76	1.69	1.69	4.46	6.66	1.15	1.79	2.42	2.56	2.56	0.82	4.39
	ORF SEQ ID NO:	20824	20825	21695	23510	26039	26759	28945		21828	23577	23753	24517	27141	28222	-	25514	20959	22225	20959	21920	22726	25407	25408		25286	20468	22178	26225	19909	19910	20897	
	Exon SEQ ID NO:	10980	10980	11816	13730		<u> </u>	18657	19403	11932	13789	13974	14737	16949	17973		15447]	12326		12023		15352	15352	18842	19143	10642	12281	16076	10092			11943
	Probe SEQ ID NO:	1064	1064	1921	2818F	2009	6685	8845	9933	2041	3878	4072	4857	7072	8082	9508	5530	1203	2449	9568	2135	3005	5432	5432	0906	9542	710	2404	6191	113	113	1141	2053

Page 207 of 413 Table 4 Single Exon Probes Expressed i

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Top Hit Descriptor	Homo sapiens HIRA interacting protein 4 (dnaJ-like) (HIRIP4), mRNA	SSU72 PROTEIN
 | zw30d01.r1 Soares ovary tumor NbHOT Homo saplens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1.2-MANNOSIDASF | 2w30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to | MP2 HTM27 160300 442 - 24 HTM201 L-ULGGGGGCCHANIOE ALLTIA-1,2-MANNOSIDASE | MR3-H 10487-150200-113-501 H 10487 Homo sapiens cDNA

 | hu09g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:002710 002710 GAG POLYPROTEIN.; | Homo sapiens mRNA for KIAA0145 protein, partial cds | QV2-HT0698-080800-293-a05 HT0698 Homo sapiens cDNA | Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds | Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA partial eds
 | AV726988 HTC Homo sapiens cDNA clone HTCAXH07 5 | Homo sapiens gene for kinesin-like protein, complete cds | CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22 788 5' | E1 beta=pyruvate dehydrogenase beta {promoter} [human, placenta, Genomic, 1280 nt] | Homo sapiens sulfotransferase-related protein (SULIX3), mRNA
 | zu62b02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
MER19 repetitive element : | Homo sapiens guanline nucleotide binding protein-like 1 (GNL1) mRNA | Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
 | Homo sapiens cyclin K (CCNK) gene, exon 7 |
| Top Hit
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 | 2.0E-38 | 2.0E-38 | 2.0E-38 | 2.0E-38 | 2.0E-38
 | 1.0E-38/ | 1.0E-38 | 1.0E-38
 | 1.0E-38 AF27083 |
| Expression
Signal | 1.11 | 1.65 | 1.65 | 0.85 | 7.17 | 7.64 | 1.78 | 1.78 | 1.58 | 1.41 | 2.6
 | 1.66 | 1. | 4.7 | 4.7

 | 1.47 | 1.66 | 5.24 | 3.69 | 3.69
 | 4.05 | 2 | 3.86 | 2.26 | 2.56
 | 2.29 | 0.94 | 1
 | 1.58 |
| ORF SEQ
ID NO: | | 23480 | 23481 | | 26083 | 26504 | 27094 | 27095 | | 19836 | 21120
 | 21390 | 21391 | | +

 | | 28063 | 28885 | 29008 | 29009
 | | | 25313 | |
 | | 21736 | 21758
 | 22221 |
| Exon
SEQ ID
NO: | 13552 | 13693 | 13693 | 14406 | 19459 | ١ | | 16902 | 17577 | 10032 | 11264
 | 11531 | 11531 | 16819 | 8 00

 | 17192 | 17820 | 18596 | 18715 | 18715
 | 18876 | 18878 | 19064 | 19099 | 19396
 | 10993 | 11849 | 11866
 | 12322 |
| Probe
SEQ ID
NO: | 3638 | 3781 | 3781 | 4513 | 6050 | 6478 | 7025 | 7025 | 7727 | 44 | 1358
 | 1627 | 1627 | 6041 | 160

 | 7316 | 7970 | 8781 | 8907 | 8907
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Table 4
Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens mRNA for KIAA1442 protein, partial cds	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA	Mus musculus otogelin (Otog), mRNA	Mus musculus otogelin (Otog), mRNA	Homo sapiens mRNA for KIAA0612 protein, partial cds	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element:	Homo saplens chromosome 21 segment HS21C084	Homo sapiens ATPase, H+ transporting, Ivsosomal (vacuolar proton primp) 16kD (ATPAC) mRNA	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (FRAGO) mRNA	wh53f10.x1 NCI_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890	Homo saniens chromosome 21 somment HS210027	CVA TYGES AND AND A TYGES AND AND AND AND AND AND AND AND AND AND	CV 1-5 10031-040900-33/-102 B 10631 Homo sapiens cDNA	7e34c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6 CE00828;	Homo saplens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	at36b04.x1 Barstead coton HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR.Q15408	disago Neo Tradicade Large Subunii ; contains LIR7. repetitive element ;	Homo sapiens hypothetical protein FL310803 (FL310803), mRNA	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds	Homo saplens chromosome 21 segment HS21C010	ae92g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains OFR.b1 OFR repetitive element:	Homo sapiens Ran GTPase activating protein 1 (RANGAP1) mBNA	QV0-FN0063-260600-278-c06 FN0063 Horno sapiens cDNA	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12.1	finfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
Jie Exon Pro	Top Hit Database Source	NT	TN	LN	L	NT	N	FZ	IN	EST HUMAN	NT	LN LN	N.	NAMI ILI TOTI	TN	CCT LUBRARI	ESI_HUMAN	EST HUMAN	TN	NAME TO THE	EST DOMAIN	Z	L	NT	EST HUMAN	NT.	EST HUMAN	EST_HUMAN	EST_HUMAN
NIN NIN	Top Hit Acession No.	1.0E-38 AB037863.1	4505016 NT	3.2	3.2	8922543 NT	7305360 NT	7305360 NT	2.1	1.0E-38 BE350127.1	4.2	4502312	4758229 NT	8 NE.39 A1823404 1				6.0E-39 BE670394.1	3.1	A OF 30 A 750454 4	00000	50707		4.0E-39 AL163210.2	4.0E-39 AA682949.1	8177			9.1
	Most Similar (Top) Hit BLAST E Value	1.0E-38 /	1.0E-38	1.0E-38 AL16320;	1.0E-38 AL16320;	1.0E-38	1.0E-38	1.0E-38	1.0E-38 AB01451	1.0E-38	1.0E-38 AL16328	8.0E-39	8.0E-39	8 0E.30	7.0E-39 AL 16322	6 OF 30 B	0.05-39 E	6.0E-39 B	5.0E-39 AF003528	70 C	20.0	3.UE-39	4.0E-39.A	4.0E-39 A	4.0E-39 A	4.0E-39	4.0E-39 B	3.0E-39 A	3.0E-39 AA63194
	Expression Signal	1.41	0.83	1.31	1.31	1.21	3.61	3.61	2.78	6.23	2.33	5.14	1.51	200	5.54	212	2.12	2.23	<u>τ</u>	7 7 3	4 54	+C	10.53	96.0	1.49	3.08	2.03	11.27	11.27
	ORF SEQ ID NO:	23743	23896	23902	23903	24173	25682	25683	26400	27489		19842	21134		21832	28310	5007		20757	22682	700,477	70000	20291	23238	26775	-		19830	19831
	Exon SEQ ID NO:	13965	14121	14127			- 1		16240	17281	19481	10036	11278	11686	<u></u>	18070	1	19337	10912	12884]	1		13441	16587	19164	19240	10029	10029
	Probe SEQ ID NO:	4063	4223	4229	4229	4493	5673	5673	6378	7414	9264	48	1372	1788	2047	8184		9838	991	2857	9556	2000	222	3525	6707	9575	9687	41	41

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	Top Hit Descriptor	finfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1	ox63a10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:G1K5_KA1 P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;	ox63a10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone !MAGE:1660986 3' similar to SW.GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;	yp51c06.s1 Scares retina N2b4HR Homo sapiens cDNA clone IMAGE:190954 3'	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5	promma-7.D01.r bytumor Homo sapiens cDNA 5	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds	PM0-BT0340-211299-003-d02 BT0340 Homo sapiens cDNA	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3	THK repetitive element;	Homo sapiens chromosome 21 segment HSZ1UU48	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA	Ing86f03.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:941693	zn06f02.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5	Human mRNA for KIAA0209 gene, partial cds	Homo sapiens myosin phosphatase, target subunit 2 (MYP12), mKINA	Homo sapiens KVLQT1 gene	Homo sapiens KVLQT1 gene	Homo sapiens DKFZp434P211 protein (UKFZP434P211), mKNA	EST364065 MAGE resequences, MAGB Homo sapiens cUNA	EST364065 MAGE resequences, MAGB Homo sapiens cDNA	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA	yd26g06,r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA cione IMAGE: 109402.5 similar to contains	Alu repetitive element contains LTX1 repetitive element,	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (NIX1 gene)	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (NIX1 gene)	Homo sapiens tubby like protein 3 (TULP3), mRNA	Homo saplens mRNA for ras-related GTP-binding protein, complete cds	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA	Homo sapiens AE-binding protein 1 (AEBP1) mRNA	Homo saplens AE-binding protein 1 (AEBP1) mRNA
	Top Hit Database Source	EST_HUMAN fi	EST HUMAN F			EST_HUMAN 6	T HUMAN		EST_HUMAN F		T HUMAN	7	- 1	EST_HUMAN I	_ (HUMAN	T HUMAN			T HUMAN				NT	LN L	NT	NT
	Top Hit Acesslon No.	-	5	5:		2.0E-39 BE409203.1	1	2.0E-39 AF000573.1				2.0E-39 AL163248.2			2.0E-39 AA080867.1		11425464 NT	1.0E-39 AJ006345.1	1.0E-39 AJ006345.1	7657020 NT	1.0E-39 AW951995.1	1.0E-39 AW951995.1	7657020 NT		1.0E-39 T80876.1	AJ278170.1	1.0E-39 AJ278170.1	11436736 NT	D78132.1	5803210 NT	4755145 NT	4755145 NT
	Most Similar (Top) Hit BLAST E Value	3.0E-39 AA631949.	3.0E-39 A1084557	3.0E-39 AI084557	3.0E-39 H37903.1	2.0E-39 E	2.0E-39 AI525119	2.0E-39	2.0E-39 AW37231		2.0E-39 /	2.0E-39 /	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39	1.0E-39	1.0E-39 /	1.0E-39	1.0E-39	1.0E-39	1.0E-39		1.0E-39	1.0E-39 AJ27817		1.0E-39	1.0E-39			9.0E-40
	Expression Signal	11.27	557	5.57	4.42	4.03	17.44	3.61	10.15		10.03	1.75	1.36	3.4	2.17	2.33	2.31	1.78	1.78	4.95	5.49	5.49	8.58		1.54	4.36	4.36	1.66			10.19	10.19
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	Exon SEQ ID NO:	10029		Ì			<u> </u>		Į		11825	12458	L			18587	19394		L		L	14453	14492		15379	15395			<u></u>		Ĺ	
	Probe SEQ ID NO:	41	40.00	200	9147	879	894	1015	1513		1930	2587	4303	5375	6360	8731	9922	1497	1497	1514	4561	4561	4604		5459	5475	5475	6083	6357	543	1215	1215

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA	Homo sapiens mRNA for KIAA1244 protein, partial cds	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5'	Human DNA polymerase garnma mRNA, nuclear gene encoding mitochondrial protein, complete cds	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds	Homo sapiens chromosome 21 segment HS21C046	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family	hz40g01.x1 NCI_CGAP_GC6 Hcmo sapiens cDNA clone IMAGE:3210480 3'	Homo sepiens fatty acid desaturase 1 (FADS1), mRNA	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'	Homo sapiens chromosome 21 segment HS21C085	tt91b01.x1 NCI_CGAP_Pr28 Home sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN;	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	Homo sabiens KIAA0433 protein (KIAA0433) mRNA	nv34e10.r1 NCL CGAP Br4 Homo sapiens cDNA clone IMAGE:1222122	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA	wh12f07.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2380549 3'	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
lle Exon Probe	Top Hit Database Source		H N			EST_HUMAN 7	EST HUMAN 6	NT T	T L	L	EST_HUMAN E	EST HUMAN E	EST HUMAN h			T_HUMAN	EST HUMAN A		EST HUMAN P			T HUMAN	EST HUMAN PI	EST_HUMAN PI	EST_HUMAN R	EST_HUMAN W	
SING	Top Hit Acession No	4507512 NT	9.0E-40 AB033070.1	4507848 NT	4507848 NT	8.0E-40 AA078165.1	8.0E-40 BE396541.1	7.0E-40 U60325.1	7.0E-40 U60325.1	7.0E-40 AL163246.2	6.0E-40 AA361275.1	6.0E-40 AA361275.1	6.0E-40 BE504766.1	11439783 NT	11439783 NT	6.0E-40 AV653028.1	6.0E-40 AV653028.1		4.0E-40 AI686005.1		62117	4.0E-40 AA742809.1	4.0E-40 BE009416.1	4.0E-40 BE009416.1	4.0E-40 AW841585.1	3.0E-40 AI925949.1	11417342 NT
	Most Similar (Top) Hit BLAST E Value	9.0E-40	9.0E-40	9.0E-40	9.0E-40	8.0E-40	8.0E-40	7.0E-40	7.0E-40	7.0E-40	6.0E-40	6.0E-40	6.0E-40	6.0E-40	6.0E-40	6.0E-40	6.0E-40	5.0E-40	4.0E-40	4.0E-40	4.0E.40	4.0E-40	4.0E-40	4.0E-40	4.0E-40	3.0E-40	3.0E-40
	Expression Signal	5.04	3.58	0.82	1.12	0.95	2.41	1.56	1.56	2.83	3.88	3.88	2.07	3.08	3.08	6.82	6.82	1.89	1.38	2.67	7.85	3.76	4.87	4.87	4.07	0.98	6.25
	ORF SEQ ID NO:	21205	23586	23923	23923	22725		26578	26579	28391	22449	22450		26124	26125	27804	27805	22326	21607		23973	26738	27308	27309	28238	23721	26030
	Exon SEQ ID NO:	11338	15069	14149		12932	13758	16399	16399	18150	12560	12560	15531	15989	15989	17581	17581	12433	11731	11951	14189	16542	17114	17114	17989	13943	15906
	Probe SEQ ID NO:	1433	3892	4250	4398	3004	3847	6541	6541	8270	2696	2696	5616	6141	6141	7731	7731	2561	1834	2061	4291	6662	7237	7237	8039	4040	6001

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Single Exon Probes Expressed in Heart	Most Similar Top Hit Acession (Top) Hit Acession Signal BLASTE No. Source	4.28 3.0E-40 5454167 NT Homo sapiens HBV associated factor (XAP4) mRNA	1.49 3.0E-40 AF078779.1 NT Rattus norvegicus putative four repeat ion channel mRNA, complete cds	1.52 3.0E-40 AF078779.1 NT Rattus norvegicus putative four repeat ion channel mRNA, complete cds	1.93 3.0E-40 BE350127.1 EST_HUMAN MER29 repetitive element;	05813 NT	xd96h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605491 3' similar to TR:Q15804 1.96 3.0E-40 AW118799.1 EST_HUMAN Q15804 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERVS	EST HUMAN	1 EST HUMAN	Г	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated 2.0E-40 4506188 NT products	4506188 NT	EST HUMAN	2.0E-40 5453592 NT	١	2.0E-40 BE275932.1 EST_HUMAN	53592 NT	1.49 2.0E-40 AL163280.2 NT Homo sapiens chromosome 21 segment HS21C080	TN	1.0E-40 AA225989.1 EST_HUMAN hc09a09.s1 NG_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007608	1.91 1.0E-40 BF036881.1 EST_HUMAN 601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5	TOTOTOTOLO OF HOT	1.0E-40 BE018348.1 EST HOMAN	1.0E-40 BF541030.1 EST HUMAN	1.0E-40 BF54103	1.0E-40 4507142 NT	1.0E-40 4508012 NT	0.88 1.0E-40 7705778 NT Homo sapiens CGI-65 protein (LOC31103), mRNA
					3.0E-40	3.0E-40														1.0E-40 A	1.0E-40 B	07 10 7	ŀ		1.0E-40 B			
	Expression Signal	4.28	1.49	1.52	1.93	11.23	1.96	12.69	2.72	1.4	2.19	2.19	1.08	2.61	2.35	1.08	3.59	1.49	1.49	1.65	1.91	7	1.92	0.92	0.92	1.81	6.28	0.88
	ORF SEQ ID NO:	26959		27389	28515	28725	28954				21664	21665	21807	21910	22112			24478	24479		22343		00,00	22460	22461		24184	
	Exon SEQ ID NO:	16761	17063	17188	18264	18456	18667	10283	10707	11681	11787	11787	11917		12214	12525	13014	14691	-		12451			0/671			ļ	14772
	Probe SEQ ID NO:	6882	7186	7312	8387	8588	8855	322	777	1783	1892	1892	2026	2123	2333	2658	3087	4807	4807	865	2580	2853	2027	7/0/7	2/0/	3258	4505	4892

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Single Exon Probes Expressed in Heart

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ביי ביילו וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים ווינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים ווינים ווינים ווינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים וויינים	Top Hit Descriptor	nj42f04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'	nj42f04.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'	AU149345 NT2RM4 Homo saplens cDNA clone NT2RM4002122 3'	qh31h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846339 3'	MR2-CT0222-211099-002-e10 CT0222 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C003	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'	Homo saplens a disintegrin and metalloprotelnase domain 22 (ADAM22), mRNA	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo sapiens DSCR5b mRNA, complete cds	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE;3682677 5'	yc03e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE: 79626 3'	Homo saplens target of myb1 (chicken) homolog (TOM1), mRNA	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA	QV0+HT0367-150200-114-g09 HT0367 Homo sapiens cDNA	AU119344 HEMBA1 Homo saplens cDNA clone HEMBA1005583 5'	ow45e06.s1 Soares_parathyroid_turnor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 CYTOCHROME C-LIKE POLYPEPTIDE.; contains LTR5.b1 LTR5 repetitive element;	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE: contains I TR5 bd 1 TR5 repairtive element	Homo sapiens gene for activin receptor type IIB, complete cds	tm98c04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element :	Homo saplens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element	AV758295 BM Homo sapiens cDNA clone BMFBHC05 5'	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'	AV710480 Cu Homo sapiens cDNA clone CuAACC07 5'	AV708431 ADC Homo sapiens cDNA clone ADCARED2 5'
oligic Exoll Topes Explessed	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	L	NT	NT	NT	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	EST HUMAN	NT	r F	LN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
5	Top Hit Acession No.	1.0E-40 AA573201.1	1.0E-40 AA573201.1	1.0E-40 AU149345.1	1.0E-40 AI239572.1	1.0E-40 BF334112.1	8.0E-41 AL163203.2	7.0E-41 Al934364.1	7.0E-41 AI934364.1	11419208 NT	11417972 NT	6.0E-41 AB037163.1	7657042 NT	BE567816.1	T62628.1	4885636 NT	5.0E-41 BE067042.1	4.0E-41 BE156318.1	4.0E-41 AU119344.1	4.0E-41 AI027117.1	4.0E-41 AI027117.1	4.0E-41 AB008681.1	AI500406.1	4.0E-41 AJ229041.1	4.0E-41 AJ229041.1	4.0E-41 X92685.1	4.0E-41 AV758295.1	4.0E-41 BF304683.1	4.0E-41 AV710480.1	4.0E-41 AV708431.1
	Most Similar (Top) Hit BLAST E Value	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	8.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41	6.0E-41	6.0E-41	6.0E-41	5.0E-41	5.0E-41	5.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41
	Expression Signal	2.03	2.03	5.72	53.3	3.93	1.73	2.36	2.36	3.27	4.82	1.72	2.19	0.94	1.31	96.0	2.55	1.91	1.28	9.42	9.42	2.12	8.5	3.03	3.03	1.89	1.39	6.01	7.62	2.31
	ORF SEQ ID NO:	26230	26231	28412	28480		26689		20586	25663		20064	21851	24044	21532				20839	21149	21150	21170	21380	22578	22579	23730		27657		
	Exon SEQ ID NO:	16081	16081	18168	18232	19622	16501	12678	12678	15567	19618	10244	11954	14260	11660	13922	15850	10332	10998	11293	11293	11309	11522	12787	12787	13954	15825	17441	18733	19510
	Probe SEQ ID NO:	6215	6215	8289	8355	9521	6621	811	811	5655	9931	279	2064	4364	1761	4018	5945	385	1082	1388	1388	1404	1618	2859	2859	4052	5920	7590	8925	6696

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	Top Hit Descriptor	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	Homo sapiens mRNA for KIAA1327 protein, partial cds	H.sapiens mRNA for putative p64 CLCP protein	Homo sapiens mRNA for KIAA1387 protein, partial cds	Human ribosomal protein L23a mRNA, complete cds	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end	Human mRNA for KIAA0207 gene, complete cds	G.gorilla DNA for ZNF80 gene homolog	Human ribosomal protein L23a mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C067	Homo sapiens chromosome 21 segment HS21C067	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds	Human B-cell specific transcription factor (BSAP) mRNA, complete cds	Human B-cell specific transcription factor (BSAP) mRNA, complete cds	EST31723 Embryo, 12 week I Homo sapiens cDNA 5' end	ZINC FINGER PROTEIN 135	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end	Mus musculus tubulin alpha 6 (Tuba6), mRNA	qf75c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3'	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA	RC0-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	ph07503 of NCI CGAD Thy Homo continue CONA clara IMACE 043508 similar to TD-042404 Curvana	367BP EXPRESSED SEQUENCE TAG MRNA;	Homo sapiens chromosome 21 segment HS21C085	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
ion Town Olfi	Top Hit Database Source	LN		NT	NT	IN	NT	NT	EST_HUMAN	NT	IN	TN	N-	NT	N	IN	LN T	EST_HUMAN	SWISSPROT	EST_HUMAN	N	EST_HUMAN	LN	EST_HUMAN	IN	IN	NT	NT		EST_HUMAN	LN	NT	NT
	Top Hit Acession No.	3.0E-41 AB030176.1		3.0E-41 AB026898.1	3.0E-41 AB037748.1	X87689.1	3.0E-41 AB037808.1	2.0E-41 U43701.1	2.0E-41 AA331940.1	J86962.1	XB9631.1	J43701.1	2.0E-41 AL163267.2	2.0E-41 AL163267.2	2.0E-41 AF038404.1	2.0E-41 M96944.1	2.0E-41 M96944.1	2.0E-41 AA328265.1	52742	2.0E-41 AA372637.1	6678468 NT	AI217868.1	11526291 NT	BE179191.1	11560151	11560151 NT	8.0E-42 AF003530.1	8 OF 42 AB026808 1	1,020,030,1	8.0E-42 AA493896.1	7.0E-42 AL163285.2	6.0E-42 AF012872.1	6.0E-42 AF012872.1
	Most Similar (Top) Hit BLAST E Value	3.0E-41		3.0E-41	3.0E-41	3.0E-41 X87689.1	3.0E-41	2.0E-41	2.0E-41	2.0E-41 D86962.1	2.0E-41 XB9631.1	2.0E-41 U43701.1	2.0E-41	2.0E-41				2.0E-41	2.0E-41 P52742	2.0E-41	1.0E-41		1.0E-41	_	9.0E-42	9.0E-42	8.0E-42	CA FINE AD	0.01-12	8.0E-42	7.0E-42	6.0E-42	6.0E-42
	Expression Signal	1.64		3.08	0.85	7.36	1.49	7.3	2.3	1.03	4.07	5.31	1.06	1.06	6.59	1.33	1.33	1.39	1.7	3.46	4.64	1.8	2.63	1.33	2.63	2.63	5.37	1 32	40.	32.6	1.83	3.25	3.25
	ORF SEQ ID NO:	20704		23914		25143	25873	21305	21688	21962	22010	21305	24199	24200	26559	26772		26786	27255	28882	24149	27494			27367	27368	20216	21840	D .				21587
	Exon SEQ ID NO:	10857		14139	14919	15296	15755	11445	11810	12059	12106	11445	14414	14414	16381	16582	16582	16596	17065	18594	14359	17287	18930	16836	17168	17168	10399	11052	70011	19625	10840	11709	11709
	Probe SEQ ID NO:	932		4240	5047	5376	6849	1782	1915	2172	2221	2798	4521	4521	6522	6702	6702	6716	7188	8777	4465	7420	9197	6958	7292	7292	455	2062	7007	9238	916	1812	1812

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Table 4
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Single Exon Probes Expressed in riedit	Top Hit Descriptor	xp29f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similer to contains L1.t1 L1 repetitive element;	qu24h09x1 NCI_CGAP_Br12 Homo sapiens cDNA clone IMAGE:1965761 similar to contains Alu repetitive element,	Homo sapiens mRNA for KIAA1067 protein, partial cds	Homo sapiens mRNA for KIAA1067 protein, partial cds	Homo sapiens Xq pseudoautosomal region; segment 1/2	hv31e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	Homo saplens ublquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA	Homo sapiens ubiquitin protein ligaso E3A (fuman papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete		Homo sapiens mRNA for KIAA1294 protein, partial cds	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA	Homo sapiens MHC class 1 region	Homo sapiens MHC class 1 region	Homo sapiens ribonuclease III (RN3) mRNA, complete cds	H.sapiens PROS-27 mRNA	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA	Homo sapiens zinc finger protein 177 (ZNF177) mRNA	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'	ab14e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains	THR.t2 THR repetitive element;	RC0-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA	2819293.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'	EST367438 MAGE resequences, MAGC Homo sapiens cDNA
e Exon Propes	Top Hit Database Source	EST_HUMAN re	HUMAN				T HUMAN												H						EST_HUMAN 6	ES	EST_HUMAN T	HUMAN		EST_HUMAN 2	_
SING	Top Hit Acession No.	6.0E-42 AW238656.1	6.0E-42 A 284770.1	<u>_</u>	6.0E-42 AB028990.1	5.0E-42 AJ271735.1	5.0E-42 BE217913.1	5730038 NT	5730038 NT	11433063 NT	11433063 NT	11417957 NT			5.0E-42 AB037715.1	8923162 NT	4.0E-42 AF055066.1		.1	4.0E-42 X59417.1	4506496 NT	4508008 NT	4.0E-42 AW818630.1	4.0E-42 AW818630.1	4.0E-42 BF035327.1		3.0E-42 AA486105.1	2.0E-42 BF376834.1	_	2.0E-42 AW250059.1	_
	Most Similar (Top) Hit BLAST E Value	6.0E-42	6.0E-42	6.0E-42	6.0E-42	5.0E-42	5.0E-42	5.0E-42	5.0E-42	5.0E-42	5 DE-42	5.0E-42		5.0E-42	5.0E-42	5.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42		3.0E-42	2.0E-42			2.0E-42
	Expression	3.51	1 04	1.81	1.72	5.44	1.17	2.94	1.27	1.76	1 76	2.75		1.57	2.76	2.15	8.89	8.89	2.67	1.61	4.52	10.26	2.07	2.07	3.22		0.78	3.63	3.86	2.15	10.2
	ORF SEO ID NO:			25105	ļ		20197			26050					27168	28494	20502	20503		23779	23830	24162						21239		22146	
	Exon SEQ ID NO:	12128	14814	15275	15275	10105	10376	10422	10423	15920				16138	16975	18243	L	10668	L		14056	14374	17932	L	上	1_	10084	11372	12241	12255	15437
	Probe SEQ ID NO:	2244	9607	5355	5504	131	431	478	479	6016	8018	6072		6274	2098	8366	736	736	1050	4100	4156	4480	8041	8041	8714		86	1467	2361	2375	5519

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Single Exon Probes Expressed in Heart

					E-2721871 3'			olog mRNA, nuclear gene	olog mRNA, nuclear gene			Ø N N N N N N N N N N N N N N N N N N N	L) mRNA, and translated																		
Single Exon Probes Expressed in Heart	Top Hit Descriptor	EST367438 MAGE resequences, MAGC Homo sapiens cDNA	601061284F1 NIH MGC 10 Homo sapiens cDNA clone IMAGE:3447620 5'	Human endogenous retrovirus pHE.1 (ERV9)	UI-H-BI1-aft-e-04-0-UI.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE: 2721871 3	Homo sapiens partial C9 gene for complement component C9, exon 1	Homo sapiens partial C9 gene for complement component C9, exon 1	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds	Homo saplens NADH-ublquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial profesir complete rets.	Homo sapiens rec (LOC51201), mRNA	Homo sapiens PDNP1 gene, expn 17	Homo sapiens major histocompatibility complex, class II. DM alpha (HI A-DMA) mRNA	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORCSL) mRNA, and translated	Homo saplens KIAA0255 gene product (KIAA0255) mBNA	Homo sapiens chromosome 21 segment HS21C067	Homo sapiens chromosome 21 segment HS21C080	RC3-ST0197-161099-012-a03 ST0197 Homo saplens cDNA	Homo sapiens proteasome inhibitor (PI31), mRNA	Homo sapiens proteasome inhibitor (PI31), mRNA	Homo saplens ryanodine receptor 3 (RYR3) mRNA	Homo sapiens mRNA for KIAA1288 protein, partial cds	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) rnRNA	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA	2t79a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728532.3'	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA	2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251.5
Jie Exon Pro	Top Hit Database Source	EST HUMAN	EST HUMAN	LN	EST HUMAN	LN	N	N	L L	Z	NT	TN	L	NT	L	L	EST_HUMAN	NT	NT	NT	. LZ	N	NT				EST_HUMAN				T HUMAN
מווס	Top Hit Acession No.	2.0E-42 AW955368.1	2.0E-42 BE538919.1		1.0E-42 AW 295809.1	1.0E-42 AJ251818.1	1.0E-42 AJ251818.1	1.0E-42 AF067166.1	1.0E-42 AF067166.1	423219	1.0E-42 AF110296.1	5174458 NT	TN 4505524	7662027 NT	1.0E-42 AL163267.2	1.0E-42 AL163280.2		5803122 NT	5803122 NT	4506758 NT	1.0E-42 AB033114.1	4501912 NT	4501912 NT	757969	1	1	8.0E-43 AV736824.1	8923276 NT	8923276 NT	8.0E-43 8923276 NT	W246442.1
	Most Similar (Top) Hit BLAST E Value	2.0E-42	2.0E-42	1.0E-42 X57147.1	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42 /	1.0E-42	1.0E-42	9.0E-43	9.0E-43 /	8.0E-43	8.0E-43	8.0E-43	8.0E-43	8.0E-43	7.0E-43
	Expression Signal	10.2	1.27	1.06	96.0	1.11	1.11	12.78	12.78	1.46	0.91	1.98	8.93	2.15	1.02	1.72	0.86	2.85	2.85	5.35	12	0.98	0.98	3.80	2.84	12.13	12.13	4.33	4.33	4.33	6.05
	ORF SEQ ID NO:	25501	27739	20478	20789	20842	20843	20983	20984	21443	21772	22264	22662	23347	23553	23827	24170	24316	24317	24348	24442	24693	24694	27893	28525	20386	20387	20441	20442	20443	23292
	Exon SEQ ID NO:	15437	17513	10648	10944	11001	11001	12688	12688	11575	11879	12372	12862	13561	13760	14053	14383	14528	14528	14555	14654	14920	14920	17655	18273	10573	10573	10618	10618	10618	13503
	Probe SEQ ID NO:	5519	7663	717	1026	1085	1085	1222	1222	1673	1986	2497	2935	3647	3849	4153	4489	4640	4640	4669	4769	5048	2048	7805	8397	636	636	685	685	685	3589

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	Top Fit Descriptor	wp69b01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2465985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;contains LTR7.b1 LTR7 repetitive element ;	ne72d06.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909803 similar to gb:L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN);	AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.t3 MER1 MER1 repetitive element ;	z35e06.r1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:665410 5' similar to TR G529641 G529641 DB1, COMPLETE CDS.; contains element PTR7 repetitive element;	DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5	Homo sapiens chromosome 21 segment HS21C013	EST96033 Testis I Homo sapiens cDNA 5' end	AV732578 HTF Homo sapiens cDNA clone HTFANC06 5'	aa33d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'	oo52c10.x5 NOL_CGAP_Lu5 Homo sapiens cDNA clone IMACE:1569810 3' similar to TR:PS0591 P90591 PV14 GENE.;	DKFZp434D0119_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D0119	MR2-\$N0007-290400-004-c02 SN0007 Homo sapiens cDNA	55a4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	Human mRNA for alpha-actinin	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	Tegrals Tegrals	FIGURE SAPIETS protocolorent beta o (FOOT IDO), III. WAS CAROCOSE OF THE PLANT OF A COST OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE	ignostatino Contranto nomo sapiena con e nomo sapiena con entro en constante de contema men lo do MER 10 repetitive element;	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1855354 3' similar to contains MER10.13	MER10 repetitive element ;	yd72h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113827 5'	yg06b05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE.31363 5' similar to contains MER10	repetitive element;	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
200	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	IN	Ŀ	- N	_	EST HUMAN		EST_HUMAN	EST_HUMAN		EST_HUMAN	NT
	Top Hit Acession No.	7.0E-43 AI936748.1	6.0E-43 AA491890.1	6.0E-43 AV708201.1	9955973 NT	6.0E-43 AW 468897.1	6.0E-43 AA195154.1	6.0E-43 AL119158.1	5.0E-43 AL163213.2	5.0E-43 AA382780.1	5.0E-43 AV732578.1	5.0E-43 AA465288.1	5.0E-43 AI733244.1	5.0E-43 AL049110.1	5.0E-43 AW863007.1	5.0E-43 W 29011.1	(15804.1	00000	4.0E-45 AF003526.1	N 58/01411	4.0E-43 AI244341.1		4.0E-43 AI244341.1	F77380.1		4.0E-43 R20950.1	3.0E-43 AF223391.1
	Most Similar (Top) Hit BLAST E Value	7.0E-43	6.0E-43	6.0E-43	6.0E-43	6.0E-43	6.0E-43	6.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43	5.0E-43 X15804.1	L	4.05-43/	4.0E-43	4.0E-43		4.0E-43	4.0E-43 T77380.1		4.0E-43	3.0E-43
	Expression Signal	1.76	10.17	4.15	2.02	2.02	1.83	6.54	1.98	3.01	1.36	4.47	2.2	1.41	5.46	2.67	2.6	L	4.83	1.72	4.49		4.49	1.8		1.89	2.84
	ORF SEQ ID NO:				25829	26111	27745			20249		27514					28146		20178		26824		26825	28761			
	Exan SEQ ID NO:	16969	11227	12421	15716	15975	l	18322	10111	10437	12745	17308	17795	17814	18033	18215	17902		12043	7609 L	16636	L	16636	18489		18915	11105
	Probe SEQ ID NO:	7092	1320	2547	5811	6128	7668	8449	137	494	2816	7390	7945	7964	8145	8338	8753		JCS .	6231	6757		6757	8624		9174	1195

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	Top Hit Descriptor		AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA		ns cDNA clone IMAGE:1017419			Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds	aa88f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR to THR reposition element	11916) mRNA	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	qd61c09.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1733968 3' similar to contains PTR7 t3		UI-H-BI1-afi-a-09-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:27217123'	mplete cds	FB1G5 Fetal brain, Stratagene Homo sapiens cDNA clone FB1G5 3'end similar to LINE-1	in (RAB27A) gene, exons 1b and 2	in (RAB27A) gene, exons 1b and 2	IS21C084	apiens cDNA clone IMAGE:4157666 5'	74) mRNA	24) mRNA	yg40e01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34732 5' similar to	EIN DN38;	CBFA2T1) gene, partial cds	Homo sapiens cDNA	iens cDNA clone IMAGE:2494705 3'	Homo sapiens calcium channei, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA	DKFZp761D1015_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761D1015 5	ens cDNA clone IMAGE:2313775 3'	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552.3'	GBC_S1 Homo sapiens cDNA clone IMAGE:18455523'	0
Chigh Lath 100cs Lapressed III I real		H.sapiens gene encoding La autoantigen	AML1-EVI-1=AML1-EVI-1 fusion protein	Mutant, 5938 nt]	nk55d06.s1 NCI_CGAP_Pr7 Homo sapiens cDNA clone IMAGE:1017419	Mus musculus otogelin (Otog), mRNA	Mus musculus otogelin (Otog), mRNA	Human ribosomal RNA upstream binding	aa88f11.s1 Stratagene fetal retina 937202	Homo sapiens hypothetical protein (HSA011916), mRNA	Homo sapiens SET domain and mariner t	qd61c09.x1 Soares_testis_NHT Homo sa	PTR7 PTR7 repetitive element;	UI-H-BI1-afi-a-09-0-UI.s1 NCI_CGAP_St	Human ribosomal protein L23a mRNA, complete cds	FB1G5 Fetal brain, Stratagene Homo sap	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2	Homo sapiens chromosome 21 segment HS21C084	602022313F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157666 5	Homo sapiens Sp4 transcription factor (SP4) mRNA	Homo sapiens Sp4 transcription factor (SP4) mRNA	yg40e01.r1 Soares infant brain 1NIB Hom	SP:BD38_MOUSE P28656 BRAIN PROTEIN DN38	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds	EST375749 MAGE resequences, MAGH Homo sapiens cDNA	wr87h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'	Homo sapiens calcium channel, voltage-d	DKFZp761D1015_r1 761 (synonym: ham	wbggb04.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE.2313775 3	Horno sapiens cadherin EGF LAG seven-	qh23g01.x1 Soares_NFL_T_GBC_S1 Ho	qh23g01.x1 Soares_NFL_T_GBC_S1 Ho	H.sapiens DNA for Cone cGMP-PDE gene
פון בייטוון וסיי	Top Hit Database Source	ZI		NT	EST_HUMAN	NT	LN.	NT	FST HIMAN	NT	Z		EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	N	TN	NT	EST_HUMAN	NT	١N		EST_HUMAN	NT		EST HUMAN	LN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	L
	Top Hit Acession No.	3.0E-43 X97869.1		3.0E-43 S69002.1	3.0E-43 AA548154.1	7305360 NT	7305360 NT	U65487.1	3 OF 43 AAA58824 1	7661721 NT	5730038 NT		2.0E-43 AI190764.1	2.0E-43 AW 207390.1		2.0E-43 T03007.1	1.0E-43 AF154836.1	1	1.0E-43 AL163284.2	1.0E-43 BF348283.1	4507168 NT	4507168 NT				.1		11424378 NT	1.0E-43 AL137964.1	1.0E-43 AI675416.1	118322		.1	
	Most Similar (Top) Hit BLAST E Value	3.0E-43		3.0E-43	3.0E-43	3.0E-43	3.0E-43	3.0E-43	3 0F-43	3.0E-43	3.0E-43		2.0E-43	2.0E-43	2.0E-43	2.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	L	1.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	1.0E-43	9.0E-44	8.0E-44	8.0E-44	8.0E-44 X94354.1
	Expression Signal	1.48		1.05	0.95	1.71	1.71	3.78	89.9	1.18	2.02		4.27	1.36	7.53	3.38	2:92	2.92	3.36	4.95	12.07	12.07			1.63	25.23	6.75	3.2	3.66	1.89	2.52	5.98	5.98	3.87
-	ORF SEQ ID NO:	21437		23237	23872	25855	25856	26072		27188	29061			26332			21394	21395	21450	22444	26014	26015	0	24800		27199	28458	28844		25311	25255	20648	20649	27037
	Exon SEQ ID NO:	11571				15743	15743	15940	16625		18769		10148	16175	16715	18404	11534	11534	11580	12557	15892	15892	1	/1101	16580	17006	18208	18560	18880	19058	19196	10798	10798	16845
	Probe SEQ ID NO:	1669		3524	4193	5837	5837	6037	6746	7120	8962		177	6312	6836	8532	1630	1630	1678	2692	5987	2882	6	8010	6700	7129	8331	8672	9117	9405	9618	872	872	8969

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Top Hit Acession Database No. Source	2.0E-44 5901933 NT Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA	INT	2.0E.44 AW864379.1	2.0E-44 11449901 NT Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA	2.0E-44 AF0389C'8.1 NT Homo sapiens general transcription factor 2-l (GTF2l) mRNA, alternatively spliced product, complete cds	2.0E-44 11419226 NT Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA	2.0E-44 11419226 NT Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA	2.0E-44 BE389058.1	2.0E.44 BE244902.1 EST_HUMAN cDNA clone TCBAP2795	2.0E.44 AB002374.1 NT Human mRNA for KIAA0376 gene, partial cds	2.0E-44 11526293 NT Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA	1.0E-44 7657334 NT Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA	7657334 NT	1.0E-44 AWB53132.1	EST_HUMAN	1.0E-44 AL163303.2 NT Homo saplens chromosome 21 segment HS21C103	2w53d02.r1 Soares_total_fetts_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to 10E-44_AA434554.1			1.0E-44 AA398099.1 EST_HUMAN Z188911.r1 Soares_bestis_NHT Homo sapiens cDNA clone IMAGE:729476 5'			1.0E-44 AA455869.1 EST_HUMAN aa01c09.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'		1.0E-44 AJ130755.1 NT Homo sapiens alpha satellite DNA, M1 monomer type	T_HUMAN	12664 NT	EST_HUMAN	AW846967.1 EST_HUMAN	9.0E-45 8922391 NT Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
je.	2.0E-44	2.0E-44 D	2.0E-44 A	2.0E-44	2.0E-44 AI	2.0E-44	2.0E-44	2.0E-44 Bi	2.0E-44 BI	2.0E-44 AI	2.0E-44	1.0E-44	1.0E-44	1.0E-44 A	1.0E-44 A	1.0E-44 AI	1 OF 44 A		1.0E-44 A	1.0E-44 A		1.0E-44 A	1.0E-44 A	1.0E-44 A	1.0E-44 A	1.0E-44 A	1.0E-44	1.0E-44 A	1.0E-44 A	9.0E-45
Expression Signal	3.32	1.36	1.76	1.39	1.46	3.86	3.86	1.88	2.22	2.72	1.38	3.64	3.64	1.85	1.52	5.54	3.53		3.53	1.05	•	1.39	5.08	0.81	0.81	10.75	4.18	3.43	3.43	1.74
ORF SEQ ID NO:		23147	24152	25719	24870			27078		24910		19839	19840	20312			21965		21966	22024		22489		24702	24703		28918	28970	28971	24159
Exon SEQ ID NO:	12438	13342	14362	15617	15107	16245	16245	16886	18816	19735	19383	10034	10034	10505	11090	11460	12064	<u> </u>	12064	12716		12594	13578	14931	14931	18255		18681	18681	14370
Probe SEQ ID NO:	2567	3425	4468	6029	2609	6383	6383	2009	9022	9710	9066	46	46	566	1179	1555	2177		2177	2237		2732	3664	5061	5061	8378	8816	8869	8869	4476

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		T	7	T	_	Т	\top	-	T-		-1	·-r		Т	Т	Т	_	+	7	1	-	_	***	Ψ.	7	***	44	10.0	~~	بهبنه	منته
Oligie Lydia I lobes Lypiessed III legit	Top Hit Descriptor	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TEG) mRNA	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW:R13A HUMAN P40429 60S RIBOSOMAL PROTFIN 113A	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (AREGAP1) mRNA	Homo sapiens chromosome 21 segment HS21C003	CM4-CN0044-180200-515-f01 CN0044 Homo sapiens cDNA	1994107 x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW.PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1.	zf72d03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element:	Homo saplens programmed cell death 5 (PDCDS) mRNA	Home capiens chirin ille screen (CE DV mDNA	H sapiens ART4 gene	601104440F1 NIH WGC 7 Homo continue a DNA alexa 1110 CF (Second)	S02084052F1 NIH MGC 83 Home saniens citing class MAGE: 3538425 5	Vd35f07.r1 Soares fetal liver spleen 1NFLS Homo seniens cPNA close MACE: 110245.F1	AV723976 HTB Homo saplens cDNA clone HTBAAGA1 5	Homo sapiens goldi autoantigen, goldin subfamily a 2 (GO) (GA2) mRNA	Homo sapiens chromosome 21 segment HS21C027	Homo sapiens chromosome 21 segment HS21C027	H.sapiens DNA for endogenous retroviral like element	Homo sapiens chromosome 21 segment HS21C018	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5	Human eosinophil Charrot-Lawfon crostal (CLC) protein (Lagarbaachaacha	601467793F1 NIH MGC 67 Homo septiens CDNA clone MAAGE-3870838 5	MR0-HT0923-190800-201-a02 HT0923 Homo sapiens CDNA	aa87112.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to	11.00 144009 G1144009 G-CLT.	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'	Xp7.2a03.X1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
gie Lauri iu	Top Hit Database Source	Z	N	N	EST HUMAN	LN L	ΙΝ	EST_HUMAN	EST HUMAN	EST HUMAN	NT	LZ	L Z	EST HIMAN	EST HUMAN	EST HUMAN	EST HUMAN	1	N	L	L	LΝ	L	L	EST HUMAN	EST_HUMAN	FOT LEMAN	LOI TOWNIN	TOT HUMAN	ESI HUMAN	Z
5	Top Hit Acession No.	8922391 NT	5174718 NT	5174718 NT	6.0E-45 AW157570.1	11418213 NT	5.0E-45 AL163203.2	3F333627.1	1523766.1	5.0E-45 AA397781.1	4759223 NT	TM 8923698	1 ***	3F265622 1	3F676077.1	71480.1	N723976.1	4758451 NT	L163227.2	3.0E-45 AL163227.2	39211.1	L163218.2	J243213.1	01665.1	2.0E-45 BE782184.1	2.0E-45 BE934350.1			20.7	1VV Z I UZBU. 1	11418157 NI
	Most Similar (Top) Hit BLAST E Value	9.0E-45	8.0E-45	8.0E-45	6.0E-45	6.0E-45	5.0E-45	5.0E-45 BF33362	5.0E-45 A152376	5.0E-45	5.0E-45	5 0F-45	4.0E-45 X95826	4 0F-45 BF26562	4.0E-45 BF67607	3.0E-45 T71480.1	3.0E-45 AV72397	3.0E-45	3.0E-45 AL16322	3.0E-45	3.0E-45 X89211.1	2.0E-45 AL16321	2.0E-45 AJ24321	2.0E-45/L01665.1	2.0E-45 B	2.0E-45 B	2 0E-45 AA45877	2.000	2.0E-40 A	2.0E-45 AW Z/UZ	Z.UE-45]
	Expression Signal	1.74	3.9	7.49	5.25	1.46	1.11	5.01	2.01	8.83	1.67	2.67	8.96	1.98	1.62	1.17	1.51	3.44	8.37	8.37	1.33	2.17	0.93	4.82	1.75	27.64	3.96	2 5	2.13	27.0	2.10
	ORF SEQ ID NO:	24160	22245	24656				21739	22904	25155	27292	29043	20883	22027				27173	27996	27997			22716	25957	26516	28315	28652	20880	28800	20000	
	Exon SEQ ID NO:	14370	12353	14889	13806	19718	10800	11852	13098	15303	17103	18748	11041	12130	19192	13210	16798	16981	17757	17757	19660	12331	12924	15834	16347	19471	18388	1860B	18608	10346	130.70
	Probe SEQ ID NO:	4476	2477	5015	3896	9707	874	1957	3173	5384	7226	8940	1127	2246	9613	3997	6920	7104	7907	7907	9814	2454	2996	5929	6489	8179	8516	8704	8794	9853	Tanna

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	Top Hit Descriptor	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA	Homo sapiens mRNA for KIAA1591 protein, partial cds	601289116F1 NIH MGC B Homo sapiens cDNA clone IMAGE:3619803 5'	Homo sapiens niban protein (NIBAN), mRNA	601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'	Human mRNA for KIAA0299 gene, partial cds	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	Homo saplens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA	Homo sapiens chramosome 21 segment HS21C009	2822449.5prime NIH_MGC_7 Homo saplens cDNA clone IMAGE:2822449 5'	tt32/08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_ma2 TUBULIN BETA-1 CHAIN (HUMAN);	t32f08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_rna2	TUBULIN BETA-1 CHAIN (HUMAN);	RC5-HT0506-280200-012-C12 HT0506 Homo sapiens cDNA	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5	RC4-BT0310-110300-015-f10 BT0310 Homo saplens cDNA	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5'	Homo sapiens chromosome 21 segment HS21C046	wm31f08.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.t2	MER19 repetitive element;	wm31f08.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.t2	MEN IS REPUBLIVE EIGHTEN.	ts56h10.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:060363 060363 SA GENE.;
	Top Hit Database Source	EST_HUMAN	EST_HUMAN	IN	TN	TN	NT	NT	EST_HUMAN	LN	EST_HUMAN	TN	NT	NT	NT	NT	NT	LN.	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	INT	EST_HUMAN	NT		EST_HUMAN	14 V M	ES! HOMAN	EST_HUMAN
	Top Hit Acession No.		1.0E-45 BE389855.1	4506412 NT	7657290 NT	U32169.1	8659558 NT	AB046811.1	1.0E-45 BE396633.1	11545796 NT	1.0E-45 BE887843.1	1.0E-45 AB002297.1	11418099 NT	11526291 NT	11418177 NT	11418157 NT	9910293 NT	9.0E-46 AL163209.2	9.0E-46 AW 246964.1	AI433261.1		AI433261.1	8.0E-46 BE167244.1	7.0E-46 BE386165.1	7.0E-46 BE064386.1	8922708 NT	7.0E-46 BF105845.1	7.0E-46 AL163246.2		6.0E-46 AI884381.1	_	6.UE-46 AI884381.1	6.0E.46 AI635448.1
	Most Similar (Top) Hit BLAST E Value	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45 AB0468	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	9.0E-46	9.0E-48	9.0E-46	8.0E-46 AI433261		8.0E-46 AI433261	8.0E-46	7.0E-46	7.0E-46	7.0E-46	7.0E-46	7.0E-46		6.0E-46	97 10 0	6.0E-40	6.0E-46
	Expression Signal	2.22	2.7	1.5	1.7	6.78	1.04	0.81	4.08	1.05	5.22	1.25	4.3	5.38	2.56	3.17	2.28	6.71	7.89	8.79		8.79	3.97	6.54	1.01	4.01	1.35	1.35		5.53	C L	5.53	8.85
	ORF SEQ ID NO:			20227	20915	22784	23171	23239	24055	24541	27347	27559	25358				26861		28077	22165		22166				25693	25943			22483		77484	25737
	Exon SEQ ID NO:	10349	10349	10407	11070	12992	13364	13442	14274	14765	17151	17355	18950	19067	19070	19324	16669	16895	17836	12270	1	12270	16572	14372	14587	15592	15818	19144		12588		12588	15634
	Probe SEQ ID NO:	118	403	464	1157	3065	3447	3526	4378	4884	7274	7485	9231	9415	9421	6820	6790	7018	986/	2392		2392	6692	4478	4701	5683	5912	9543		2726	2020	27.70	5727

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Single Extra Probes Explessed in Real	Top Hit Descriptor	601478409F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880995 5	Homo sapiens chromosome 21 segment HS21C010	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'	naa38107.x1 NC_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258757 3' similar to TR:O75202 O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC;	602021164F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'	no54e09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);	hl86c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gio.X14008_rns1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element;	hI86c03.X1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similer to gb.X14008_rna1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element :	Human endogenous retrovirus RTVL-H2	Homo sapiens mRNA for KIAA0622 protein, partial cds	Homo sapiens mRNA for KIAA0622 protein, partial cds	Human ig germiline gamma-3 heavy-chain gene V region, partial cds	Human ig germline gamma-3 heavy-chain gene V region, partial cds	Homo sapiens DNA for Human P2XM, complete cds	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline, Ig-Light-Lambda; VLambda	wJ49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMACE:2406150 3' similar to contains THR.b2 THR repetitive element;	Human mRNA for KIAA0061 gene, partial cds	ne06a09.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;	zi27a11.s1 Soares_feta_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3'	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
Jie Exoli Prop	Top Hit Database Source	EST_HUMAN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		_ LZ	LN	LN		L		NT	5	EST_HUMAN	LZ ⊢Z	EST_HUMAN	EST_HUMAN	NT TN
110	Top Hit Acession No.	6.0E-46 BE784971.1	5.0E-46 AL163210.2	5.0E-46 BE677194.1	5.0E-46 BE677194.1	5.0E-46 BF590442.1	5.0E-46 BF347229.1	4.0E-46 AA601143.1	4.0E-46 AW770544.1	4.0E-46 AW 770544.1	4.0E-46 M18048.1	4.0E-46 AB014522.1	4.0E-46 AB014522.1	M36852.1	4.0E-46 M36852.1	4.0E-46 AB002059.1	4506376 NT	273660.1	273660.1	3.0E-46 AI831462.1		2.0E-46 AA468646.1	2.0E-46 AA678246.1	
	Most Similar (Top) Hit BLAST E Value	6.0E-46	5.0E-46	5.0E-46	5.0E-46	5.0E-46	5.0E-46	4.0E-46	4.0E-46	4.0E-46	4.0E-46	4.0E-46	4.0E-46	4.0E-46 M36852.1	4.0E-46	4.0E-46	3.0E-46	3.0E-46 Z73660.1	3.0E-46 Z73660.1	3.0E-46	3.0E-46 D31765.1	2.0E-46	2.0E-46	2.0E-46 U78027.1
•	Expression Signal	3.03	6.41	1.12	1.12	1.79	3.52	1.51	3.57	3.57	3.55	1.07	1.07	1.84	1.84	1.91	0.8	1.13	1.13	8.3	2.63	5.91	1.32	2.43
	ORF SEQ ID NO:		_	23205		26074	26155		21446	21447	22464	23999	24000	25082	25083	25237	23976	24343	24344	27151	28955	, 20594		21385
	Exan SEQ ID NO:		10169	13400	13400	15942	16017	10562	11578	11578	12573	14217				19221	14192	14552	14552	16958	18668	10747	11447	11527
	Probe SEQ ID NO:	8694	197	3484	3484	6038	6144	625	1676	1676	2710	4320	4320	5338	5338	0996	4294	4666	4666	7081	8856	819	1542	1623

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4899	14779	24555	1.15	2.0E-46	AA399286.1	EST_HUMAN	2459e02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE Q01730 RSP-1 PROTEIN.;
6418	16280		6.78	2.0E-46		NT	Mus musculus sperm tail associated protein (Stap), mRNA
6703	16583		1.17	2.0E-46	2.0E-46 BE869151.1 EST	EST_HUMAN	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849297 5'
8571	18439		1.87	2.0E-46		NT	Homo sapiens small acidic protein (IMAGE145052), mRNA
9157	19629		1.75		2.0E-46 BF028854.1	EST HUMAN	601765225F1 NIH_MGC_53 Ното sapiens cDNA clone IMAGE:3997326 5'
9409	19525		1.44		2.0E-46 H48391.1	EST_HUMAN	yr32d01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:206977 5'
9728	19515	25136	3.81	2.0E-46	2.0E-46 AW277214.1	EST_HUMAN	xq78h03.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
1213	11121	20970	5.19	1.0E-46	4502694 NT	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2236	12121	L	4.6		1.0E-46 AW978516.1	EST_HUMAN	EST390625 MAGE resequences, MAGP Homo sapiens cDNA
2351	12231	L	2.59	1.0E-46		EST_HUMAN	EST48b095 WATM1 Homo sapiens cDNA clone 48b095
3211		_		1.0E-46	1.0E-46 AA631912.1	EST HUMAN	np78b02.s1 NCL_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H sapiens MT-1I mRNA. (HUMAN);
4772					 -	LN	Homo sapiens mRNA for KIAA0980 protein, partial cds
5495	_	25477			1.0E-46 BF194707.1	EST HUMAN	7692501.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
5636	19449	25639	5.66		8923762 NT	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
5636		_	5.66		8923762 NT	LΝ	Homo sapiens centaurin-apha 2 protein (HSA272195), mRNA
8236	15414	25477	4.26		1.0E-46 BF194707.1	EST_HUMAN	7692b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
9188	18923	25348	1.43		1.0E-46 BF531102.1	EST_HUMAN	602072264F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4215398 5'
9188	18923	25349	1.43	Ì	1.0E-46 BF531102.1	EST_HUMAN	602072264F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215398 5'
9925	19397		1.53		1.0E-46 AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
749	10679		4.51			NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
	l			1	7 00 00 00 00 00 00 00 00 00 00 00 00 00	1	higaed4x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:075703 075703
9682	19617	25001	1 84		9.0E-47 AVI 10320.1	LO LO	Homo saplens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
176B					V18536 1	TN.	Home saniens HI A-C dene exen 5 individual 19323
					7,0000	1	Home regions LII A Course E judicidad A0222
1766	11665	21540	14.02		8.0E-47 Y18536.1	Z	Homo sapiens FLA-C gene, exon 5, Individual 19323
2684	12549	22439	1.74	8.0E-47	5453955 NT	N L	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
2989	12917	7 22712			8.0E-47 AJ229043.1	LN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
2501	12376	3 22266	3.05		6.0E-47 AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7344	17212	27411	6.27		6.0E-47 AI695189.1 EST	EST_HUMAN	tz98h02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296659 3'
5963	Ŀ	3 25990	5.27		11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
8174	18062		3.91		5.0E-47 M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
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Table 4
Single Exon Probes Expressed in Heart

Top -lit Descriptor	Homo sapiens E1A binding protein p300 (EP300) mRNA	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5	xx66b07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE	Q64222 VIKAL IN LEGRATION SITE PROTEIN IN 1-6, [1].	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMACE:3899721 5	yy54b04.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:277327 3'	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens KIAA0439 mRNA, partial cds	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds	UI-HF-BM0-adx-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'	UI-HF-BM0-adx-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'	qh04e07x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:18437163'	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens chromosome 21 segment HS21C009	wq96b02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2479851 3'	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA	ng43h12.s1 NCI_CGAP_Co3 Homo saplens cDNA clone IMAGE:937607 3'	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds			Inf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652	Homo saplens Rev/Rex activation domain binding protein-related (RAB-R) mRNA			601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5	Homo saplens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo saplens SPH-binding factor mRNA, partial cds	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
Top Hit Database Source	NT	EST_HUMAN	EST_HUMAN	1	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	TN	LZ	EST_HUMAN	EST_HUMAN	EST_HUMAN	ΝΤ	NT	NT	EST HUMAN	INT	EST_HUMAN	NT	NT	EST HUMAN	EST HUMAN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	LN	LN	LN	NT
Top Hit Acession No.	4557556 NT	4.0E-47 BE616483.1	4.0E-47 BE616483.1		4.0E-47 AW 515509.1	3.0E-47 BE907634.1	3.0E-47 BE907634.1	3.0E-47 N57483.1	3.0E-47 AL163284.2	3.0E-47 AB007899.1	3.0E-47 U93181.1	3.0E-47 M12959.1	3.0E-47 AW 408800.1	3.0E-47 AW 408800.1	3.0E-47 AI222413.1	4505318 NT	2.0E-47 AL163209.2	2.0E-47 AL163209.2	2.0E-47 AI969279.1	7662109 NT	2.0E-47 AA524514.1	2.0E-47 AF060568.1	4504866 NT	2.0E-47 AA569592.1	2.0E-47 AA569592.1	5174648 NT	2.0E-47 AW965166.1		2.0E-47 BE778475.1	2.0E-47 L09731.1	2.0E-47 D87675.1	2.0E-47 D87675.1	2.0E-47 AF071771.1	4505318 NT
Most Similar (Top) Hit BLAST E Value	4.0E-47	4.0E-47	4.0E-47		4.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	3.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47
Expression Signal	3.41	2.06	2.06		4.84	1.75	1.75	5.17	8.9	1.5	4.99	76.0	4.26	4.26	1.89	4.27	2.18	2.18	1.18	1.22	4.44	2.3	1.66	1.75	1.75	2.06	1.1	1.6	1.6	1.33	2.1	2.1	1.77	5.77
ORF SEQ ID NO:	21140		ļ			20287	20288		20703	21770		23941	25666	25667		19936	20722	20723		21338		21974	23924	23967	23968	24084	24384		25638		26716			19936
Exon SEQ ID NO:	11284	16816	16816		18713	10474	10474	10730	10855	11877	13796	14164	15571	15571	15858	10116	10876	10876	11453	11479	11557	12072	14150	14186	14186	14300	14593	15549	15549	19464	16523	16523	16937	10116
Probe SEQ ID NO:	1379	6938	6938		8905	532	532	801	930	1984	3885	4265	5659	699	5953	142	952	952	1548	1575	1654	2185	4251	4287	4287	4406	4707	5635	5635	6532	6643	6643	7060	9070

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Single Exon Probes Expressed in Heart

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Top Hit Descriptor	yf92e08.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE.29966 3' similar to contains OFR repetitive element;	Hamo sapiens chromosome 21 segment HS21C009	qp99h03.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3'	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE;3138893 5'	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA	at19e06.x1 Barstead aorta HPLRB6 Horno sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995 RAS-RELATED PROTEIN RAP-1A (HUMAN);	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	CM2-MT0100-310700-290-f05 MT0100 Homo sapiens cDNA	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5	Homo sapiens aminoacylase 1 (ACY1), mRNA	Homo sapiens aminoacylase 1 (ACY1), mRNA	hk61b03.x1 NCI_CGAP_Lym12 Homo saplens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);	hk61b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb.X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN):	Homo sapiens mRNA for KIAA1209 protein, partial cds	Homo sapiens mRNA for KIAA1209 protein, partial cds	Homo sapiens touslod-like kinase 1 (TLK1), mRNA	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	Homo saplens histidy-tRNA synthetase (HARS), mRNA	Homo sapiens putative oncogene protein mRNA, partial cds	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA	zq45b06.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA	tu47a02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2254154 3'	AV690964 GKC Homo sapiens cDNA clone GKCDRE12 5'	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA	Homo estiane chromosoma V men reading from a (OVODE) DAIA
Top Hit Database Source	EST_HUMAN	NT	EST_HUMAN	HOMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	L	N⊤	EST HUMAN	EST HUMAN		N	EST_HUMAN	EST HUMAN	T	NT	占	LN L	LN	LN	LN	T HUMAN	NT	EST HUMAN	EST_HUMAN	N	
Top Hit Acession No.	342423.1	2.0E-47 AL163209.2	1	.1		1.0E-47 AW813906.1	A1880886.1		· -	9.0E-48 BF359947.1	9.0E-48 BE393813.1	4501900 NT	4501900 NT	8.0E-48 AW768477.1	8.0E-48 AW 768477.1		7.0E-48 AB033035.1	6912719 NT	5730038 NT	11416831 NT	6.0E-48 AF026816.1	11427428 NT	6.0E-48 AA189080.1	26891	4.0E-48 AI620420.1	3.0E-48 AV690964.1	4885170 NT	4885170 NIT
Most Similar (Top) Hit BLAST E Value	2.0E-47 R42423.1	2.0E-47 #	1.0E-47 Al333429	1.0E-47 BE280477	1.0E-47	1.0E-47	1.0E-47 AI880886.	1.0E-47 L30115.1	9.0E-48 AF223391	9.0E-48	9.0E-48	8.0E-48	8.0E-48	8.0E-48 /	8.0E-48/A	7.0E-48 /	7.0E-48 ₽	7.0E-48	7.0E-48	7.0E-48	6.0E-48	6.0E-48	6.0E-48 △	5.0E-48	4.0E-48 /	3.0E-48	3.0E-48	3 OF.48
Expression Signal	1.98	1.32	4.5	0.79	0.79	2.59	7.68	1.75	2.34	0.83	3.22	1.32	1.51	3.62	3.62	1.37	13.37	1.12	3.49	22.88	1.52	1.9	3.38	1.39	3.55	0.92	18.97	18 97
ORF SEQ ID NO:	24988		21142	23443	23444	24648	26086	28017	21358	23228	28595			22818	22819			21250	21382	25975	27348	27577	27654	22989	28451	21124	21710	21711
Exon SEQ ID NO:	19658	19659	11288		13662	14882	15954	17778	11499	13425	18333	11138	11138	13023	13023	10426	10426	11387	11524	15852	17152	17370	17438	15067	18202	11269	11828	11878
Probe SEQ ID NO.	9219	9257	1383	3749	3749	5008	6194	7928	1595	3509	8460	1230	1231	3096	3096	482	483	1482	1620	5947	7275	7500	7587	3269	8325	1363	1933	1933

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Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	h14b12.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCRB_HUMAN P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B.;	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA	nv03f05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219137.3' similar to contains PTR5.b1	PTR5 repetitive element ;	UI-H-BW1-ani-a-10-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'	fmfc7 Regional genomic DNA specific cDNA library Homo saplens cDNA clone CR17-26	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukernia Baylor-HGSC project=TCBA Homo sapiens cDNA cione TCBAP3842	no18g01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'	no18g01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:11010723'	Homo sapiens mRNA for KIAA1501 protein, partial cds	Homo sapiens mRNA for KIAA1501 protein, partial cds	Homo sapiens v-rel avian reticulcendotheliosis viral oncogene homolog A (nuclear factor of kappa light	polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA	AV743451 CB Homo sapiens cDNA clone CBCCGG10 5'	zx80c03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810052.5'	601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'	Homo sapiens cisplatin resistance associated overexpressed protein (LOC51747), mRNA	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA	Homo sapiens RNA binding motif protein 6 (RBM6) mRNA	Homo saplens chromosome 21 segment HS21C102	Homo sapiens chromosome 21 segment HS21C046	Human endogenous retroviral DNA (4-1), complete retroviral segment	Homo sapiens huntingtin (Huntington disease) (HD) mRNA	Homo sapiens mRNA for KIAA1245 protein, partial cds	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5	Homo sapiens B cell linker protein (SLP65), mRNA	Homo sapiens B cell linker protein (SLP65), mRNA	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds	15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	Mus musculus T-box 20 (Tbx20), mRNA
	Top Hit Database Source	EST_HUMAN	EST_HUMAN		EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	님	N		LZ	EST_HUMAN	EST HUMAN	EST_HUMAN	TN	LN	IN	NT	LN	NT	LN	NT	EST_HUMAN	NT	LN	LN	TN	1.1 EST HUMAN	N.
	Top Hit Acession No.	31.1	1.1			3.0E-48 BF514170.1	A631940.1	2.0E-48 BE246065.1	<u></u>	 -	<u>_</u>	2.0E-48 AB040934.1		11496238 NT	2.0E-48 AV743451.1	2.0E-48 AA465007.1	2.0E-48 BE737154.1	7706534 NT	4502166 NT	5032032 NT	1.0E-48 AL163302.2	AL163246.2		4755137 NT	1.0E-48 AB033071.1	1.0E-48 BF304683.1	11429808 NT	11429808 NT	1.0E-48 AF119117.1	AF119117.1	1.0E-48 W 26785.1	10048417
	Most Similar (Top) Hit BLAST E Value	3.0E-48 AW6645	3.0E-48 BE08457		3.0E-48 /	3.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48 AA613171	2.0E-48	2.0E-48		2.0E-48	2.0E-48	2.0E-48	2.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48 M10976	1.0E-48	1.0E-48	1.0E-48	1.0E-48		1.0E-48	1.0E-48 AF11911		8.0E-49
	Expression Signal	0.88	2.35		2.86	7.08	1.18	1.35	72.29	72.29	4.29	4.29		2.9	2.39	2.45	1.63	0.85	6.93	3.26	44.65	1.23	1.1	2.21	5.72	4.48	5.06	5.05	1.73	1.73	1.56	2.95
	ORF SEQ ID NO:	23284				28376	19827	24114			26464	L		26473	26936	24828	25070	19844	20632			23167	24728	26325			L	28024	29094	29095		25702
	Exon SEQ ID NO:	13493		l	16768	18128	10027	14326	15469	15469	16301			16308	16743	15082	19579	10037	10782	11182		13360	14952	16167	17205		_	17784	18802	18802	19606	15601
	Probe SEQ ID NO:	3579	5592		6889	8248	39	4431	5553	5553	6440	6440		6447	6864	9184	9511	S	855	1274	1876	3443	5082	6303	7337	7526	7934	7934	8999	8999	9145	5692
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Single Exon Probes Expressed in Heart

Single Exoli Probes Expressed in near	Expression (Top) Hit Acession Signal Top Hit Acession Signal Top Hit Descriptor Signal Value Value Top Hit Descriptor Source	2.95 8.0E-49 10048417 NT Mus musculus T-box 20 (Tbx20), mRNA	3.19 8.0E-49 U23850.1 NT Human inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds	1.47 7.0E-49 5729990 NT Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA	1.47 7.0E-49 5729990 NT		7.0E-49 5729990 NT	7.0E-49 5729990 NT		4.05 7.0E-49 AL163284.2 NT	0.95 7.0E-49 G60811 SWISSPROT HYPOTHETICAL PROTEIN DJ845024.3	7.0E-49 Al807191.1 EST HUMAN 054923 RSEC15.	1.34 7.0E-49 AL120937.1 EST_HUMAN DKFZp762C033_s1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762C033 3'		11.77 SUCE-49 AW 13 140.1 EST HOMAN COMPRERE (MOUSE);	6 0F-49 AA366556 1 FST HIMAN	6 0F-49 AA366556 1 FST HIMAN	6.0E-49 AA707567.1 EST HUMAN	Homo sapiens chromosome 21 segment HS21C010	3.37 5.0E-49 AL163210.2 NT Homo sapiens chromosome 21 segment HS21C010	229c07.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE.610860 5 similar to 1.94 5.0E-49 AA172121.1 EST HUMAN TR:G233226 G233226 RTVL-H PROTEIN ; contains LTR7.f3 LTR7 LTR7 repetitive element	Г	5.13 5.0E-49 11436355 NT Homo sapiens similar to ribosomal protein S27 (metallopanstimulin 1) (H. sapiens) (LOC63362) mRNA	37.46 4.0E-49 AW189533.1 EST HUMAN CE06703 : CEGAP_Ut4 Home sapiens cDNA clone IMAGE:2675593.3 similar to WP:B0350.2B	4.0E-49 AA210798.1	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	0.93 3.0E-49 XB8968.1 NT H.sapiens mRNA for acetyl-CoA carboxylase
	Most Similar (Top) Hit BLAST E Value		8.0E-49															ĺ									
	Exon ORF SEQ E SEQ ID NO:	15601 25703	16706 26900	10335 20157	10335 20158	10335 20157			10335 20158	11112 20958	14443 24227	15271 25100	15277 25107					19498	10628 20452	10628 20453	11653 21524	12583 22477	13159 22957	10456 20266	19710	19090	10489 20298
	Probe Ex SEQ ID SEC NO: NC	5692 15	6827 16	134 10	134 10	388 10			389 10		4550 14	5351 15	5357 16	9		1_	L	9507 19	Ĺ.,		1753 11	2721 12	3235 13	514 10	9376 19		548 10

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Single Exon Probes Expressed in Heart

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onige Lyon Flores Lypiessed in real	Top Hit Descriptor	ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380584 5' similar to contains L1 t3 L1 repetitive element;	Human type IV collagen (COL4A6) gene, exon 40	EST25e12 WATM1 Homo sapiens cDNA clone 25e12	EST42572 Endometrial tumor Homo sapiens cDNA 5' end	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA	yx23d06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE.262571 5'	Homo sapiens RNA binding protein II (RBMII) gene, complete cds	oz88d02.xt Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA cione IMAGE:1682403 3' similar to gb:M31470 RAS-LIKE PROTEIN TC10 (HUMAN);contains Alu repetitive element;contains element MER22 repetitive element.		U-H-BI4-abs-d-uz-u-U.S1 NCI_C:3AP_Sub8 Homo saplens cDNA clone IMAGE:3088538 3	AV717838 DCB Homo sapiens cDNA clone DCBALB01 5	EST02558 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY50	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5	601115769F1 NIH_MGC_16 Homo sapiens cDNA clone IMACE:3356273 5'	601820053F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052052 5'	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5	601290330F1 NIH_MGC_8 Homo sapiens cDNA done IMAGE:3620863 5'	w78g12.s1 Soares_placenta_8to9weeks_ZNbHP8to9W Homo sapiens cDNA clone IMAGE.258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);	yw78g12.s1 Soares_placenta_8to9weeks_2NbHP8to8W Homo sapiens cDNA clone IMAGE.258406 3 similar to gb.X65873 KINESIN HEAVY CHAIN (HUMAN);	Homo saplens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA	601300992F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'	DKFZp434D2423_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2423 5	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA	MR0-HT0407-010200-006-f02 HT0407 Homo sapiens cDNA	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds	Homo sapions chromosome 21 segment HS21C002	Homo sapiens mRNA for VIP receptor 2
שום ביוחעים פול	Top Hit Database Source	EST_HUMAN	IN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	NT	NAMUH TZA	איטאיטו איט			EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	LN	L	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN	TN	NT	⊢N	N.
	Top Hit Acession No.	3.0E-49 AA016131.1	3.0E-49 U46999.1	139479.1	3.0E-49 AA337561.1	2.0E-49 BE165980.1	V26446.1	2.0E-49 AF026564.1	2 OF-49 A1167357 1	TE440404	2.0E-49 BF511845.1	2.0E-49 AV /1/938.1	VI86033.1	2.0E-49 AF163864.1	1.0E-49 BF035327.1	1.0E-49 BE255216.1	1.0E-49 BF131007.1	1.0E-49 BE398110.1	1.0E-49 BE398110.1	125884.1	V25884.1	11321580 NT	11321580 NT	BE409340.1	1.0E-49 AL043129.2	11427366 NT	1.0E-49 BE159343.1	11418322 NT	9.0E-50 AF101475.1	8.0E-50 AL163202.2	(95097.2
	Most Similar (Top) Hlt BLAST E Value	3.0E-49	3.0E-49	3.0E-49 H39479.1	3.0E-49	2.0E-49	2.0E-49	2.0E-49	2 0F-49	20.2	2.0E-49	2.0E-49 /	2.0E-49 M86033.1	2.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49 N25884.1	1.0E-49 N25884.1	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	9.0E-50 /	8.0E-50 /	8.0E-50 X95097.2
	Expression Signal	2.01	2.08	9.6	2.3	2.66	1.4	0.93	1 12	100	67.	1.47	1.97	1.53	3.95	2.58	4.97	2.93	2.93	2.17	2.17	1.29	1.29	1.22	1.21	3.88	1.73	2	1.06	2.59	1.89
ľ	ORF SEQ ID NO:		24564	26409	28759		22914		24373		24381	c/09Z						26307	26308	26346	26347	26777	26778		27924	28769					20460
	Exon SEQ ID NO:	12479	14788	16248	18487	10582	13110	13437	14579	7 4500	14590	15943	16597	19599	10807		Li	16151	16151	16185	16185	16589	16589	17077	17680	18495	18813	19035	14802	10136	10635
	Probe SEQ ID NO:	2611	4909	6386	8621	645	3185	3521	4693	7307	4/04	5040	6717	9467	881	1760	5289	6287	6287	6322	6322	6209	6209	7200	7830	8630	9018	9367	4923	163	702

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						יייי יייייי טולי	Onigo Exert Tobac Expression
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
761	10691		4.91	2.0E-50	2.0E-50 AF055066.1	.LN	Homo sapiens MHC class 1 region
1063	10979	20823	4.6	2.0E-50	4557752 NT	L	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
1425	11330	21197	18.02	2.0E-50	2.0E-50 AF138303.1	IN	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
6924	16802	26995	6.27	2.0E-50	2.0E-50 X06956.1	TN	Human HALPHA44 gene for alpha-tubulin, exons 1-3
6924	16802	26996		2.0E-50	2.0E-50 X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
7686	17536	27761	1.53	2.0E-50	9910293 NT	TN	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
7686	17536	27762	1.53	2.0E-50	9910293 NT	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
235	10204	20018	1	1.0E-50	1.0E-50 BE007080.1	EST_HUMAN	PM3-BN0137-290300-002-g11 BN0137 Homo sapiens cDNA
235	10204		-	1.0E-50		EST_HUMAN	PM3-BN0137-290300-002-g11 BN0137 Homo sapiens cDNA
454	10398	20215	2.1	1.0E-50	1.0E-50 AL163209.2	LN	Homo sapiens chromosome 21 segment HS21C009
2314	12195		86.8	1.0E-50	1	IN	Homo sapiens Xq pseudoautosomal region; segment 1/2
7375	17244	27450	1.22	9.0E-51	9.0E-51 AA043738.1	EST_HUMAN	zk51c09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486352 5'
4467	14361	24151	4.89	8.0E-51	8.0E-51 AA610842.1	EST HUMAN	np98e09.s1 NC_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6510	16369		2.34	8.0E-51	11439587 NT	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
7448	17257		1.28	8.0E-51	8.0E-51 AU138590.1	EST_HUMAN	AU138590 PLACE1 Homo sapiens cDNA clone PLACE1008887 5'
3245	13168	22967	1.36	7.0E-51	7.0E-51 AW889219.1	EST HUMAN	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
3317	13238		0.83	7.0E-51	7.0E-51 AW274720.1	EST_HUMAN	xn34a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE.2695564 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN .;
4076	13978		1.26	7.0E-51	1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4076	13978		1.26	7.0E-51	7.0E-51 AL079628.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4254	14153		2.38	7.0E-51	7.0E-51 AW295603.1	EST_HUMAN	UI-H-BW0-alp-b-05-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729817 3'
1936	11831	21714	5.3	6.0E-51	7657266 NT	TN	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3428	13345	23150	12.92	6.0E-51		LN	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4212	14110	23887	0.78			NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
4212	14110		0.78	6.0E-51		NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
5645	15558		2.26		6.0E-51 X01788.1	LΝ	Human haptoglobin related (Hpr) gene exon 3
5650	15562		6.68		.1	LN	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
5650	j				6.0E-51 AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6158					1	LN	Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA
7583				6.0E-51	7	NT	Homo sapiens B9 protein (B9), mRNA
8580	18448	28716	1.72	6.0E-51	11526289[NT	LZ	Homo sapiens interfeukin 17 receptor (IL17R), mRNA

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ſ		T		Т	T	Г	Γ	Т		Τ		T	1	4	Τ-	T	T	Ť	T	T ₌	Т		T	Τ	T	<u></u>	ΪÏ
olligie excit frobes expressed iii fregit	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Novel human gene mapping to chomosome X	Homo sapiens 26S proteasome associated pad1 homolog (POH1) mRNA	Homo sapiens mRNA for nucleoporin 155	Human Ku (p70/p80) subunit mRNA, complete cds	Human Ku (p70/p80) subunit mRNA, complete cds	Homo sapiens mRNA for KIAA1411 protein, partial cds	Homo saplens RNA binding motif protein 3 (RBM3), mRNA	tr81c09.x1 NC_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);	tr81c09.x1 NCL_CGAP_Pan1 Homo septens cDNA clone IMAGE.2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN):	Novel human gene mapping to chomosome 22	ya47c08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);contains LTR5 repetitive element;	Human hnRNP C2 protein mRNA	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'	2/30a05.11 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE.664880 5' similar to TR:G233226 G233226 RTVL-H PROTEIN, contains LTR7.t3 LTR7 repetitive element:	ti27g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732.3'	UI-H-BI1-adj-d-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'	601470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'	ts74a07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:1RKC_HUMAN Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR;	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
JIE EXOII PIOD	Top Hit Database Source	NT	NT	LN	LN	TN	ΙN	LN	LN LN	NT	EST_HUMAN	EST HUMAN	LN	EST HUMAN	TN	LN LN	L	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	5.0E-51 AL163203.2	4507500 NT	5.0E-51 AL133204.1	5031980 NT	.1			5.0E-51 AB037832.1	5803136 NT	3.0E-51 Al587348.1	AI587348.1	1	315914.1	M29063.1	3.0E-51 AF003528.1	TN 867798	2.0E-51 BE391063.1	2.0E-51 BE391063.1	AA233352.1	2.0E-51 AI492415.1	2.0E-51 AW137826.1	2.0E-51 BE782015.1	2.0E-51 BE901994.1	2.0E-51 BE901994.1	2.0E-51 AI917078.1	3E165980.1
	Most Similar (Top) Hit BLAST E Value	5.0E-51	5.0E-51	5.0E-51	5.0E-51	5.0E-51	5.0E-51 M30938.1	5.0E-51 M30938.1	5.0E-51	5.0E-51	3.0E-51	3.0E-51	3.0E-51	3.0E-51 R15914.1	3.0E-51 M29063.1	3.0E-51	2 0F-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51
	Expression Signal	10.92	1.47	1.37	0.84	11.48	1.08	1.08	2.34	3.72	0.92	4.16	2.13	1.73	5.87	1,58	181	1.08	1.08	2.24	2.21	1.02	2.95	1.61	1.61	1.68	5.25
	ORF SEQ ID NO:	20543	20557	20745	21354	22311	23566	23567	24643	28739	19926	20917	23906	26500			20139		20425	21431	23373	24071		27114	27115		27600
	Exon SEQ ID NO:	10704	10715	12682	11494	12422	13774	13774	14879	18468	10104	11072	14130	16333	17008	19233	10318	10607	10607	11564	13586	14288	15573	16924	16924	17348	17390
	Probe SEQ ID NO:	774	786	975	1590	2548	3863	3863	5004	8601	130	1159	4232	6474	7131	9675	362	673	673	1662	3672	4392	2995	7047	7047	7478	7539

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		- 1																		·	السد		11. 11. 4. 41. 0. 11
oligie Exori Frobes Expressed in Healt	Top Hit Descriptor	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5	ob34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT FPSII ON 1 PRECLIPSOR	033409.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE INMDA! RECEPTOR SURINIT EPS!! ON 1 PDECLIDENCE	Homo saplens myelodd/ymphold or mked-lineage feukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLT4), mRNA	Homo sabiens eukarvotic translation initiation factor 44 incferm 1/EIE4441 Entry	AV742248 CB Homo sapiens cDNA clone CRERCC12 5	Homo sapiens small inducible cytokine subfamily A (Ora-Ora) member 15 (SCVA15)	Homo sapiens small inducible cytokine subfamily A (Ox. Ox), member 15 (SOXA15), mixiva	1012056t Testis 1 Homo saciens chine Aranis Aranis	AV760590 MDS Homo sabiens cDNA clone MDSCRR02 5'	295e07.s1 Soures_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR to THR repetitive element	nw21g02.s1 NGI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR t3	H.sapiens mRNA for laminin-5 alpha3b chain	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	nomo sapiens nypotnetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA	Homo sapiens hypothetical protein FLJ13556 similar to N-mx; downstream remilated 3 / E1 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE2 143 EE	zc59a06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element:	QV3-BT0537-271299-049-d07 BT0537 Homo sapiens cDNA	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds	tz46h04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PGBM_MOUSE Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR;
gie Lauri r ru	Top Hit Database Source	EST HUMAN	EST_HUMAN	EST HUMAN	LN	TN	EST HUMAN	ï	LN	EST HUMAN	EST HUMAN	EST HUMAN	MANI H TSE	N	LIA LIA	2	LN	LNT	LN.	EST HUMAN	EST_HUMAN	N	EST_HUMAN
5	Top Hit Acession No.	2.0E-51 AV682474.1	2.0E-51 AI732851.1	2.0E-51 AI732851.1	11419159 NT	4503528 NT	1.0E-51 AV742248.1	4759071 NT	4759071 NT	T18862.1	1.0E-51 AV760590.1	AA777621.1	AA720574 1		14060000	1 1800020	11968028 NT	11968028 NT	11968028 NT		6.0E-52 BE072409.1	1	6.0E-52 BE048172.1
	Most Similar (Top) Hit BLAST E Value	2.0E-51	2.0E-51	2.0E-51	2.0E-51	1.0E-51	1.0E-51	1.0E-51	1.0E-51	1.0E-51	1.0E-51	9.0E-52 AA77762	8.0E-52.AA72057	8.0E-52 X84900.1	C T L	0.0L-3k	8.0E-52	8.0E-52	8.0E-52	7.0E-52 W56471.1	6.0E-52	6.0E-52 AF109907	6.0E-52
	Expression	1.71	8.63	8.63	1.33	4.4	22.7	96.0	0.96	3.12	3.57	3.28	7.31	1.33	2.05	2	2.05	6.44	6.44	1.48	0.86	2.25	2.23
	ORF SEQ ID NO:	28054	25084	25085	25240	19905		23989	23990	25036			19939	21249	21397		21398	21397	21398	27278		21438	28678
	Exon SEQ ID NO:	17812	15259	15259	19227	10090	11383	14206	14206	15231	19771	19086	10120	11386	11537		11537	11537	11537	17088	11082	11570	18412
	Probe SEQ (D NO:	7962	8640	3640	3668	109	1478	4309	4309	5310	8980	9454	146	1481	1633		1633	3913	3913	7211	1170	1668	8540

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Single Exon Probes Expressed in Heart

Exon NO: 14237 CRF SEQ 24021 Expression Signal Value Most Similar (Top) Hit Value Top Hit Acession Source Top Hit Acession Value Top Hit Source 14237 24021 2.07 5.0E-52 Z78898.1 NT 11648 2.1616 8.58 4.0E-52 AF287318.1 NT 11648 2.1656 0.82 4.0E-52 AF287318.1 NT 11648 2.1656 0.82 4.0E-52 AF287318.1 NT 11648 2.1656 0.82 4.0E-52 AF587318.1 NT 16866 2.6760 1.24 4.0E-52 BE622032.1 EST HUMAN 16873 2.7035 2.0E-52 BE622032.1 EST HUMAN 16873 2.0259 4.0E-52 BE677892.1 NT 10491 2.0259 1.39 2.0E-52 A11418477 NT 10491 2.0250 1.75 2.0E-52 BE77892.1 EST HUMAN 1559 2.0550 2.0E-52 A1478804.1 RT HUMAN 15747
Probe Ex SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID

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Table 4
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			T	T	T	Т		T	7	Т			T	1	Τ	7		T	T	Т	7	T	T	T		1	7	Т	Т	т.	77 700
Chigo Lyon Lobos Lypicosed III Ieali	Тор Hit Descriptor	Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL) mRNA	Homo sapiens arykulfatase D (ARSD), transcript variant 1, mRNA	pol=reverse transcriptase homolog {rotroviral element} [human, endogenous retroviral element RTVL-Hp1,	Human P-alycoprotein (MDR1) gene even 4	Human PMS2 related (hPMSR2) dene, complete ads	Human aldolase C gene for fructose-1.6-bisphosophate aldolase	Homo sapiens chromosome 21 segment HS21C027	Homo sapiens chromosome 21 segment HS21C002	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA complete cds	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMR2), mRNA	Homo sapiens protein kinase, cAMP-dependent, regulatory type heta (PRKAR2R) mENA	Homo sapiens core binding factor alpha1 subunit (CBFA1) acne exon 3	Homo sapiens predicted osteoblast protein (GS3786), mRNA	601904771F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132793 5	#44f07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2099077 3' similar to contains THR.:1 THR repetitive element:	Homo sapiens beterodened is nuclear ribonic learning (C1/C2) (LNISBC)	RC3-ST0197-151099-011-010 ST0197 Home canisms COM	Homo saplens chromosome 21 segment HS21C085	Homo saplens chromosome 21 segment HS21C085	Homo sapiens hook1 protein (HOOK1), mRNA	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes,	Full Dieter Cds)	WZZZUJI XI Soales Dreckgrede Colon, NHCD Homo sapiens cDNA clone IMAGE: 2558796 3'	10-V3-RT0381-270100-77-406 BT0381 12-2-2-2011	GF=growth Inhibition factor fluman brain Garamic 2045 at	Homo sapiens FGFR1 oncorane narhar (FOP) mRNA	EST77525 Pancreas tumor III Homo sapiens cDNA 5 end	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
שום באטוו רוכ	Top Hit Database Source	NT	LN	LIV	LZ	IN	N L	TN	L	Z	LN	Z	FZ	Z	EST HUMAN	EST HIMAN	1.	EST HUMAN		LN	Z	EST_HUMAN	EST HUMAN	H	TOT CLANN	EST HIMAN	EST HIMAN	LN LN	Z-L	EST_HUMAN	LN-
	Top Hit Acession No.	4504026 NT	4502238 NT	564070 4	A29426.1	J38964.1	(07292.1		1.0E-52 AL163202.2	148296.1	11426321 NT	4506064 NT	9.0E-53 AF001446.1	7661713 NT	7.0E-53 BF238465.1	<u> </u>	4758543	3.1	2		7705414 NT	.1	.1				-		5901953	+	
	Most Similar (Top) Hit BLAST E Value	1.0E-52	1.0E-52	1 0E-50 S61020 1	1.0E-52 M29426.1	1.0E-52 U38964.1	1.0E-52 X07292.1	1.0E-52 AL163227	1.0E-52	1.0E-52 U48296.1	1.0E-52	9.0E-53	9.0E-53	9.0E-53	7.0E-53	7.0E-53 AI421782	5.0E-53	5.0E-53 AW81356	4.0E-53 AL163285.	4.0E-53 A	4.0E-53	4.0E-53 BF128701	4.0E-53 BF128701	3 OE_53 AB026808	3 0E-53 A	3.0F-53 AW803563	3 0F-53 BF069344	3.0E-53 S72043.1	3.0E-53	2.0E-53 AA366556	2.0E-53 U78027.1
	Expression Signal	8.25	1.2	1 41	3.59	2.11	3.19	1.64	1.61	1.84	2.04	1.03	1.01	0.93	2.06	2.98	2.2	1.72	1.92	1.92	1.09	3.33	3.33	2 50	1 20	1 18	0.85	9.88	8.59	4.25	2.98
	ORF SEQ ID NO:	21111		22741		25875				28283			23975	24611			23690		19834	19835	24387	28685	28686	22384	23371	24167	24498				22060
	Exon SEQ ID NO:	11255	12364	12949	15192	15757	16256	16810	17873	18035	18094	13635	14191	14841	19018	19632	13915	19048	10031	10031	14601	18417	18417	12493	13584	14380	14715	16712	17115	10394	12163
	Probe SEQ ID NO:	1349	2489	3021	5270	5851	6394	6932	8023	8147	8210	3723	4293	4966	9338	9752	4009	9389	43	43	4715	8545	8545	2625	3670	4486	4833	6833	7238	450	2279

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Single Expires Expressed in Real	Top Hit Descriptor	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton purrp) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin Detaled (CBFA2T1) mRNA	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene exon 6	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds	Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA	Homo sapiens chromosome 21 segment HS21C081	Homo sapiens chromosome 21 segment HS21C081	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA	2822665.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822665 5'	Homo saplens Xq pseudoautosomal region; segment 2/2	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	Conjuste cus)	H senions mRNA for hardness section 8 due 1 de 1 de 1 de 1 de 1 de 1 de 1 de	Homo saniens T-cell lymphoma invasion and matastasis 4 /TIAM41ON A	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	Homo sapiens ublquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA	ai 79c12.s1 Soares testis NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.t3 MER30 repetitive element:	Homo sapiens mRNA for monocyte chemotactic protein-2	yw68d12.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7.b3 LTR7 repetitive element;
JIE EXULI PIUL	Top Hit Database Source	N	TN	Į.	NT	LN LN	TN	L	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	l l	EST HIMANI		L	LN LN	NT	EST_HUMAN	ΙΝ	TN	NT	N T	NT	TN	EST HUMAN	NT	EST_HUMAN
310	Top Hit Acession No.	4502316 NT	4757915 NT	4757915 NT	2.0E-53 AF083822.1	2.0E-53 M61873.1	4506962 NT	2.0E-53 AL163281.2	2.0E-53 AL163281.2	2.0E-53 BF334740.1	2.0E-53 BF334740.1	5.1	1.0E-53 AJ271736.1	4 00 000000 4			4507500	4507500 NT	4506786 NT	BE386785.1	4504610 NT	4507848 NT	4507848 NT	4507848 NT	4507848 NT	6005700 NT	7.0E-54 AA812537.1		
	Most Similar (Top) Hit BLAST E Value	2.0E-53	2.0E-53	2.0E-53	2.0E-53	2.0E-53	2.0E-53				2.0E-53	2.0E-53	1.0E-53	70.7	1.0E-53	1 0F.53	9.0E-54	9.0E-54	9.0E-54	8.0E-54	8.0E-54				8.0E-54	8.0E-54	7.0E-54	7.0E-54 Y16645.1	7.0E-54 N27177.1
	Expression Signal	10.54	6.93	6.93	1.18	2.06	1.07	1.12	1.12	3.11	3.11	5.6	6.0	*	1 42	5 14	0.8	0.8	4.71	3.09	1.33	1.25	1.25	1.08	1.08	20.81	1.26	1.54	4.61
	ORF SEQ ID NO:		22446	22447	22933	23653		24735	24736	25056	25057		21200	20000			24787	24788	24939	19988	21568	24307	24308	24307	24308	25612	20186	21563	21945
	Exon SEQ ID NO:	12365	12559	12559	13131	13877	14286	14961	14961	15251	15251	17280	11334	12083	15925	17129	15019	15019	19439	10172	11692	14517	14517	14517	14517	15529	10363	11687	12045
	Probe SEQ ID NO:	2490	2694	2694	3207	3970	4390	5091	5091	5331	5331	7413	1429	7366	6021	7252	5152	5152	5244	200	1794	4629	4629	5030	5030	5614	379	1789	2158

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Single Exon Probes Expressed in Heart

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Olligie Lauri Fiudes Lapressed III Feat	Top Hit Descriptor	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA	db67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204.3' similar to contains OFR.t1 OFR repetitive element;	Homo sapiens DNA for MICB, exon 4, 5 and partial cds	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA	Homo sapiens chloride channel 6 (CLCN6) mRNA	AV754746 TP Homo saplens cDNA clone TPGAAC10 5'	H.sapiens shc pseudogene, p66 isoform	H.sapiens shc pseudogene, p66 isoform	RC3-ST0197-151099-011-f08 ST0197 Homo sapiens cDNA	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)	Tupaia belangeri beta-actin mRNA, partial cds	EST177696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate	dehydrogenase	Human mRNA for KIAA0077 gene, partial cds	Human mRNA for KIAA0077 gene, partial cds	wd26d11x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:O02711 D02711 PRO-POL-DUTPASE POLYPROTEIN :	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end	DKFZp434E0731_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0731 5'	IL-BT189-190399-007 BT189 Homo sapiens cDNA	Homo saplens BMX non-receptor tyrosine kinase (BMX) mRNA	ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3	ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'	602019408F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155121 5	270f12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315 G191315 G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN.;	EST366629 MAGE resequences, MAGC Homo sapiens cDNA	RC1-BT0313-131199-011-b09 BT0313 Homo saplens cDNA	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
ביים ביים	Top Hit Database Source	LN	EST HUMAN	NT TN	NT.	IN	NT	NT	EST_HUMAN	NT	닐	EST_HUMAN	SWISSPROT	NT		EST_HUMAN	TN	LN	EST HIMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	NT	N
31110	Top Hit Acession No.	11417222 NT	7.0E-54 AI160189.1	8.1	4505052 NT	4505052 NT	8922148 NT	4502872 NT	6.1	Y09846.1	709846.1	6.0E-54 AW813567.1	>51523	4.0E-54 AF110103.1		4.0E-54 AA306764.1	J39521.1	J38521.1	4 OF-54 A1035086 1			AI908757.1	4502434 NT	3.0E-54 AA844061.1	3.0E-54 AA844061.1	3.0E-54 BF345600.1	3.0E-54 AA393362.1		1	TN 0091505	4507164 NT
	Most Similar (Top) Hit BLAST E Value	7.0E-54	7.0E-54 /	6.0E-54 AB00361	6.0E-54	6.0E-54	6.0E-54	6.0E-54	6.0E-54	6.0E-54 Y09846.1	6.0E-54	6.0E-54	5.0E-54 P51523	4.0E-54 /		4.0E-54	4.0E-54 D39521.	4.0E-54 D38521.	4 OF-54 4	3.0E-54	3.0E-54	3.0E-54 AI908757	3.0E-54	3.0E-54	3.0E-54	3.0E-54	3.0E-54	3.0E-54/	3.0E-54	2.0E-54	2.0E-54
	Expression Signal	2.23	6.24	1.54	78.0	78.0	0.84	2.4	1.24	1.7.1	1.3	1.77	2.25	106.86		41.94	3.24	3.24	1 17	5.11	0.92	0.88	1.48	1.58	1.68	4.17	3.34	2.86	7	6.29	1.94
	ORF SEQ ID NO:	27925		19802	21605	21606	22968	23612	24040			28143	21893	-		20712	21536	21537		19888	22287	-	25590	26394	26395	28565	28847			20374	21105
	Exon SEQ ID NO:	17681	18478	10009	11730	11730	13169	13832	14255	14658	14658	17899	11993	10147		10865	11663	11663	13003	10072	12396	12454	15512	16235	1	18309	18563	1			11248
	Probe SEQ ID NO:	7831	8611	22	1833	1833	3246	3923	4359	4774	4930	8750	2104	176		940	1764	1764	3168	3 88	2522	2583	5598	6373	6373	8435	8675	9199	9242	626	1342

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	ent L1			similar to											(NF1),						-luman					0	· ie	<u> </u>	
Top Hit Descriptor	nt78a09.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element;	au92g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783784 5' similar to SW:CUL1_HUMAN Q13616 CULLIN HOMOLOG 1.	Homo sapiens chromosome 21 segment HS21C010	wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING;	nj45g09.s1 NCI_CGAP_Pr9 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN);	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA	Homo sapiens chromosome 21 segment HS21C001	Homo sapiens peptidylarginine deiminase type III (LOC51702), mRNA	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 7	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA	1243c11.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291348 5'	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA	Homo sapiens mRNA for KIAA1591 protein, partial cds	Homo sapiens mRNA for KIAA1591 protein, partial cds	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen cisease, Watson disease) (NF1), mRNA	Homo sapiens mRNA for brain ryanodine receptor, complete cds	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA	601899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'	AU077341 Sugano cDNA library Homo sapiens cDNA clone Zrv6C880 similar to 5'-end region of Human	gamma-glutamy/ transpeptidase mRNA, 5 end	Homo sapiens RFB30 gene for RING finger protein	Homo sapiens RFB30 gene for RING finger protein	fh02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960907 5'	V/26e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127998 5' similar to	STATE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P	ak28a11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407260 3'	AU139909 PLACE1 Homo sapiens cDNA clone PLACE1011576 5'
Top Hit Database Source	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	LV	NT	LZ	NT	NT	EST_HUMAN	NT	NT	NT	ZZ	N	L	NT	LN	EST_HUMAN		EST_HUMAN	LN	LN	EST_HUMAN	MARKILL TOD	NAMOL I CE	EST HUMAN	EST_HUMAN
Top Hit Aœssion No.	2.0E-54 AA655008.1	\W163175.1	2.0E-54 AL163210.2	2.0E-54 AW057524.1	2.0E-54 AA532925.1	4502642 NT	2.0E-54 AL163201.2	7706446 NT	2.0E-54 AF083823.1	4759069 NT	2.0E-54 BE047864.1	126657	1	2.0E-54 AB046811.1	11426544 NT	AB001025.1	11429127 NT	7657454 NT	8567387 NT	1.0E-54 BF315418.1		1.0E-54 AU077341.1			8.0E-55 AW 409714.1	000346.4	7.0E-33 N08340.	VA889581.1	7.0E-55 AU139909.1
Most Similar (Top) Hit BLAST E Value	2.0E-54 /	2.0E-54 /	2.0E-54 /	2.0E-54 /	2.0E-54	2.0E-54	2.0E-54 /	2.0E-54	2.0E-54	2.0E-54	2.0E-54	2.0E-54	2.0E-54	2.0E-54 /	2.0E-54	2.0E-54 /	2.0E-54	2.0E-54	2.0E-54	1.0E-54	-	1.0E-54 /	8.0E-55 Y07829.2	8.0E-55 Y07829.2	8.0E-55	7.05 55	1.00-30.7	7.0E-55/	7.0E-55/
Expression Signal	1.6	1.3	1.82	1.65	4.06	2.03	1.13	1.45	0.84	3.75	1.34	3.59	18.19	18.19	8.14	3.62	1.26	2.57	1.46	1.07		2.26	14.56	2.32	2.76	7	9.	1.26	1.59
ORF SEQ ID NO:	21290	22261	22321	22587				24450	24790	25116	25417	25503	25564	25565	26243	27617	27821		25216							SCBUC	20070	27373	27393
Exen SEQ ID NO:	11434	12367	ļ	12793	13418	14010	14240	14664		15283	15360		15488	15488	16093	17403	17599	18770	19244	14259		19345	11201	11204	18402	40084	j	_]	17191
Probe SEQ ID NO:	1529	2493	2556	2865	3501	4110	4343	4780	5156	5363	5440	5521	5673	5573	6227	7552	7749	8963	6693	4363		9852	1294	1297	8530	1065	0001	7297	7315

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Table 4
Single Exon Probes Expressed in Heart

															AN			similar to																
Top Hit Descriptor	tq29f09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2210249 3'	tq29f09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2210249 3'	ym57g07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52444 5'	Homo sapiens mRNA for KIAA1501 protein, partial cds	zj95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3	zj95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA	Homo saplens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA	Homo sapiens mRNA for KIAA0611 protein, partial cds	Homo sapiens mRNA for KIAA0611 protein, partial cds	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	EST370064 MAGE resequences, MAGE Homo sapiens cDNA	Homo sapiens RNA binding motif protein, Y chromosome, family 1, mentser A1 (RBMY1A1) mRNA	Homo sapiens predicted osteoblast protein (GS3786), mRNA	Homo sapiens predicted osteoblast protein (GS3786), mRNA	7J52b10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:3390043 3' similar to	contains L1.t3 L1 repetitive element ;	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA	Homo sapiens diacy/glycerol kinase, gamma (90kD) (DGKG) mRNA	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA	Homo saplens Xq pseudoautosomal region; segment 1/2	Homo sapiens chromosome 21 segment HS21C100	Homo sapiens chromosome 21 segment HS21C010	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	601886575F2 NIH MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C084	Human endogenous retrovirus pHE.1 (ERV9)	Human endogenous retroviral DNA (4-1), complete retroviral segment	Homo saplens syntaxin-binding protein 1 (STXBP1) mRNA, and translated products
 Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST HUMAN	EST_HUMAN	LN	NT	IN	LN	۲N	NT	N.	EST_HUMAN	LN	NT	LN		EST_HUMAN	NT	LN	TN	LN	IN	LΝ	TN	N	EST_HUMAN	EST_HUMAN	EST HUMAN	١	N⊤	LN	LN
Top Hit Acession No.	7.0E-55 AI561056.1	7.0E-55 AI561056.1	123396.1	6.0E-55 AB040934.1	5.0E-55 AA704971.1	5.0E-55 AA704971.1	4502240 NT	4502240 NT	4506302 NT	5.0E-55 AB014511.1	5.0E-55 AB014511.1	5453765 NT	11417972 NT	4.0E-55 AW957994.1	4826973 NT	7661713 NT	7661713		4.0E-55 BF061411.1	4506180 NT	4506180 NT	4503314 NT	4503314 NT	4.0E-55 4507794 NT	AJ271735.1	4.0E-55 AL163300.2	4.0E-55 AL163210.2	4.0E-55 W28189.1	4.0E-55 BF303941.1	3.0E-55 BE178519.1	3.0E-55 AL163284.2	X57147.1	2.0E-55 M10976.1	4507296 NT
Most Similar (Top) Hit BLAST E Value	7.0E-55	7.0E-55	7.0E-55 HZ3396.1	6.0E-55 /	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	4.0E-55 /	4.0E-55	4.0E-55	4.0E-55		4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55 /	4.0E-55	4.0E-55	3.0E-55	3.0E-55	2.0E-55 X57147.1	2.0E-55	2.0E-55
Expression Signal	12.75	12.75	4.3	1.98	1.12	1.12	1.82	1.82	2.06	1.86	1.86	1.19	2.13	1.36	33.95	1.89	1.89		1.26	1.53	1.53	7.73	7.73	1.25	1.04	1.38	8.44	4.46	2.38	2.76	1.65	2.3	0.89	3.08
ORF SEQ ID NO:	28679	28680		28908	21500	21501	25969	25970	27296	27851	27852	27965		19843	20409	21193	21194			21763		21824	21825	22046		22964						20150		20383
Exon SEQ ID NO:	18413	18413	19648	18617	11633	11633	15846	15846	17106	17620	17620	17719	18985	12658	10591	11328	11328			11872	11872	11930	11930	12146	12419	13165	16736	18429	18933	18894	19356	10327		10570
Probe SEQ (D NO:	8541	8541	9823	8803	1732	1732	5941	5941	7229	7770	7770	7869	9283	49	959	1422	1422		1498	1979	1979	5033	2039	2262	2545	3242	6857	8559	9200	. 9138	9986	373	539	633

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Table 4

You Probes Expressed in Heart

Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA	CM1-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA	am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element;	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabeflaz) mRNA, complete cds	Homo sapiens mRNA for KIAA0903 protein, partial cds	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE,2967027 5'	Homo sapiens SMA3 (SMA3), mRNA	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds	Human mRNA for HLA-A11E, a MHC class I molecule (major histoccmpattbility complex)	Homo sapiens mRNA for KIAA0406 protein, pertial cds	Homo sapiens mRNA for KIAA0406 protein, partial cds	Homo sapiens CLP mRNA, partial cds	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C067	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens DSCR5b mRNA, complete cds	Homo sapiens DSCR5b mRNA, complete cds	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA	Homo sapiens hect domain and RLD 2 (HERC2), mRNA	Homo sapiens hect domain and RLD 2 (HERC2), mRNA	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens chromosome 21 segment HS21C010	Human infant brain unknown product mRNA, complete cds	Homo sapiens DNA-binding protein (LOC56242), mRNA	601237702F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3809552 5'	yn62g03.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element;	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
le Exon Probe	Top Hit Database Source		EST_HUMAN C	EST_HUMAN TI	T_HUMAN					T_HUMAN			H		NT		T HUMAN	TN		TN	TN TN				INT IN	- LN	- IN		EST_HUMAN 6		EST_HUMAN
Sing	Top Hit Acession No.	4507798	5.1	2.0E-55 A1002836.1		5060		0.1	1.0E-55 BE277891.1	1.0E-55 BE277861.1	3174	0.1	X13111.1	1.0E-55 AB007866.2	1.0E-55 AB007866.2	1.0E-55 L54057.1	W28189.1	1.0E-55 AL163267.2	AL163210.2	1.0E-55 AB037163.1	1.0E-55 AB037163.1	8923125 NT	11433046 NT	11433046 NT	AL163210.2	1.0E-55 AL163210.2	U50950.1	10567821 NT	9.0E-56 BE379074.1	+-	213.1
	Most Similar (Top) Hit BLAST E Value	2.0E-55	2.0E-55 BE71998	2.0E-55	2.0E-55	1.0E-55	1.0E-55	1.0E-55 AB02071	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-55 X13111.1	1.0E-55	1.0E-55	1.0E-55	1.0E-55 W28189.	1.0E-55	1.0E-55 AL16321	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-55	1.0E-55 AL16321	1.0E-55	1.0E-55 U50950.	1.0E-55	9.0E-56	7.0E-56 H19934.	7.0E-56
	Expression Signal	0.79	2.97	4.3	2.2	1.6	11.9	3.55	0.86	98.0	2.3	1.03	33.19	4.71	4.71	1.35	1.15	3.47	1.04	0.98	0.98	1.19	5.75	5.75	4.74	4.74	2.58	2.04	1.81	5.18	1.84
	ORF SEQ ID NO:	22656			28446	19891	19969	20888	21680	21681		22071	22238	22271	22272	22331	23082	23597	23878			24727	25809							22457	
	Exon SEQ ID NO:	12855	14551	17160	18196	10075	10154	11046	11802	11802	12161	12651	12346	<u> </u>	12381	12439	_	13817	14097	14607	14607	14951	15700	15700	L	_	<u></u>		16221	12567	
	Probe SEQ ID NO:	2928	4665	7284	8319	91	182	1132	1907	1907	2277	2290	2470	2507	2507	2568	3363	3907	4197	4721	4721	5081	5794	5794	8284	8284	8745	8859	6358	2703	6504

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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'	Homo sapiens beta-tubulin mRNA, complete cds	Homo sapiens beta-tubulin mRNA, complete cds	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds	tm65g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163046 3'	Im65g12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE.2163046 3'	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA	Homo saplens oncogene TC21 (TC21), mRNA	EST28889 Cerebellum II Homo sapiens cDNA 5' end	EST28889 Cerebellum II Homo sapiens cDNA 5' end	Homo sapiens MHC class 1 region	Homo sapiens chromosome 21 segment HS21C068	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA	Homo sapiens mRNA, similar to rat myomegalin, complete cds	Homo sapiens nuclear pore complex Interacting protein (NPIP), mRNA	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA	Homo sapiens caveolin 3 (CAV3), mRNA	Homo sapiens caveolin 3 (CAV3), mRNA
אור באמון ומד	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	IN	LN	LN	₽	Z-L	N	LN	EST HUMAN	EST_HUMAN	LN	LN	EST_HUMAN	EST_HUMAN	NT	LN	TN	NT	FZ	L	NT	NT	LN	LN	NT	NT	NT
	Top Hit Acession No.	7.0E-56 AW361213.1	5.0E-56 AW997712.1	N 28189.1	5.0E-56 H55099.1	4.0E-56 AF141349.1	4.0E-56 AF141349.1	4507728 NT	4507728 NT	4 0E-56 AE003528 1	4.0E-56 AF217508.1	4.0E-56 AF217508.1	4.0E-56 AF043349.1	4.0E-56 AI498066.1	4.0E-56 Al498056.1	8924029 NT	6912697 NT	3.0E-56 AA325826.1	AA325826.1	3.0E-56 AF055066.1	3.0E-56 AL163268.2	5902085 NT	4759163 NT	4759163 NT	11421124 NT	11418704 NT	11434956 NT	3.0E-56 AB042556.1	5902013 NT	5902013 NT	11434876 NT	11434876 NT
	Most Similar (Top) Hit BLAST E Value	7.0E-56	5.0E-56	5.0E-56	5.0E-56	4.0E-56 /	4.0E-56	4.0E-56	4.0E-56	4 0E-56	4.0E-56	4.0E-56	4.0E-56	4.0E-56	4.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56
	Expression Signal	1.84	2.26	1.31	2.68	6.15	6.15	4.11	4.11	3.05	629	6.29	1.23	8.75	8.75	9.85	2.7	1.58	1.58	1.39	4.05	2.14	1.57	1.57	6.34	5.74	1.52	10.72	3.89	3.89	2.3	2.3
	ORF SEQ ID NO:		21434		24902	19805		22431	22432	20268		25803			28418	21081	21892		22805		24006	24154	25467	25468	26141	27185	28078	28259				25316
	Exan SEQ ID NO:	16363	11568	17790	19701	10012	10012	12541	12541	10457			<u> </u>	18174	18174	11225	11992		13013	13674	14224	14364	15405	15405	16003	16994	17837	18012				18955
	Probe SEQ ID NO:	6504	1666	7940	9375	25	25	2676	2676	2781	5788	5788	7999	8295	8295	1318	2103	3086	3086	3761	4327	4470	5486	5486	6109	7117	7987	8124	8632	8632	9240	9240

Page 241 of 413 Table 4 Single Exon Probes Expressed in Heart

		Τ	T	Γ	Τ	Τ	Γ	Τ	Ī		Τ	T	T	Τ		Τ		T	\top	Ť	T	Τ	Ť	Ť	T	Ť	Τ	T	T	Γ	Τ	T	T	T
Origin Lyones Lybrassed III realt	Top Hit Descriptor	zq52a08.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645206 3'	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds	Homo saplens mRNA for KIAA1414 protein, partial cds	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds	hg23c11.x1 NCi_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946452 3'	hg23c11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946452 3'	QV-BT077-130199-079 BT077 Homo sapiens cDNA	RC2-CT0163-220999-001-E02 CT0163 Homo sapiens cDNA	QV0-OT0033-070300-152-h03 OT0033 Homo sapiens cDNA	Homo sapiens EphA4 (EPHA4) mRNA	Homo sapiens EphA4 (EPHA4) mRNA	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA	QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA	x05d10.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:∪05875 INTERFERON-GAMMA RECEPTOR BETA CHAIN PRFCI IRSOR (HIJMAN)	zv51b12.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:7571515	Homo sapiens EphA4 (EPHA4) mRNA	Homo sapiens EphA4 (EPHA4) mRNA	op67h02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1581939 3'	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA	Homo sapiens mRNA for KIAA0960 profein, partial cds	Homo sapiens mRNA for KIAA0960 protein, partial cds	Homo sapiens mRNA for KIAA0837 protein, partial cds	Homo saplens mRNA for KIAA0837 protein, partial cds	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA	Homo sapiens monocarboxylate transporter 3 (SLC16A8), mRNA	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
אום רעמון ב זמר	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	Z	N L	N	EST_HUMAN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	N	Z.	N	EST_HUMAN	EST HUMAN	EST HUMAN	LN	NT	EST_HUMAN	LN	NT	NT	NT	NT	L	NT	NT	N	NT	NT
5	Top Hit Acession No.	2.0E-56 AA199818.1	2.0E-56 BE064386.1	2.0E-56 BE064386.1	J26061.1	A26061.1	2.0E-56 AB037835.1	2.0E-56 AV703184.1	1.0E-56 AF190930.1	1.0E-56 AW 589833.1	1.0E-56 AW 589833.1	1905162.1	W845987.1	VW880885.1	4758279 NT	4758279 NT	8923349 NT	8.0E-57 AW816405.1	8.0E-57 AW 264599.1	AA496109.1	4758279 NT	4758279 NT	8.0E-57 AA971001.1	11418185 NT	4B023177.1	\B023177.1	AB020644.1	AB020644.1	8923349 NT	7019528 NT	11545732 NT	11545732 NT	7657592 NT	7657592 NT
	Most Similar (Top) Hit BLAST E Value	2.0E-56	2.0E-56	2.0E-56	2.0E-56 M26061.1	2.0E-56 M26061.1	2.0E-56	2.0E-56	1.0E-56	1.0E-56	1.0E-56 /	1.0E-56 AI905162.	1.0E-56 AW84598	9.0E-57 AW88088	9.0E-57	9.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57 AB023177	8.0E-57 AB023177		8.0E-57	8.0E-67	8.0E-57	8.0E-57	8.0E-57	7.0E-57	7.0E-57
	Expression Signal	2.94	1.19	1.19	1.02	1.02	0.93	1.08	1.44	1.79	1.79	1.52	1.86	1.97	1.17	1.17	1.55	2.91	5.79	1.63	1.02	1.02	96'0	6.35	11.76	11.76	67.76	67.76	3.32	1.27	2.02	1.39	2.02	2.02
	ORF SEQ. ID NO:		20476	20477	22113	22114	22684				23322	24606	27863		23786	23787	19790	20079	20642	21551	23060	23061	24750	25004	25915	25916	26594	26595	19790		25251	25251	22353	22354
	Exon SEQ ID NO:	10455	12675	12675	12215	12215	12886		10887		13536	14838	17630	10545	14009	_	6666	10258	10792	11673	13255	13255	14975	19624	15794	15794	16415	16415		19097	19188		_]	12462
	Probe SEQ ID NO:	513	716	716	2334	2334	2959	3489	964	3622	3622	4963	7780	609	4109	4109	13	294	866	1774	3335	3335	5107	5207	5888	5888	6557	6557	8771	9468	3607	9622	2592	2592

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
0700	10100	7,0000	C	77 70 57	TOLOGE	1	Unempropriate NIME 7 (AIME 7) DNIA
3212		10677	75.0	70-30.7	0017471	12	TOUTO Sapletis NIVIET (NIVIET), ITINIA
3212	13136	22938	0.92	7.0E-57	7242158 NT	LN	Homo sapiens NME7 (NME7), mRNA
3233	13157	22956	6.49	7.0E-57	E005979 NT	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3801	13713	23500	2.17	7.0E-57	7.0E-57 AF012872.1	NT	Homo sapiens phosphatidylinosital 4-kinase 230 (pi4K230) mRNA, complete cds
3801	13713	23501	2.17	7.0E-57	7.0E-57 AF012872.1	LN	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
9934	19656		2.99	5.0E-57	5.0E-57 AJ271735.1	Z	Homo sapiens Xq pseudoautosomal region; segment 1/2
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,
3694		23393	1,23	4.0E-57	4.0E-57 AB026898.1	NT	complete cds)
4935	14813	24581	0.96	4.0E-57	4.0E-57 BE783649.1	EST HUMAN	601471226F1 NIH_MGC_67 Homo sapiens cDNA clone INAGE:3874135 5
787	10716	20558	0.70	3.05.57	TN 807708	l-	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman
		2002	2	10.0	0671001		
1309	11215		11.34	3.0E-57	3.0E-57 AA230279.1	EST_HUMAN	nd13f07.s1 NCL_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1008037 sImilar to SW:RS10_HUMAN P46783 40S RIBOSOMAL PROTEIN S10.;
2342	12222	22119	2.83	3.0E-57	3.0E-57 AA348335.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' end
	!						733b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP: Y47H9C.2
2670	12535	22425	1.62	3.0E-57	BE676622.1	EST HUMAN	CE20263;
2670	12535	22426	1.62	3.0E-57	3.0E-57 BE676622.1	EST HUMAN	7f33b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 CE20263;
3514	13430	23230	1.15	3.0E-57	3.0E-57 AF232708.1	LN	Homo sapiens cell-line tsA201a chloride ion current inducer protein ((Cin) gene, complete cds
3639	13553		115.94	3.0E-57	3.0E-57 AW853964.1	EST_HUMAN	RC3-CT0254-110300-027-d10 CT0254 Homo sapiens cDNA
5723	15630	25733	3.34	3.0E-57	3.0E-57 BE796537.1	EST HUMAN	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5
6736		26805	3.95	3.0E-57	3.0E-57 W28130.1	EST_HUMAN	42f6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
6751	16630	26817	1.95	3.0E-57	11545798 NT	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
6751		26818	1.95	3.0E-57	11545798 NT	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
7142	l	27212	4.65	3.0E-57	3.0E-57 AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5
8279		28400	20.31	3.0E-57	3.0E-57 AW248374.1	EST_HUMAN	2820473.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
9247		24907	5.2	3.0E-57	3.0E-57 W23871.1	EST_HUMAN	2b45d11.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306549 5
9608	19628		2.15	3.0E-57	3.0E-57 AW 178575.1	EST_HUMAN	RC0-HT0112-080999-001-C06 HT0112 Homo sapiens cDNA
			-				ak02b02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to
2699		22453	1.19	2.0E-57		EST_HUMAN	contains Alu repetitive element contains element MER22 repetitive element :
3392	_ İ		2.91	2.0E-57	1.2	NT	Homo sapiens chromosome 21 segment HS210004
3504	l	23223	0.84	2.0E-57		HUMAN	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5
3504		23224	0.84	2.0E-57		T HUMAN	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 6'
4409	14303	24086	6.88	2.0E-57	2.0E-57 AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083

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12798 22593 1.19 6.0E-58 BE242150.1 EST HUMAN 17759 28000 1.3 6.0E-58 11434746 NT 109700 1.8 6.0E-58 11526201 NT	Probe SEQ ID NO: NO: 5676 7017 7665 8592 8892 2184 7045 7045 863 874 8231 8231 8231 8330 8330 8330 8330 8330 8330 8330 83	Exon SEQ ID NO: NO: 15398 15398 15894 17515 17515 18460 12077 19223 10575 10575 10575 10575 10575 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 11710 1171	ORF SEQ ID NO: 27084 27742 28729 28730 21973 21973 21589 21589 21589 21589 21589 21589 21589 21589 21589 21589 21589	Expression Signal 1.43 1.43 1.29 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.129 1.1	Most (ΤΕ (ΤΕ (ΤΕ (ΤΕ (ΤΕ (ΤΕ (ΤΕ (ΤΕ (ΤΕ (ΤΕ	4ST E No. AST E No. AST E No. AST E No. AST E No. AST E No. AST E No. AST E No. AST E C. C. E. C. E. E. C. E. E. E. E. E. E. E. E. E. E. E. E. E.	Top Hit Database Source Source Source Source EST_HUMAN NT NT NT EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN	Top Hit Descriptor ze31c05.r1 Soares retine N2b4HR Homo sepiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 Tre96t04.x1 NCI_CGAP_Ov18 Homo sepiens cDNA clone IMAGE:3570956 3' similar to contains TAR1111 MERZ2 repetitive element; Homo sepiens Gall-Hit MCS1 transcriptional regulatory protein p54 mRNA, complete cds Homo sepiens for the GS1 transcriptional regulatory protein p54 mRNA, complete cds Homo sepiens hypothetical protein FL120041 (FL120041), mRNA Homo sepiens hypothetical protein FL120041 (FL120041), mRNA Homo sepiens hypothetical protein FL120041 (FL120041), mRNA Homo sepiens hypothetical protein FL120041 (FL120041), mRNA Homo sepiens hypothetical protein FL120041 (FL120041), mRNA HYPOTHETICAL 9.3 KD PROTEIN; HYPOTHETICAL 9.3 KD PROTEIN; HOMO-GCAP_CAP_CAP_CAP_CAP_CAP_CAP_CAP_CAP_CAP_
17759 28000 1.3 6.0E-58 11434746 NT	2871				6.0E-58	BE2421	⊢'J	TCAAP1E1219 Pediatric acute myelogenous leukernia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
18 6 0E-58 1150601NT	7905				6.0E-58		F	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
1.01 0.01 0.01 0.01	9492	19109		1.8		11526291 NT	L	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA

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Table 4
Single Exon Probes Expressed in Heart

		_	_						-		_,_			,	_								-										
Oligie Lyon I lobes Lypressed III reall	Top Hit Descriptor	Homo sapiens synaptojanin 1 (SYNJ1), mRNA	RC4-NT0057-160600-016-b05 NT0057 Homo sapiens cDNA	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cUNA	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA	CM3-UM0043-240300-127-e07 UM0043 Homo saplens cDNA	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA	or98e07.s1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'	Homo sapiens placenta-specific 1 (PLAC1), mRNA	ym51h07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52071 5'	Homo sapiens apical protein, Xenopus Iaevis-like (APXL), mRNA	Homo saplens hypothetical protein FLJ10826 (FLJ10826), mRNA	Homo sapiens chromosome 21 segment HS21C018	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, herriophilia B)	(F9) mKNA	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mF.NA, complete cds	Human beta-prime-adaptin (BAM22) gene, exon 3	Human mRNA, Xq terminal portion	Homo sapiens EGF-like repeats and discoidin Hiko domains 3 (EDIL3), mRNA	Homo sapiens E18-55kDa-associated protein 5 (E18-AP5), mRNA	yg10e02.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'	Homo sapiens peptide YY (PYY) mRNA	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'	AV712977 DCA Homo sapiens cDNA clone DCAAZG04 5'	Homo saplens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds	ba08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391 60S	RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE):	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5
gie Lauii Fio	Top Hit Database Source	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	Ā	EST_HUMAN	LN	Į,	LN	N	Ę	F	N		LN	NT	LV.	LN	N	NT	EST HUMAN	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	NT		EST HUMAN	EST HUMAN
	Top Hit Acession No.	4507334 NT	5.0E-58 BE763984.1	5.0E-58 AW 797948.1	5.0E-58 AW 797948.1	5.0E-58 AW797948.1	5.0E-58 AW 797948.1	5.0E-58 AA988183.1	11496282 NT		11421330 NT	8922693 NT	5.0E-58 AL163218.2	11526293 NT	11418177 NT	4502302 NT	4504634 NT		4503648 NT	4.0E-58 AF265555.1	J36251.1	016470.1	5031660 NT	11424059 NT	317879.1	4758981 NT	3.0E-58 BF569848.1	3.0E-58 BF569848.1	3.0E-58 AV712977.1	1F068624.1		2.0E-58 BE208532.1	2.0E-58 BE907186.1
	Most Similar (Top) HIt BLAST E Value	5.0E-58	5.0E-58	5.0E-58	5.0E-58	5.0E-58	5.0E-58	5.0E-58	5.0E-58	5.0E-58 H23072.1	5.0E-58	5.0E-58	5.0E-58	5.0E-58	5.0E-58	4.0E-58	4.0E-58		4.0E-58	4.0E-58	4.0E-58 U36251.1	4.0E-58 D16470.1	4.0E-58	4.0E-58	3.0E-58 R17879.1	3.0E-58	3.0E-58	3.0E-58	3.0E-58	2.0E-58		2.0E-58	2.0E-58
	Expression Signal	2.9	5.87	4.47	4.47	2.99	2.99	3.56	2.21	5.86	1.45	6.77	1.56	3.26	2.49	17.97	1.58		1.24	0.97	2.7	1.1	2.11	7.54	1.17	2.34	2.91	291	1.39	8.16		12.06	4.42
	ORF SEQ ID NO:	20081			20933	20932	20933	23002			25924	26721	27923			20147			21221	22297	22351	23004	23380	28798		21129	22864	22865	26031	20698			24986
	Exan SEQ ID NO:	10261	10626	11088	11088	11088	11088	13202	15378	15656	15800	16527	17679	19650	19362	10325	10709		1135/	12405	12461	13204	13594	18515	10291	11273	13066	13066	15907	10850		11175	19441
	Probe SEQ ID NO:	297	693	1176	1176	1177	1177	3281	5458	5748	5894	6647	7829	9215	9876	369	779	1	1452	2531	2590	3283	3680	8651	332	1367	3141	3141	6002	925		1268	5288

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Table 4
Single Exon Probes Expressed in Heart

										-			_	_	-,-														_			
Single Exoll Flobes Expressed III near	Top Hit Descriptor	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3601911 5	am57e02.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP.2K3.28.1 CE05065 UBIQUITIN CONJUGATING ENZYMEI; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM DINITING EDATEIN.	BinDiNG PROTEIN; Homo sapiens endocytic recentor Endot80 (ENDO480) mRNA complete add	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA complete cos	601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5	hm25f08 x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3	Human complement component C5 mRNA, 3'end	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex. 9 (22k) R22) (NDLIFRG) mRNA	EST369252 MAGE resequences, MAGD Homo sablens cONA	EST369252 MAGE resequences, MAGD Homo sapiens cDNA	Homo sapiens partial AF4 gene, exons 2 to 7 and Alu repeat elements	hy10f08.x1 NCI_CGAP_GC6 Horno sapiens cDNA clone IMAGE:3196935 3	Homo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP1) mRNA	Human prohormone converting enzyme (NEC2) gene, exon 4	oz43h01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE: 1678129 3'	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA	H.sapiens immunoglobulin kappa light chain variable region L14	Homo sapiens TATA box binding protein (TBP) mRNA	wh50d06.x1 NCL CGAP Kid11 Homo sapiens cDNA clone IMAGE.23841713'	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5	Wf48c11.x1 Soares NFL T GBC 51 Homo sapiens cDNA clone IMAGE 23588363'	H.saplens DNA for ZNF80-linked ERV9 long terminal repeat	au66c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains	element TAR1 repetitive element;	AV762869 MDS Homo saplens cDNA clone MDSEIC12 5'	Homo sapiens hypothetical protein (LOC57143), mRNA	Human mRNA for KIAA0184 gene, partial cds	Homo saplens ryanodine receptor 3 (RYR3) mRNA
JIE LAULI FIU	Top Hit Database Source	EST HUMAN	F C	NT NT	Z.L	EST_HUMAN	EST HUMAN	NT	NT	EST HUMAN	EST_HUMAN	F	EST_HUMAN	LN L	N	Z F	LN	IN	EST_HUMAN	TN	IN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN		EST HUMAN	EST_HUMAN	NT	NT	LΠ
3.12	Top Hit Acession No.	2.0E-58 BE907186.1	2 0 0 E 60				2.0E-58 AW872641.1	1.0E-58 M65134.1	6274549 NT	1.0E-58 AW957182.1	17	_	1.0E-58 BE466132.1	4759169 NT	4758081 NT	4758081 NT	4507628 NT	1.0E-58 M95963.1	1.0E-58 A/141063.1	4505314 NT	1.0E-58 X63392.1	4507378 NT	1	.1	.1			_	5.0E-59 AV762869.1	11434908 NT	4.0E-59 D80006.1	4506758 NT
	Most Similar (Top) Hit BLAST E Value	2.0E-58	- C	2.0E-38	2.0E-58	2.0E-58	2.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	8.0E-59	8.0E-59	6.0E-59	5.0E-59	5.0E-59		5.0E-59	5.0E-59	5.0E-59	4.0E-59	4.0E-59
	Expression Signal	4.42		2.76	2.76	10.79	2.26	0.93	5.45	2.17	2.17	1.07	2.02	96.0	0.98	0.98	0.84	0.89	4.86	6.7	3.46	27.47	1.2	1.63	6.21	5.85		7.46	1.71	2.8	2.42	1.2
	ORF SEQ ID NO:	25010	26731					20463	20811	21067		21136					23360	24306		27217		21971			22807	24237		24850	27662		İ	24368
	Exon SEQ ID NO:	19441	15679	16112	16112	18011	18209	10638	10969	11212	11212	11281	11545	12633	13409	13409	13573	14515	14775	17023	18790	12069	16638	12660	13015	14451		15130	17447	18158	10706	14571
	Probe SEQ ID NO:	5288	7724	6246	6246	8123	8332	705	1052	1305	1305	1375	1641	2771	3493	3493	3659	4627	4895	7146	8985	2182	6229	171	3088	4559		6173	7596	8278	776	4685

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens ryanodine receptor 3 (RYR3) mRNA	Homo saplens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1	EST377582 MAGE resequences, MAGI Homo sapiens cDNA	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA	Homo sapiens plasminogen activator, tissue (PLATa) mRNA	Homo sapiens plasminogen activator, tissue (PLATa) mRNA	Homo sapiens mRNA for KIAA112 protein, partial cds	Homo sapiens mRNA for KIAA1112 protein, partial cds	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	Homo saplens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA	Homo sapiens Testis-specific XK-related protein on Y (XKRY) mRNA	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA	Horno sapiens hypothetical protein PRO1741 (PRO1741), mRNA	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA	Human mRNA for dbi proto-oncogene	Human mRNA for dbl proto-oncogene	Homo sapiens gamma-glutamyltransferase-like activity (GGTLA1), mRNA	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end	RC0-NT0036-100700-032-a07 NT0036 Homo sapiens cDNA	fh07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 51	Ph07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE.2961654 5'	wa36c12x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542	Geodaz KIVCH PRO I Eliv.; contains LIK7.01 LIK7 repetitive element;	Homo sapiens alpha-tubulin mRNA, complete cds	601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'	oa56h11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13537	G1333/ MERS/ TRANSPOSABLE ELEMEN!, COMPLETE CONSENSUS SEQUENCE	Homo sapiens mRNA for transcription factor	Homo sapiens zinc finger protein 275 (ZNF275), mRNA	Homo sapiens mRNA for transcription factor	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
jie Exon Pro	Top Hit Database Source	NT	LN	EST HUMAN	NT	NT	LN L	NT	IN	NT	NT	NT	L	NT	LN	LΝ	LN	L	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	1	ESI HOMAN	N	EST_HUMAN	1	ES HOMAN	L	NT	N	N
Suis	Top Hit Acession No.	4506758 NT		3.0E-59 AW965524.1	7682247 NT	4505860 NT	5860	3.0E-59 AB029035.1	3.0E-59 AB029035.1	4502014 NT	4502014 NT	4508044	4759329 NT	7427522 NT	8924074 NT	5454137 NT			11417866 NT	1866			8.1	W410698.1	,			E296411.1			1.0E-59 AJ130894.1	419630	-	4759159 NT
	Most Similar (Top) Hit BLAST E Value	4.0E-59	4.0E-59	3.0E-59 A	3.0E-59	3.0E-59	3.0E-59	3.0E-59 A	3.0E-59 A	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59 X12556.1	3.0E-59 X12556.1	3.0E-59	3.0E-59	2.0E-59 A	2.0E-59 E	2.0E-59 A	2.0E-59 AW41069	L	Z.UE-59 AI531809	2.0E-59 L11645.1	1.0E-59 BE296411	L	1.0E-39.	1.0E-59 A	1.0E-59	1.0E-59 AJ130894	8.0E-60
	Expression	1.2	2.16	5.96	4.12	9.87	9.87	7.68	7.68	3.71	3.71	1.17	1.07	1.85	2.03	1.82	1.23	1.23	1.64	3.9	5.01	2.47	1.84	1.84		5.14	2.75	3.58		2.40	1.29	1.22	8.32	2.71
	ORF SEQ ID NO:	24369			20002	21455	21456	21866	21867	22811	22812	23449	24366	24406	25786	26377	26697	26698					28341	28342	C	Z9328	24997				26488	27524	26488	21224
	Exon SEQ ID NO:	14571	19586	9995	10191	11584	11584	11972	11972	13017	13017	13666	14569	14619	15679	16215	16509	16509	19014	19101	17406	17853	18089	18089		18933	19611	10131	0,707	12440	16322	17318	16322	11360
	Probe SEQ ID (9 NO:	4685	9356	6	221	1682	1682	2082	2082	3090	3090	3753	4683	4734	5772	6352	6239	6239	9333	9474	7555	8003	8205	8205	L	9235	9756	157	7	c/c7	6463	7400	8229	1455

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Table 4
Single Exon Probes Expressed in Heart

July Cavol Flobes Laplessed III Teal	Top Hit Descriptor	ox56d09.xt Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660337 3' similar to SW:FORM_MOUSE Q05860 FORMIN;	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA	601646227F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3930990 5'	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds: nuclear gene for mitochondrial product	H.sapiens 41kDa protein kinase related to rat ERK2	Human bor protein mRNA, 5' end	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens pro-alpha 2(1) collagen (COL1A2) gene, complete cds	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	Homo sanjans non-histona chromosoma protain 2/S corenistra, libe (Alubby) 4/	Homo sapiens somatostatio receptor surbhore 3 (SCTR3) dene 5 familian region and martial of	Homo sapiens similar to HSPC022 protein (H. sapiens) (1 OCG3504) mRNA	Homo sapiens gene for AF-6, complete cds	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA	PM3-HT0605-270200-001-e06 HT0605 Homo sapiens cDNA	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'	Homo sapiens chromosome 21 segment HS21 C085	nc04e12.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.t1 L1	repetitive element;	AV754081 TP Homo sapiens cDNA clone TPGAED05 5'	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'	wt05b10.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE 2506555 3'	wt05b10.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:25065553'	Human endogenous retrovirus pHE.1 (ERV9)
G LAUII F IUDES	Top Hit Database Source	est HUMAN SW		EST_HUMAN 601	NT Hor	NT H.s	NT Hu	NT	NT			EST_HUMAN ES	HUMAN										EST_HUMAN AU	NT		HUMAN		EST HUMAN AU		T HUMAN	NT
נוייט	Top Hit Acession No.	3.0E-60 AI040235.1 E	5174644 NT	3.0E-60 BF102612.1 E	2.0E-60 AY008285.1				2.0E-60 AF004877.1	4503044 NT	4503044 NT	-	2.0E-60 AA311159.1 E		11991659 NT	140046E0	11418192 NI	AF068757 1	11418068	4B011399.1	11418157 NT	1.0E-60 BE178586.1 E	1.0E-60 AU143389.1 E	1.0E-60 AL163285.2 N					+	78.1	
	Most Similar (Top) Hit BLAST E Value	3.0E-60 /	3.0E-60	3.0E-60 E	2.0E-60	2.0E-60 Z11694.1	2.0E-60 M24603.1	2.0E-60 /	2.0E-60	2.0E-60	2.0E-60	2.0E-60	2.0E-60	2.0E-60 L36033.1	2.0E-60	70 110 100	2.0E-00	2.0F-60.4	2.0E-60	2.0E-60 /	2.0E-60	1.0E-60 E	1.0E-60 /	1.0E-60 /		1.0E-60 /	1.0E-60 /	9.0E-61	8.0E-61	8.0E-61	8.0E-61 X57147.1
	Expression Signal	2.59	4.7	3.84	1.79	2.89	1.29	0.78	1.57	2.44	2.44	3.22	3.22	3.86	1.89	C C	98.6	131	1.46	1.47	1.4	1.56	1.12	1.1	!	2.9	1.58	1.9	1.39	1.39	1.74
	ORF SEQ ID NO:	27061	27147	27637	19810	21171	21462	23543	25941	24880	24881	26238	26239	27216	27806	77876	10017				25169	20264	23531	24533			27170	20840	22395	22396	
	Exon SEQ ID NO:	16867	16954	17420	10015	11310	11593	13750	15816	15103	15103	16088	16088	17022	17582	47582	19123	19573	19209	19220	19420	10453	13739	14754		16963	16978	10999	12502	12502	12848
	Probe SEQ ID NO:	0669	7077	7569	28	1405	1691	3839	5910	6093	6093	6222	6222	7145	7732	0577	9509	9639	9641	9658	9957	511	3827	4874		7086	7101	1083	2635	2635	2921

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Table 4.
Single Exon Probes Expressed in Heart

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Sligie Exul Flobes Expressed III Tealt	Top Hit Descriptor	Homo sapiens PXR2b protein (PXR2b), mRNA	Homo sapiens PXR2b protein (PXR2b), mRNA	Homo sapiens PXR2b protein (PXR2b), mRNA	Homo sapiens PXR2b protein (PXR2b), mRNA	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635460 5'	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'	Homo sapiens PRO2014 mRNA, complete cds	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'	nn66h09.s1 NC _CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'	Ig-beta/B29=CD79b {alternatively spliced} [human, B cells, mRNA Partial, 375 nt]	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene	Homo sapiens general transcription factor 2-I (GTF2I) mRNA, complete cds	601300938F1 NIH_MGC_Z1 Homo sepiens cDNA clone IMAGE:3635480 5'	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA	Homo sapiens chromosome 21 segment HS21C079	Homo sapiens mRNA for KIAA0825 protein, partial cds	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), เมหิNA	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3	AV731140 HTF Homo sapiens cDNA clone HTFARB01 5'	601309785F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631220 5'	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA	yv53d11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246453 3' similar to gb:L25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);	Homo saplens calmegin (CLGN), mRNA	yy03f11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270189 5'	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA	AV694317 GKC Homo sapiens cDNA clone GKCELG06 5'	UI-HF-BN0-akd-f-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
gie Exuli Piol	Top Hit Database Source	NT	LN	NT	TN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	LI	NT	LN	EST HUMAN	NT	NT	NT	Ł	NT	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST HUMAN	EST HUMAN	4758003 NT	EST_HUMAN	NT	EST HUMAN	EST HUMAN	님
	Top Hit Acession No.	7706670 NT	7706670 NT	7706670 NT	7706670 NT	6.0E-61 BE409310.1	6.0E-61 BE409310.1	6.0E-61 AF119860.1	BE257400.1	6.0E-61 AA596033.1	6.0E-61 AU130689.1	6.0E-61 S79249.1	6.0E-61 U24498.1	6.0E-61 AF035737.1	BE409310.1	4506008 NT	5.0E-61 AL163279.2	5.0E-61 AB020632.1	4502166 NT	5.0E-61 AJ229041.1		3.0E-61 BE396279.1	8922829 NT	2.0E-61 BE168410.1		N53039.1	4758003	N39397.1	11426166 NT	2.0E-61 AV694317.1	2.0E-61 AW 500256.1	11421778 NT
	Most Similar (Top) Hit BLAST E Value	7.0E-61	7.0E-61	7.0E-61	7.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-61		5.0E-61	5.0E-61	5.0E-61	5.0E-61	5.0E-61	4.0E-61	3.0E-61	2.0E-61	2.0E-61	2.0E-61	2.0E-61	2.0E-61	2.0E-61	2.0E-61	2.0E-61	2.0E-61	2.0E-61
	Expression Signal	0.94	0.94	0.86	0.86	2	1.69	10.28	0.95	2.12	8.19	2:92	1.93	2.03	1.43	1.78	1.92	0.84	1.0	1.68	2.76	1.13	1.5	1.35	1.35	1.31	1.41	1.16	1.7	1.33	1.62	3.09
	ORF SEQ ID NO:	19918	19919	19918	19919	20045	20564	21060		21392	22987	25684	26370	26521	20564	21421	22720	22835	22890			23797	20246	20950	20951	21407			25896	27279		27979
	Exan SEQ ID NO:	10098	10098	10098	10098	10230	10723	11206		11532	13189	15583	16207	16351	10723	11558	12928	13039	13086	13809	18941	14019	10433		11104	11546	11998	12472	15777	17089		17735
	Probe SEQ ID NO:	122	122	123	123	265	794	1299	1612	1628	3266	5674	6344	6492	9417	1655	3000	3114	3161	3899	9213	4119	490	1194	1194	1642	2109	2604	5871	7212	7077	7885

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Table 4
Single Exon Probes Expressed in Heart

	r		_	-	-									_						_								****	****				
	Top Hit Descriptor	Homo sapiens ribosomal protein L44 (RPL44), mRNA	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA	Homo sapiens chromosome 21 segment HS21C003	Human polymorphic trinucleotide repeat in X-linked retinitis pigmentosa (RP3) gene region	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA	xn11b09.y1 NCI_CGAP_Li5 Homo sapiens cDNA clone IMAGE:2693369 5' similar to contains element	Mort repetitive element;	UNIZABIONE VIA ANGOLE CONTRACTOR SEDIMA CIGNE IMAGE 35 TANDER CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONTRACTOR VIA ANGOLE CONT	1 W.2 HTGETZ AGGOD 077 AGE UTDETZ USES CONTRACTORS	AVIDS SINGLE TOOL TOOL TOOL TOOL TOOL TOOL TOOL TO	Homo sapiens I NAF family member-associated NFKB activator (TANK) mRNA	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA	UI-H-BW0-ajt-b-08-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:27328713'	UI-H-BW0-ajt-b-08-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:27328713'	Homo sapiens chromosome 21 segment HS21C010	Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA	Homo sapiens growth hormone releasing hormone (GHRH), mRNA	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3	(VOEZZLS) genes, complete cas MR0-BN0070-040400-010-h01 BN0070 Homo saniens c/NA	Homo sapiens KIAA0971 protein (KIAA0971), mRNA	Homo saplens actinin, alpha 4 (ACTN4), mRNA	Homo sapiens gene for AF-6, complete cds	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo saplens low density lipoprotein-related protein 2 (LRP2), mRNA	Human kappa-immunoglobulin germline pseudogene (Chr1) variable region (subcroup V kappa I)	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA	oc66h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POI_MLVRK	nz75g01.st NCI CGAP GCR1 Home seniens cDNA clone IMA CE 123/1909 2	AV714334 DCB Homo sapiens cDNA clone DCBAMA08 5
	Top Hit Database Source	NT	TN	N	LN LN	LZ LZ	Ε	1448 ti	EST HUMAN	EST TOWAIN	EST HI MAN	NOW PLANT	2	. 1	EST_HUMAN	EST_HUMAN	LN	L	LN LN	L	FZ	H	EST HUMAN	N	NT	LN	LN	L	N	NT	HOT HIMAN	EST HUMAN	EST_HUMAN
5	Top Hit Acession No.	11419729 NT	1.0E-61 AL163203.2	5453820	1.0E-61 AL163203.2 NT	1.0E-61 U32657.1	6005983 NT	A NOCEOUTON A NO	1.0E-01 AW 627.201.1	ZESSONS.I	1.0E-01 1.0E-61 1.0E-61 1.0E-61	4750040	4/58249(N)	4759249 NT	1.0E-61 AW 298181.1	1.0E-61 AW 298181.1	1.0E-61 AL163210.2	1.0E-61 M30135.1	8923130 NT	8923130 NT	11034840 NT	4 OE 64 NED34660 4	1.0E-61 AW 999726.1	11428892 NT	11425578 NT	1.0E-61 AB011399.1	11430460 NT	11430460 NT	M20809.1	11418127 NT	8 0F-62 AAB30420 1	8.0E-62 AA768861.1	7.0E-62 AV714334.1
	Most Similar (Top) Hit BLAST E Value	2.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	10.4	1.0E-01	10E-01	10.101	10.1	1.0E-01	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	10 10	1.0E-01	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61		1.0E-61	8 0F-62	8.0E-62	7.0E-62
	Expression Signal	7.14	0.85	1.32	1.09	76.0	4.47	•	1.49	10.1	1 47	30.0	0.80	0.95	7.63	7.63	0.85	7.19	1.4	1,4	3.38	2 50	2.79	6.28	1.96	1.26	2.96	2.96	1.8	8.25	62 0	1.56	1.27
	ORF SEQ ID NO:				21138		21590	34035		22,333								26107	26287	26288	26800	28040	01807	27840	28169		25002	25003		25205	24138		20848
	Exon SEQ ID NO:	18138	10373	10686	11283	11632	11711	42030	10734	13250	13585	44036	14230	14236	14636	14636	14758	15971	16133	16133	16609	18717	17216	17613	17923	19631	19620	19620	19128	19317	14345	19417	11007
	Probe SEQ ID NO:	8228	428	992	1377	1731	1814	2450	2000	3330	3671	4330	8004 6004	4339	4751	4751	4878	6124	8268	6268	6729	8888	7348	7763	8031	9110	9149	9149	9515	9805	4451	9953	1091

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Top Hit Database Source	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) PROT (AUTOANTIGEN NOR-90)	qg56a04.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1839150 3' similar to TR:015103	1	Homo sapiens CGI-56 protein (CGI-56), mRNA	HUMAN wi04d02.x1 NCI_CGAP_CLL1 Homo saplens cDNA clone IMAGE.2389251 3'		Homo sapiens CGI-18 protein (LOC51008), mRNA	UMAN MR3-ST0203-130100-025-a09 ST0203 Homo sapiens cDNA		Γ	Homo sapiens Xq pseudoautosomal region; secment 1/2	Homo sapiens ryanodine receptor 3 (RYR3) mRNA		UMAN fn07g09.x1 NIH MGC 17 Homo sapiens cDNA clone IMAGE 2961616 5'		Homo sapiens muscle specific gene (M9), mRNA						wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to HUMAN gb:X57138_mat HISTONE H2B.2 (HUMAN);	wf12b08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to JMAN gb:X57138_mat HISTONE H2B.2 (HUMAN);	Г
	SWISSPROT	EST H	LN.	418255 NT	l⊢'	EST H	11431139 NT	3.1 EST_HUMAN	EST HUMAN	N	N	506758 NT	1 EST HUMAN	1 EST HUMAN	11425574 NT	11425574 NT	1 EST HUMAN	.1 EST_HUMAN	1 EST HUMAN	1 EST HUMAN	EST_HUMAN	EST_HU	EST HUMAN	57887 NT
Top Hit Acession No.	P17480	7.0E-62 AI208681.1	6.0E-62 U09410.1	11	6.0E-62 AI762801.1	6.0E-62 Ai762801.1	117	6.0E-62 AW814393	5.0E-62 AI950528.1	5.0E-62 AJ271735.1	AJ271735.1	4	5.0E-62 AA431093.	AW410687			4.0E-62 AW161479	4.0E-62 AW161479	4.0E-62 AW161479.1	4.0E-62 AW161479.1	4.0E-62 AA311281.1	4.0E-62 AI827900.1	4.0E-62 AI827900.1	
Most Similar (Top) Hit BLAST E Vafue	7.0E-62	7.0E-62	6.0E-62	6.0E-62	6.0E-62	6.0E-62	6.0E-62	6.0E-62	5.0E-62	5.0E-62	5.0E-62	5.0E-62	5.0E-62	5.0E-62	5.0E-62	5.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62
Expression Signal	62.0	4	1.07	3.93	3.33	3.33	1.4	2.76	1.49	3.26	3.26	2.17	1.65	6.17	4.91	4.91	3.47	3.47	4.63	4.63	0.89	1.39	1.39	6.6
ORF SEQ ID NO:	23184	28829			26525	26526		27460		22132		23090	23907		28723	28724	20597	20598	20597	20598		22183	22184	
Exon SEQ ID NO:	13378	18546	12896	13258		16355	16683	17255	10356	12236		13291	14131	17352	18455	18455	10750	10750	10750	10750	11351	12286	12286	13273
Probe SEQ ID NO:	3462	8657	2969	3338	6496	6496	6804	7386	410	2356	2356	3372	4233	7482	8587	8587	822	822	823	823	1446	2409	2409	3353

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Oligic Lyons Lyprosed in Tear.	Top Hit Database Source	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate 'ransporter), member 2 (SLC13A2) mRNA	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X). mRNA					H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3							Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA	Homo sapiens mRNA for KIAA1476 protein, partial cds	Homo sapiens mRNA for KIAA1476 protein, partial cds	Human cyclophilir-related processed pseudogene	wa33f04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2299903 3' similar to contains THR.t2	NOMO	T HUMAN	Т	(UBE2D3) genes, complete ods	HUMAN	Homo sepiens intersectin 2 (SH3D1B) mRNA, complete cds	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds	ar70e11.r1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1 EST_HUMAN CE03453;	
Signio	Top Hit Acession No.	243213.1 NT	4506978 NT	11420654 NT	11421041 NT	7657057 NT	7657057 NT	033089.1 NT	8766.1 NT	8766.1 NT	11418086 NT	11418192 NT	11418322 NT	11417862 NT	11417862 NT	11430460 NT	4557794 NT	040909.1 NT	040909.1 NT	2858.1 NT					224669.1 NT	330676.1 EST	248540.1 NT	3810.1 NT		
	Most Similar (Top) Hit To BLAST E Value	4.0E-62 AJ243213.	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62 AB033089.	4.0E-62 Z78766.1	4.0E-62 Z78766.1	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	4.0E-62	3.0E-62	3.0E-62 AB040909.1	3.0E-62 AB040909.	3.0E-62 X52858.1	2 OF 60 Alecanas 4	2.0E-62 AI 163284.2	2.0E-62 BF	2.0E-62 BF329911.	2.0E-62 AF224669.	2.0E-62 BF330676.	1.0E-62 AF248540.1	1.0E-62 L78810.1	1.0E-62 AA625207.1	1.0E-62 AL039044.1
	Expression Signal	2.03	1.66	2.42	1.68	2.21	2.21	6.3	2.43	2.43	2.95	2.98	1.99	4.2	4.2	1.51	1.12	0.95	0.95	1.92	1 25	25.7	8,4	4.8	3.94	8.93	1.24	6.83	1.02	1.12
	ORF SEQ ID NO:		25606	25822	26273	26528	26529	27204	28505	28506	28792		25201	25198	25199	25210	19868	22728	22729	23340	02020	20802	27165	27166			20791	21288	21528	22606
	Exon SEQ ID NO:	14824	15524	15709	16120	16357	16357	17011	18254	18254	18891	19578	19305	19302	19302	19335	10053	12936		13554	16946		16973	16973	17696	18744	10946	11431	11657	12811
	Probe SEQ ID NO:	4947	5609	5804	6254	6498	6498	7134	8377	8377	9135	9355	9743	9792	9792	9835	83	3008	3008	3640	9080	1211	7096	2096	7846	8936	1028	1526	1758	2884

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		T	Τ	T	T	Γ	Τ	Τ	Τ	Τ	Τ	Τ	Τ	Т	T	T	T	Τ	Τ	Τ	T	T	T	Τ	Τ	Τ	Γ	Т	Т	Т	$\overline{}$	T	T
origin Event Topics Explicated III realit	Top Hit Descriptor	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE,409771 3'	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:4097713'	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9	aa33d08.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815355 3'	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA14D8	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA	C18159 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-558C10 5'	Homo sapiens mRNA for KIAA0350 protein, partial cds	Homo saplens mRNA for KIAA0350 protein, partial cds	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA	Homo sapiens mRNA for PkB kinase	Homo sapiens nucleoporin 88kD (NUP88), mRNA	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein mRNA	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C068	wm55g11.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2439908 3'	nc83f02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S RIROSOMAI PROTEIN (4) IMAAN:	Homo sabiens chromosome 21 segment HS210078	CM3-BT0595-190400-072-a09 RT0595 Homo caniene cDMA	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA	UI-H-BI1-abq-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3	UI-H-BI1-abq-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'	Homo sapiens mRNA for KIAA0717 protein, partial cds
אוס בעסון ו וסף	Top Hit Database Source	TN	EST HUMAN	EST HUMAN	NT	NT	TN	LN LN	EST HUMAN	NT	N	NT	EST_HUMAN	EST_HUMAN	N L	N	N	N	Z	NT	TN	LZ LZ	NT	NT	NT	EST_HUMAN	H H	L	FST HIMAN	EST HUMAN	EST HUMAN	EST HUMAN	NT
5	Top Hit Acession No.	8923201 NT	1.0E-62 AA722878.1	1.0E-62 AA722878.1	7662289 NT	7662289 NT	(15533.1	(15533.1	1.0E-62 AA465170.1	78698.1	11418322 NT	11430460 NT	9.0E-63 AW816405.1	318159.1	9.0E-63 AB002348.2	9.0E-63 AB002348.2	11418185 NT	15056.1	11426985 NT	11421160 NT	4557734 NT	5031810 NT	8.0E-63 AF198349.1	8.0E-63 AF198349.1	2	7.0E-63 AI872137.1	6 0F-63 AA420803 1	4 0F-63 Al 163278 2	4 0F-63 AW 750372 1	4.0E-63 AW750372.1	4.0E-63 AW134709.1	4.0E-63 AW134709.1	3.0E-63 AB018260.1
·	Most Similar (Top) Hit BLAST E Value	1.0E-62	1.0E-62	1.0E-62	1.0E-62	1.0E-62	1.0E-62 X15533.1	1.0E-62 X15533.1	1.0E-62	1.0E-62 Z78698.1	1.0E-62	1.0E-62	9.0E-63	9.0E-63 C18159.1	9.0E-63	9.0E-63	9.0E-63	9.0E-63 Y15056.1	9.0E-63	9.0E-63	8.0E-63	8.0E-63	8.0E-63	8.0E-63	8.0E-63	7.0E-63	6.0F-63	4 0F-63 /	4 0F-63 /	4.0E-63	4.0E-63 /	4.0E-63 /	3.0E-63/
	Expression Signal	1.32	2.17	2.17	1.53	1.53	1.81	1.81	2.81	2.13	1.94	2.3	2.14	1.51	7.42	7.42	6.51	1.31	4.39	1.37	1.52	2.17	3.81	3.81	3.37	1.78	40.61	0.98	2 86	2.86	2	2	1.97
	ORF SEQ ID NO:	24108	26251		27310	27311	27331	27332	27507	28845			20109			23639	29106	25104	26281	26917	22077	22102	23134	23135	23843			23001			28611	28612	21666
	Exon SEQ ID NO:	14321	16102	16102	17116	17116	17139	17139	17300	18561	19199	19322	10294	12179	13863	13863	15088	15274	16127	16724	12178	12203	13332	13332	14068	10837	15196	13200	15785	15785	18347	18347	11788
	Probe SEQ ID NO:	4426	6236	6236	7239	7239	7262	7262	7512	8673	9623	9815	335	2297	3955	3925	5210	5354	6262	6845	2296	2322	3415	3415	4168	913	5274	3279	5879	5879	8474	8474	1893

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Top Hit Descriptor	Human Met-fRNA-i gene 1	Homo sapiens zinc finger protein 144 (Mel-18) (ZNF144), mRNA	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA			Human DNA topoisomerase I mRNA, partial cds	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcystelne synthetase), catalytic (72.8kD) (GLCLC)	MANA MANA MANA MANA MANA MANA MANA MANA	Home sapiens Down syndrome candidate region 1 (DSCR1), mixing	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide complete cds	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA	Homo sapiens chromosome 3 subtelomeric region	Homo sapiens polycystic kidney disease associated protein (PKD1) gene, complete cds	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	VV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3,	TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A11, TCRBV13S3, TCRBVAS3P TCRRV7S3A9T TCRBV13S34T TCRBV9S2A2PT TCRBV7S2A1N4T.	TCRBV13S9/13S>	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA	Homo sepiens Carbonic anhydrase-related protein 10 (LOC55934), mRNA	Homo sapiens chromosome 21 segment HS21C010	_		Homo sapiens neurexin III-alpha gene, partial cds	Homo sapiens neurexin III-alpha gene, partial cds	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
Top Hit Database Source	LN	NT	LN T	EST HUMAN	EST HUMAN	NT	NT		Z	LN	ī	٦N	NT.	NT	LN	NT	EST HUMAN	EST_HUMAN			Z	LZ LZ	N	F		EST_HUMAN	NT	NT	NT	FZ	EST_HUMAN
Top Hit Acession No.	J00310.1	6005963 NT	11545810 NT	3.0E-63 BE876158.1	BE876158.1	2.0E-63 U07804.1	4885226 NT		4557624 NT	7657042 NT	AB030388.1	2.0E-63 AB030388.1	4502166 NT	2.0E-63 AF109718.1	2.0E-63 L39891.1	2.0E-63 AF111167.2	2.0E-63 BF373541.1	2.0E-63 BF373541.1			U66059.1	D910365 NT	2.0E-63 9910365 NT	AL163210.2		2.0E-63 N78945.1	2.0E-63 AF099810.1	AF09981	1	11418157 NT	1.0E-63 F08485.1
Most Similar (Top) Hit BLAST E Value	3.0E-63	3.0E-63	3.0E-63	3.0E-63	3.0E-63	2.0E-63	2.0E-63		2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63			2.0E-63	2.0E-63	2.0E-63	2.0E-63		2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63	1.0E-63
Expression	1.34	8.97	27.69	1.82	1.82	1.11	1.74		1.39	5.29	2.47	2.47	1.68	1.78	1.86	1.13	2.45	2.45			1 37	1.41	1.41	3.8		12.54	3.02	3.02	10.85	1.39	291
ORF SEQ ID NO:	22506	20978	25926	27663	27664	19972	19980		-	İ	21312	21313	22841								26061					28265	28292	28293	25058	25186	23918
Exon SEQ ID NO:	12615	11127	15802	17448	17448	10156	10163		10432	10738	11452	11452	<u> </u>	_	13743	J		15502			15920	1				18017	18042	18042	19523	19354	14145
Probe SEQ ID NO:	2753	2791	5896	7597	7597	184	191		489	808	1547	1547	3119	3248	3831	4760	5587	5587			8025	6208	6208	6964		8129	8154	8154	9243	9864	4246

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		~		_	-,-	 -		-	-,	-	-,												-					****	10.00					
	Top Hit Descriptor	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zyd11	QV0-ST0215-060100-083-b09 ST0215 Homo sapiens cDNA	Homo saplens chromosome 21 segment HS21C047	Homo sapiens chromosome 21 segment HS21C007	tm50b07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161525 31	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 51	601508968F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5	Homo sapiens Ran GTPase activating protein 1 (RANGAP1). mRNA	y698b02.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE 79179 5	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA	Homo sapiens thirmet oligopeptidase 1 (THOP1) mRNA	Homo sapiens EWS, gar22, rrp22 and bam22 genes	wb51e07.x1 NCI_CGAP_GC6 Homo sepiens cDNA clone IMAGE:2309220 3' similar to qb:M15182 BETA.	GLUCURONIDASE PRECURSOR (HUMAN);	wb51e07.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BE FA-GLUCURONIDASE PRECURSOR (HUMAN):	wv13e03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGF 2529436 31	wv13e03.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE-2529436 3'	Homo sapiens MCP-1 gene and enhancer region	Homo sapiens MCP-1 gene and enhancer region	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA	Homo sapiens mesenchyme homes box 1 (MEOX1), mRNA	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds	trkC [human, brain, mRNA, 2715 nt]	Homo sapiens stromal antigen 3 (STAG3), mRNA	Homo sapiens stromal antigen 3 (STAG3), mRNA	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
ביים ביים	Top Hit Database Source	EST_HUMAN	EST HUMAN	NT	N	EST HUMAN	EST_HUMAN	EST HUMAN	LN LN	EST_HUMAN	EST HUMAN	N	LN	NT		EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LN LN	N	N	NT	NT	LN⊤	ŢN	N	L	N	N	NT	NT	NT	NT
5	Top Hit Acession No.	F08485.1	1.0E-63 AW 582266.1	1.0E-63 AL163247.2	1.0E-63 AL163207.2	9.0E-64 AI478186.1	8.0E-64 BE280796.1	BE885755.1	11418177 NT	8.0E-64 T60651.1	7.0E-64 BE394321.1	4507490 NT	4507490 NT	Y07848.1		6.0E-64 AI651992.1	6.0E-64 AI651992.1	AW026445.1	AW026445.1	Y18933.1		-	11525879 NT	11525879 NT	11420555 NT	AF274753.1	S76475.1	11420197 NT	11420197 NT	11526198 NT		9.1		
	Most Similar (Top) Hit BLAST E Value	1.0E-63 F08485.1	1.0E-63	1.0E-63	1.0E-63	9.0E-64	8.0E-64	8.0E-64	8.0E-64	8.0E-64	7.0E-64	7.0E-64	7.0E-64	7.0E-64 Y07848.1		6.0E-64	6.0E-64	6.0E-64 AW0264	6.0E-64 AW0264	6.0E-64 Y18933.1	6.0E-64 Y18933.1	6.0E-64 M13975.	6.0E-64	6.0E-64	6.0E-64	6.0E-64 AF27475		6.0E-64	6.0E-64	6.0E-64	5.0E-64 AF231919	5.0E-64	5.0E-64 L40933.1	5.0E-64 L40933.1
	Expression Signal	2.91	1.39	2.3	3.02	4.78	7.89	3.16	2.61	2.56	66.0	2.44	2.44	2.13		1.7	1.7	3.7	3.7	2.64	2.64	4.41	2.58	2.58	7.8	2.06	2.34	7.57	7.57	4.06	2.44	2.44	2.42	2.42
	ORF SEQ ID NO:	23919				26661		25747				24303	24304	27844		21463	21464	22801	22802	25433	25434	25444	26312	26313	27451	27538	27669	28287	28288	25321	20574	20575	21167	21168
	Exon SEQ ID NO:	14145	15443	16813	19633	16471	10948	15641	18841	18875	13402	14513	14513	17616		11594	11594	13011	13011	15375	15375	15384	16157	16157	17245	17332	17455	18039	18039	18967	10732	10732	11307	11307
	Probe SEQ ID NO:	4246	5526	6935	9879	6591	1030	5733	9059	9111	3486	4625	4625	7766		1692	1692	3084	3084	5454	5454	5464	6293	6293	7376	7472	7604	8151	8151	9262	803	803	1402	1402

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		T	T	T	Τ	T	1	7	1	T		T	T	$\overline{}$	T	7		T		\top	Ī	T	T	i	T	T	T		T	Т	1		7	7	Ť
Single Exon Probes Expressed in Heart	Top Hit Descriptor	Human ((3)mbt protein homolog mRNA, complete cds	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA	RC3-ST0197-120200-015-a03 ST0197 Homo saplens cDNA	C18895 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-569E02 5	601589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'	H.sapiens isoform 1 gene for L-type calcium channel, exon 28	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds	Homo saplens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds	bb72h12.y1 NIH MGC 12 Homo sapiens cDNA clone IMAGE 3047975 5' similar to ah-1 nanga DNA 1	PROTEIN HOMOLOG 2 (HUMAN);	bb72h12.y1 NIH_MGC_12 Home sapiens cDNA clone IMAGE:3047975 5' similar to qb:L08069 DNAJ	PROTEIN HOMOLOG 2 (HUMAN);	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C027	af09d08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3/	Homo saplens elF4E-like cap-binding protein (4EHP) mRNA	wo87b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMACE.2462281 3' similar to contains element	L1 repetitive element;	Homo sapiens cirromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo saplens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2).	nuclear gene encoding mitochondrial protein, mRNA	EST370215 MAGE resequences, MAGE Homo sapiens cDNA	EST370215 MAGE resequences, MAGE Homo sapiens cDNA	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
jle Exon Proi	Top Hit Database Source	LN	NT	N	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	N	EST HUMAN	N	IN		EST_HUMAN		EST HUMAN	NT	NT	NT	NT	NT	EST HUMAN	NT		EST HUMAN	2	NT	Ŀ		EST HUMAN	EST_HUMAN	EST_HUMAN
Sing	Top Hit Acession No.	U89358.1	7662205 NT	7662205 NT	3.1	W813783.1	4.0E-64 AW813783.1	18895.1	3.0E-64 BE794381.1	4.1	4.1		3.0E-64 BF370000.1				E206521.1								0.1	4757701 NT				2.0E-64 AL163246.2	00000	200			2.0E-64 AU124387.1
	Most Similar (Top) Hit BLAST E Value	5.0E-64	5.0E-64	5.0E-64	5.0E-64 AF01743	4.0E-64 AW8137	4.0E-64	3.0E-64 C18895.	3.0E-64	3.0E-64 AV71171	3.0E-64 AV71171	3.0E-64 Z26273.1	3.0E-64 E	3.0E-64	3.0E-64 A		3.0E-64 BE20652		3.0E-64 BE20652	3.0E-64 A	3.0E-64 A	3.0E-64 A	3.0E-64 A	3.0E-64 AL16322	2.0E-64 AA609940	2.0E-64	L	2.0E-64 A	Z.UE-04 A	2.0E-64 A	20 E	Z.UE-04	2.0E-64 A	2.0E-64 A	2.0E-64IA
	Expression Signal	1.67	2.66	2.66	5.61	3.9	3.9	3.85	0.95	1.51	1.51	1.34	3.39	1.81	1.81		1.3		1.3	1.26	1.26	1.76	1.76	4.59	0.94	1.32	ç	1.78	3.03	3.03	7 86	2.30	1.33	1.33	2.62
	ORF SEQ ID NO:	21457	21235	21236				21936	22943	23112	23113	25713	25942	27005	27006		27016	!	27017	27497	27498	28703	28704	29040	20831	21137		22252	20777	22253	22873	2077	23416	23417	25662
	Exen SEQ ID NO:	11585	11370	ŀ			_ (- 1	ı	- 1	1	_		_	16811		16824		- }	17289	- 1	- 1	- 1	18746	10988	11282	10067	12350	12000	12359	13027	12067	13831	13031	15565
	Probe SEQ ID NO:	1683	2796	2796	3876	8188	8188	2151	3216	3396	3396	5703	5911	6933	6933		6946		6946	7422	7422	8565	8565	8638	1072	1376	2478	2484		2484	3101	2740	3718	8175	5653

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Single Exon Probes Expressed in Heart

Probe				_			
SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5783	15689	25799	1.3	2.0E-64	2.0E-64 AF113708.1	NT	Homo sapiens angiopoietin 4 (ANG4) mRNA, partial cds
5906	15812	25938	4.97	2.0E-64	2.0E-64 BF668537.1	EST_HUMAN	602123474F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4280395 5'
9269	15880	26004	1.31	2.0E-64	2.0E-64 AI078387.1	EST_HUMAN	oz29b03.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676717 3'
6024	15928	26060	3.86	2.0E-64	2.0E-64 M77185.1	Z	H.sapiens dopamine receptor D5 pseudogene 1, partial cds
8144	18032	28279	2.85	2.0E-64	2.0E-64 BF528114.1	EST_HUMAN	602042882F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180556 5'
8406	18282	28534	6.4	2.0E-64	2.0E-64 AI922911.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2452211 3'
8406	18282	28535	6.4	2.0E-64	2.0E-64 AI922911.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE;2452211 3'
9182	18921	25347	1.73	2.0E-64	2.0E-64 8567387 NT	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
9617	19195		2.68	2.0E-64	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exan Homo sapiens cDNA clone C22_132 5'
258	10224	20039	1.74	1.0E-64	1.0E-64 AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1740	11641	21508	5.88	1.0E-64	1.0E-64 Al929419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE.2519136 3' similar to gb:L21696_cds1 PROTHYMOSIN ALPHA (HU:AAN);contains element MSR1 repetitive element;
							Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein. M10 protein A4 differentiating dependent protein; triple IM domain protein.
3466	13382	23188	5.61	1.0E-64	1.0E-64 AF196779.1	LZ.	complete cds; and L-type calcium channel a>
3536	13452	23248	1.32	1.0E-64	1.0E-64 AF228527.1	N	Homo sapiens TRIAD3 mRNA, partial cds
3536	13452	23249	1.32	1.0E-64	1.0E-64 AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
9154	18904		1.62	1.0E-64	1.0E-64 AL163246.2	NT	Homo saplens chromosome 21 segment HS21C046
2230	12115	22017	0.93	9.0E-65	9.0E-65 X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2230	12115	22018	0.93	9.0E-65	9.0E-65 X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
8822	18635		15.1	9.0E-65	9.0E-65 BF330676.1	EST_HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
8799	18613	28903	10.83	8.0E-65	A1929244.1	EST_HUMAN	au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21.
7841	17691	27936	2.05	7.0E-65	7.0E-65 BE081653.1	EST_HUMAN	QV2-BT0635-240400-162-c02 BT0635 Homo sapiens cDNA
1040	10958	20801	1.52	6.0E-65	6.0E-65 AV721898.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC06 5'
1880	11776		8.32	6.0E-65	6.0E-65 AA550929.1	EST_HUMAN	nj86d10.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:999379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
7080	16957	27150	2.52	6.0E-65	6.0E-65 AW 083252.1	EST HUMAN	xc07b09.x1 NCI_CGAP_Co21 Homo sepiens cDNA clone IMACE:2583545 3' similar to 7R.Q63306 Q63306 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORF'S, contains L1 b2 L1 reneitive element
7209	17086	27275	4.25	6.0E-65	6.0E-65 AA427878.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:77374737
7209			4.25	6.0E-65	6.0E-65 AA427878.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
8247		28375	6.18	6.0E-65	6.0E-65 BE567816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
8787	18602	28892	4.76	6.0E-65	6.0E-65 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

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Single Exon Probes Expressed in Heart

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Single Choice Lybrassed in real	Top Hit Descriptor	Homo sapiens KE03 protein mRNA, partial cds	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	Horno sapiens ubiquitin specific protease 13 (Isopeptidase T-3) (USP13) mRNA	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'	qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800.3°	qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA	Homo sapiens ribosomal protein L34 (RPL34) mRNA	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDIT), mRNA	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDIT), mRNA	Homo sapiens mRNA for KIAA1267 protein, partial cds	Homo sapiens mRNA for KIAA1267 protein, partial cds	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor	Homo sapiens PRO1474 mRNA, complete cds	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	H.sapiens HZF9 mRNA for zinc finger protein	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element. MSR1 repetitive element:	Homo sapiens laminin, beta 1 (LAMB1), mRNA	ov23f03 s1 Soares festis NHT Homo saniens cDNA clone IMAGE 1638173.3' similar to contains element	MSR1 repetitive element;	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA	601479686F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5
וב באטוו רוטם	Top Hit Database Source	NT	LN	NT	TN	LN	NT	EST HUMAN	EST_HUMAN	EST_HUMAN	LN	NT	EST_HUMAN	EST HUMAN	NT	NT	L	NT	NT	NT	LN	NT	NT	LN-	EST HUMAN	NT		EST_HUMAN	۲N	EST_HUMAN
GIIIO	Top Hit Acession No.	4.1	7861951 NT	7661951 NT	5.0E-65 AB033768.1	4507848 NT	4507848 NT	L120419.1	4.0E-65 Al266468.1	4.0E-65 Al266468.1	4826735 NT	4506636 NT	4.0E-65 BE221469.1	4.0E-65 BE221469.1	9055269 NT	. 9055269 NT		4.0E-65 AB033093.1	11545780 NT	1277546.2	4.0E-65 AF119846.1	4826735 NT	11430460 NT	478932.1	1,000692.1	4504950 NT		A1000692.1	6912385 NT	3.0E-65 BE787366.1
	Most Similar (Top) Hit BLAST E Value	5.0E-65 AF06460	5.0E-65	5.0E-65	5.0E-65 ∤	5.0E-65	5.0E-65	4.0E-65 AL12041	4.0E-65 /	4.0E-65	4.0E-65	4.0E-65	4.0E-65	4.0E-65	4.0E-65	4.0E-65	4.0E-65 /	4.0E-65	4.0E-65	4.0E-65 AJ27754	4.0E-65	4.0E-65	4.0E-65	3.0E-65 X78932.	3 0E-65 A1000692	3 0F-65		3.0E-65 A1000693	3.0E-65	3.0E-65
	Expression Signal	0.91	1.62	1.62	1.02	1.91	1.91	1.09	1.56	1.56	1.88	8.28	1.03	1.03	0.95	0.95	3.93	3.93	2.29	2.17	7.47	1.34	1.58	5.37	1 14	1 30	3	0.98	1.4.1	1.43
	ORF SEQ ID NO:	20362	21094	21095	21898	22944	22945	19975	20491	20492	20822	21240	22068	22069	24775	24776	25754	25755	26304		28579	20822	25152		21557	L		23361	24228	27876
	Exon SEQ ID NO:	10551	11238	11238	11999	13141	13141	10158	10660	10860	10978	11375	12171	12171	15005	15005	15648	15648	16149	17870	18320	10978	19434	12646	11679	13162	70101	13574	14444	17643
	Probe SEQ ID NO:	615	1331	1331	2110	3217	3217	186	728	728	1062	1470	2288	2288	5138	5138	5740	5740	6285	8020	8446	9471	9875	1212	17RU	3230	335	3660	4551	7793

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The Event House Explicated III Theat.	Top Hit Descriptor	ts76a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237170 3' similer to gb:L15533_ma1 PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA	Novel human gene mapping to chomosome 22	Novel human gene mapping to chomosome 22	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA	Human transposon-like element, partial	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	zv90c05.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767048 5'	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A CE18595;	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15C9.4A	CE18595;	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597.3' similar to WP:F15G9.4A CE18595;	H.sapiens mRNA for ribosomal protein L31	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA	H.sapiens DNA for endogenous retroviral like element	Homo sapiens germ-line DNA upstream of Jkappa locus	Human endogenous retrovirus, complete genome	Homo sapiens methylene telrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate	cyclohydrolase (MTHFD2), mRNA	QV1-DT0069-110200-067-g10 DT0069 Homo sapiens cDNA	EST377546 MAGE resequences, MAGI Homo sapiens cDNA	Homo sapiens cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
שום בייוסעים פול	Top Hit Database Source	EST_HUMAN	N	NT	NT	NT	NT	ΝΤ	FZ	N	N	N	EST_HUMAN	EST HUMAN	EST_HUMAN		EST HUMAN	EST HUMAN	N	EST_HUMAN	FN	LN	N-	LZ	Z		L	EST_HUMAN	EST HUMAN	TN	NT
	Top Hit Acession No.	1.0E-65 AI621017.1	11418041 NT	11418322 NT	11418248 NT	AL160311.1	9.0E-66 AL160311.1	5031980	5031980 NT	9.0E-66 M87299.1	M72393.1	M72393.1	۲.	7.0E-66 BE064410.1	_		6.0E-66 Al924653.1	6.0E-66 Al924653.1	(69181.1	5.0E-66 BE064410.1	11420557 NT	6679816 NT	(89211.1	4.0E-66 AJ223364.1	9635487 NT		8		4.0E-66 AW965473.1		11421638 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-65	1.0E-65	1.0E-65	1.0E-65	9.0E-66	9.0E-66	9.0E-66	9.0E-66	9.0E-66	9.0E-66 M72393.1	9.0E-66 M72393.1	8.0E-66	7.0E-66	6.0E-66 AI924653.		6.0E-66	6.0E-66	6.0E-66 X69181.1	5.0E-66	5.0E-66	4.0E-66	4.0E-66 X89211.1	4.0E-66	4.0E-66	L	4.0E-66	4.0E-66	4.0E-66/	4.0E-66 U78168.1	4.0E-66
	Expression	2.35	2.27	4.85	1.44	1.51	1.51	2.49	2.49	4.18	6.0	6.0	0.88	1.73	1.22		1.22	1.22	70.7	2.25	12.31	0.79	1.94	3.66	5.15	i d	3.35	1.78	4.71	6.89	6.38
	ORF SEQ ID NO:	28681		25318		19864		21096	21097		23529	23530	24266		23944		23945	23946	28636	21107	27424	20542	22022			1 0	25376	25494	24869		26776
	Exon SEQ ID NO:	18414	18905	18963	19225	10051	10051	11239	11239	11373	13738	13738	14479	18543	14168		14168	14168	18372	11250	17225	10703	12120	12302	14560	7	15326	15430	15106	16098	16588
	Probe SEQ ID NO:	8542	9155	9254	9965	65	65	1332	1332	1468	3826	3826	4591	8654	4269		4269	4269	8439	1344	7357	773	2235	2425	4674	107.1	2407	5512	9609	6232	6708

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	Top Hit Descriptor	UI-H-BW1-amr-a-10-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070747 31	Homo saplens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA	yz27g12.r1 Soares_multiple_sclerosis_ZNbHMSP Homo sapiens cDNA clone IMAGE.284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B5661.2	yzZig12.r1 Soares multiple_sclerosis_ZNbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2, [2] PIR:B56612.	yz27g12.r1 Soares multiple_scierosis_ZNbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.11H2B.2_{21}PIR:B56612.	Homo sapiens TGF(beta)-induced transcription factor 2 (TGF2) mRNA	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA	Homo saplens protein phosphatase 2, regulatory subunit B (B58) ainha isoform (PPD2R54) mDNA	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORCSL) mRNA, and translated products	Homo sapiens chromosome 21 segment HS21C101	H. sapiens pseudogene for the low affinity IL-8 receptor	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA complete cols	Homo sapiens HLA-B gene for human leucocyte antigen B	Homo sapiens HLA-B gene for human leucocyte antigen B	39502.r1 Soares, multiple, sclerosis, 2NbHMSP Homo sapiens cDNA clone IMAGE: 277826.53	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'	AV717817 DCB Hamo sapiens cDNA clone DCBADC07 5	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
מוס בעמון זו ומ	Top Hit Database Source	EST_HUMAN	ΤZ	μN	EST HUMAN	EST_HUMAN	EST HUMAN	LN	NT	LN	TN	TN	N	₽N	۲	LN LN	NT	N	LN	NT	LN	EST_HUMAN	N	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN
5	Top Hit Acession No.	BF507493.1	4502098 NT	4502098 NT	3.0E-66 N55323.1	V55323.1	3.0E-66 N55323.1	11141880 NT	7662223 NT	11417946 NT	11417946 NT	5453949 NT	7657334	7657334 NT	4505524 NT	4505524 NT	1.2		9.1		2.0E-66 AJ133267.2		11418318 NT	_		1.0E-66 AV717817.1	1.0E-66 AV717817.1
	Most Similar (Top) Hit BLAST E Value	4.0E-66	3.0E-66	3.0E-66	3.0E-66	3.0E-66 N55323.1	3.0E-66	3.0E-66	3.0E-66	3.0E-66	3.0E-66	3.0E-66	2.0E-66	2.0E-66	2.0E-66	2.0E-66	2.0E-66	2.0E-66 X65859.1	2.0E-66/	2.0E-66/	2.0E-66/	2.0E-66 N45480.1	2.0E-66	1.0E-66	1.0E-66 /	1.0E-66	1.0E-66 ⊅
	Expression Signal	1.96	24.62	24.62	0.84	0.84	0.84	2.91	5.47	1.64	1.64	8.3	1.02	1.02	0.93	0.93	2.02	96'0	0.86	12.69	12.69	2.16	2.22	1.38	1.38	3.26	3.26
	ORF SEQ ID NO:	28193	21175	21176	21717	21718	21719	22430	22797	25511		28904	19837	19838	19774	19775	21560	22669	23657			27205		22585	22586	22585	22586
	Exan SEQ ID NO:	17943	11313	11313	11834	11834	11834	12540	13006	15445	15445	18614	10033	10033	9983	9983	11682	12871	13882	14448	14448	17012	19712	12792	12792	12792	12792
	Probe SEQ ID NO:	8052	1408	1408	1939	1939	1939	2675	3079	5528	5528	8800	45	45	416	416	1784	2944	3975	4556	4556	7135	9475	2864	2864	4288	4288

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Probe SEQ ID Exan NO: ORF SEQ ID NO: NO: NO: ID NO: 5306 16227 2503 6143 15991 26126 6926 16804 26996 8312 18189 28438 9260 18965 20186 4829 14711 21126 1360 11266 21126 1535 11439 21296 1535 11439 21297 1538 11881 2177 1988 11881 2177	SEQ Expression IO: Signal		Top Hit Acession	Top Hit	
15227 15891 16804 18189 18965 14711 10360 11266 11439 11439 11881		BLAST E Value	o Z	Database Source	Top Hit Descriptor
15991 16804 18189 18965 14711 10360 11266 11439 11439 118811	2000			EST_HUMAN	602152996F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294151 5'
18804 18965 18965 14711 10360 11266 11439 11439 118811	26126 1.49		1.0E-66 BF328623.1	EST_HUMAN	RC5-BN0193-010900-034-G06 BN0193 Homo sapiens cDNA
18189 18955 14711 10360 11266 11439 11439 118811	26998 1.37		1.0E-66 AA668858.1	EST_HUMAN	aa80e04.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:827262 3'
14711 10360 11286 11439 11439 11881	28438 2.39		1.0E-66 AF111167.2	- E	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
14711 10360 11286 11439 11439 11881			11418177 NT		Homo saplens Ran GTPase activating protein 1 (RANGAP1), mRNA
10360 11266 11439 11439 11881	0.84		8.0E-67 M78158.1	EST_HUMAN	EST01750 Subtracted Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCPN31 similar to L1 repetitive element
11266 11439 11439 11881	20184 6.19		7.0E-67 AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
11439 11439 11881 11881	21122 2.63		7.0E-67 AA383416.1	EST_HUMAN	EST96812 Testis I Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK353
11439	21296	1 7.0E-67		EST_HUMAN	zh56b05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:416049 5'
11881	21297	1 7.0E-67	7.0E-67 W85947.1	EST_HUMAN	zh56b05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
11881	21773 1.06			NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
	21774 1.06	6 7.0E-67	7657243 NT		Homo saplens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
2779 10360 20	20184		7.0E-67 AW162232.1	T_HUMAN	au75d02.xt Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
15699	25807 2.04				Homo saplens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
	25808 2.04				Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
18826					Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
18826			11430460		Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
19116	25292 3.33		7.0E-67 AB011399.1		Homo sapiens gene for AF-6, complete cds
19357	1.43		1421527		Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA
547 10488 20	20297 1.32		X68968.1		H.saplens mRNA for acetyl-CoA carboxylase
10708	20547 1.5				Homo sapiens mRNA for transmebrane receptor protein
11159			Y14320.1	LN.	Homo sapiens PMP69 gene, exons 3,4,5,6 & 7
13056	22856 1.24	4 6.0E-67			Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
13308	3106 1.2		4507332 NT		Homo sapiens Synapsin III (SYN3) mRNA, and translated products
13308	23107		4507332 NT	LN	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4035 13938 2:	23714 1.28		6.0E-67 AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
13938	23715 1.28		6.0E-67 AL163201.2		Homo sapiens chromosome 21 segment HS21C001
14495					Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4607 14495 2.	24284 3.37	7 6.0E-67	7657020 NT		Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA

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Suigle Explessed III healt	EQ ID ID NO: Signal Average Most Similar Top Hit Acession ID NO: Top Hit Acession Signal Average Top Hit Descriptor Source Value Yalue Source Source	14761 2.1 6.0E-67 4507848 NT Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	22913 2.45 5.0E-67 AF009660.1 NT	2.1 5.0E-67 BE010038.1 EST HUMAN	21069 1.83 4.0E-67 R90819.1 EST_HUMAN	1.22 4.0E-67 BF357321.1 EST_HUMAN	2.3 4.0E-67 AA714294.1 EST HUMAN	20365 0.93 3.0E-67 AA333768.1 EST HUMAN	23125 1.14 3.0E-67 BE064410.1 EST HUMAN	24270 3.14 3.0E-67 AW869159.1 EST HUMAN	26827 1.22 3.0E-67 BF196068.1 EST HUMAN	19.27 3.0E-67 AA927874.1 EST HUMAN	19967 1.94 2.0E-67 BE348354.1 EST HUMAN	20604 6 2.0E-67/AW816405.1 EST HUMAN	1.74 2.0E-67 AF167460.1 NT	21614 1.5 2.0E-67 BE303037.1 EST_HUMAN	21615 1.5 2.0E-67 BE303037.1 EST HUMAN	22116 0.98 2.0E-67 AF309561.1 NT	22153 1.2 2.0E-67 4758795 NT	23144 3.9 2.0E-67 AA625755.1 EST_HUMAN	23610 2.33 2.0E-67 AL163300.2 NT	25734 4.22 2.0E-67 BF240758.1 EST_HUMAN	25820 2.17 2.0E-67 AB051763.1 NT	25821 2.17 2.0E-67 AB051763.1 NT	27264 1.34 2.0E-67 AW602635.1 EST_HUMAN	27265 1.34 2.0E-67 AW 602635.1 EST_HUMAN	3.26 2.0E-67 11436448 NT	28698 1.77 2.0E-67 BE295714.1 EST_HUMAN	28144 2.26 2.0E-67 BF377169.1 EST HUMAN	25069 2.0E-67 11418189 NT
	ORF SEQ ID NO:															21614														
	Exon SEQ ID NO:	5 14761	4 13109	2 18229	6 11213	3 16762	6 18290	2 10553	7 13324	14484	16639	3 18451	0 10152	7 10754	11005	1 11737	11737	3 12216		╛					_					3 19577
	Probe SEQ ID NO:	5125	3184	8352	1306	6883	8416	2782	3407	4596	6760	8583	180	827	1089	1841	1841	2336	2381	3422	3921	5724	5803	5803	7202	720.	8409	8558	8751	9388

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Strigle Exott Flodes Expressed in Healt	Most Similar (Top Hit Acession Database BLAST E No. Source Source	1.0E-67 4502166 NT Homo sapiens amyloid beta (A4) precursor protein (protease nexin-il, Alzheimer discase) (APP), mRNA	8.0E-68 BE87073	2492h10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN.;	8.0E-68 AA209456.1 EST HUMAN	6.0E-68 AW 503842.1	6.0E-68 11422086 NT	6.0E-68 AF133901.1	6.0E-68 BE612554.1	6.0E-68 BF310675.1 EST HUMAN	5.0E-68 AF231919.1 NT		5.0E-68 AF231919.1	57 5.0E-68 AF231919.1 NT Homo sapiens chromosome 21 unknown mRNA	5.0E-68 AB037852.1 NT		4.0E-68 11421388 NT	4.0E-68 P04406 SWISSPROT	4.0E-68 110	4.0E-68 11055991 NT	4.0E-68 D63479.2 NT	4.0E-68 D63479.2 NT	4.0E-68 AB040918.1 NT	3.0E-68 AF236082.1 NT		3.0E-68 AI342323.1 EST HUMAN	3.0E-68 F28784.1 EST_HUMAN	3.0E-68 AW939485.1 EST_HUMAN		2.0E-68 AB008681.1 NT	8 2.0E-68 R45088.1 EST_HUMAN yg38g04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34896 3'
		1.0E-67	8.0E-68 BE87073	8.0E-68 AA2094	8.0E-68 AA2094	6.0E-68 AW 5038	6.0E-68	6.0E-68 AF13390	6.0E-68 BE6125	6.0E-68 BF31067	5.0E-68 AF23191	5.0E-68 AF23191	5.0E-68 AF23191	5.0E-68 AF23191	5.0E-68 AB0378			4.0E-68 P04406			4.0E-68 D63479.	4.0E-68 D63479.	4.0E-68 AB0409	3.0E-68 AF23608	0	3.0E-68 AI34232	3.0E-68 F28784.	3.0E-68 AW9394	2.0E-68 D00522	2.0E-68 AB00868	2.0E-68 R45088.
	Expression Signal	4.37	2.46	4.96	4.96	22	2.46	1.93	1.42	1.36	0.87	0.87	3.87	3.87	29.2	1.01	1.01	17.24	5.64	5.64	5.41	5.41	2.39	5.61		4.44	1.45	1.53	12.26	1.66	8
	ORF SEQ ID NO:	20036	21915	23492		L	28064	28627		25178	20555		20572	20573	22830	22247	22248							23312			28088			24261	
	Exon SEQ ID NO:	10219	12017	13706	13706	11745	17821	18362	19234	19391	12642	12642	10731	10731	13034	12356	12356	14780	16044	16044	17102	17102	17171	13525		16454	_1		1		16004
	Probe SEQ ID NO:	253	2129	3794	3794	1849	7971	8489	9676	9918	785	785	802	802	3108	2480	2480	4800	6061	6061	7225	7225	7295	3611		(441	7997	9872	2832	4583	6110

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	Top Hit Descriptor	601458514F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862034 5		Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA			Homo sapiens mRNA for KIAA0577 protein, complete cds	Γ		Γ	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA	Homo sapiens phosphodiesterase 7B (PDE7B), rnRNA	Homo sapiens MIF2 suppressor (HSMT3) mRNA, complete cds	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2). mRNA	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA	Homo sapiens 26S proteasome associated pad1 homolog (POH1) mRNA	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA	Homo saplens v-raf murine sarcome viral oncogene homolog 81 (RRAF) mRNA		Homo sapiens RIBIIR gene (partial), exon 12	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA	qe62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601.3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN):		gold 1300 ous RIBUSUMAL PROTEIN L18 (HUMAN); WMD8H11 v1 NCL CCAP 1144 Home content CDNA close 1846 CE 2122 212E 21	Т	055137 ACYL-COA THIOESTERASE. :	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA	Homo sapiens latent transforming growth factor beta binding protein 2 (LTI3P2) mRNA	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3361352 5'	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
3.5	Top Hit Database Source	EST_HUMAN	EST HUMAN	Z	EST HUMAN	NT	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN LN	N	NT	Z	ZI	LN	N L	F	LN	LN	NT	EST_HUMAN	Z Z	NT	EST HUMAN	1444	FST HIMAN		EST_HUMAN	N	NT	EST_HUMAN	NT
	Top Hit Acession No.	2.0E-68 BF035316.1	2.0E-68 BE897376.1	4505222 NT	1.0E-68 AW816405.1	AB011149.1	1.0E-68 AB011149.1	1.0E-68 AW451832.1	1.0E-68 BE296032.1	1.0E-68 AA897343.1	7662349 NT	11418869 NT	11418869 NT	L76416.	4505222 NT	11430460 NT	5031976 NT	TN 9761505	5031980 NT	5031980 NT	4757867 NT	9.0E-69 AU117241.1	8.0E-69 AJ237744.1	9966912 NT	6.0E-69 AI192764.1	6 OF 60 A 400364 4			4.0E-69 AI764973.1	4557732 NT	4557732 NT		3.0E-69 AF221712.1
	Most Similar (Top) Hit BLAST E Value	2.0E-68	2.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-68	9.0E-69	9.0E-69	9.0E-69	9.0E-69	9.0E-69	9.0€-69	8.0E-69	7.0E-69	6.0E-69	90 50	4.0E-69.4		4.0E-69	4.0E-69	4.0E-69	3.0E-69	3.0E-69/
	Expression Signal	4.79	1.92	1.31	92.6	1.32	1.32	1.01	0.95	86.0	1.57	2.44	2.44	2.29	1.95	1.38	1.82	1.82	1.63	1.63	0.78	9.27	1.21	80'9	3.61	200	188		4.12	2.43	2.43	2.81	1.64
	ORF SEQ ID NO:	26095		19873	20078	21994		22486	23617	24598	24959		28362	28396	19873	24991	19797	19798	20772	20773	23718			25852	26659	26660	20007		25554	28024	26025	20187	20340
	Exan SEQ ID NO:	15962	19731			12092				14831	15183		18108	18155		19669	10006	10006	10929	10929	13940	18143	13260	15740	16469	16460	10451		15481	15900	15900	10364	10532
	Probe SEQ ID NO:	6202	9148	72	293	2205	2205	2728	3928	4954	5261	8226	8228	8275	9659	9862	19	19	1011	1011	4037	8263	3340	5834	6288	GSRQ	509		5565	5995	5995	380	596

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				Most Similar			
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1536	11440		1.35	3.0E-69	3.0E-69 T80514.1	EST HUMAN	yd08a02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE.24880 5' similar to SP:A48836 A48836 SPEGF II=EGF REPEAT-CONTAINING FIBROPELLIN-LIKE PROTEIN - SEA URCHIN
2325	12206		0.88	3.0E-69	5729910 NT	N	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
3990	13897	23674	0.86	3.0E-69	3.0E-69 AI765888.1	EST_HUMAN	wh66g08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385758 3'
5209	15087	29105	5.94	3.0E-69	11418185 NT	L	Homo saplens aconitase 2, mitochondrial (ACO2), mRNA
6387	16249	26410	1.37	3.0E-69	3.0E-69 U52351.1	N	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds
6457	16318	26485	8.43	3.0E-69	3.0E-69 AF268075.1	N	Homo sapiens TRAF6-binding protein T6BP mRNA, complete cds
7091	16968		1.26	3.0E-69	3.0E-69 AA376399.1	EST_HUMAN	EST88807 HSC172 cells II Homo saplens cDNA 5' end similar to similar to ribosomal protein S18
7417	17284	27491	1.54	3.0E-69	3.0E-69 X13223.1	Z	H. sapiens mRNA for N-acetyglucosamide-(beta 1-4) galactosytransferase
							Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory facto:
7493	17363	27568	2.24	3.0E-69	X06233.1	NT	(MIF)-related protein
8036	17928	28174	3.07	3.0E-69		N	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
8215			7.12	3.0E-69	AA3763	199.1 EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
9168			4.13	3.0E-69		NT	Homo sapiens HGC6.2 protein (HGC6.2), mRNA
124	10344	20170	1	2.0E-69	2.0E-69 AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds, and alphallb protein gene, partial cds
124	10344	20171	1	2.0E-69	2.0E-69 AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alphallb protein gene, partial cds
398	10344	20170	4.94	2.0E-69	2.0E-69 AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alphallb protein gene, partial cds
398		20171	4.94	2.0E-69	2.0E-69 AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds, and alphallb protein gene, partial cds
1842	11738	21616	1.2	2.0E-69	2.0E-69 BE257857.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
2813	12742		2.73	2.0E-69	2.0E-69 AA431157.1	EST_HUMAN	zw71g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781682 5'
1675		21445	2.35	1.0E-69	1.0E-69 AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
5981		26008	3.68	1.0E-69	1.0E-69 AW393969.1	EST_HUMAN	QV0-TT0010-031199-045-c07 TT0010 Homo sapiens cDNA
9080	16063	26211	1.55	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6080	16063	26212	1.55	1.0E-69	7662263 NT	IN	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6088	16033	26173	2.93	1.0E-69	1.0E-69 AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial ods
6088	16033	26174	2.93	1.0E-69	1.0E-69 AB032973.1	N	Homo sapiens mRNA for KIAA1147 protein, partial cds
							TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens.
7847	17697	27942	5.29	1.0E-69	1.0E-69 BE245070.1	EST_HUMAN	cDNA clone TCBAP2678
							TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
7847		27943	5.29	1.0E-69	BE24507	EST_HUMAN	cDNA clone TCBAP2678
8246			23.27	1.0E-69	4504918 NT		Homo sapiens keratin 8 (KRT8) mRNA
9105	18872	28785	1.53	1.0E-69	1.0E-69 BF125887.1	EST_HUMAN	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'

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Table 4
Single Exon Probes Expressed in Heart

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Top Hit Descriptor	wf84e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Alurepetitive element.
 | Homo sapiens MIST mRNA, partial cds

 | Homo sapiens gene encoding splicing factor SF1, exons 2-8 | Homo sapiens mRNA for KIAA1294 protein, partial cds

 | Homo sapiens mRNA for KIAA1294 protein, partial cds | Human displacement protein (CCAAT) mRNA | Human displacement protein (CCAAT) mRNA | Human PBX3 mRNA
 | Human PBX3 mRNA | Homo saplens phospholipid scrambiase 1 gene, exon 1 and 5' flanking region | Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA | Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA | Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
 | Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
 | | Suppliers supplied between (A4) precursor protein (protease nextin-ri, Alzheimer disease) (APP), mRNA | Human Ku (p/o/pau) subunit mRNA, complete cds | Homo sapiens CMP-N-acetyineuraminic acid synthase (LOC55907), mRNA
 | Homo sapiens KIAA0792 gene product (KIAA0792), mRNA | Homo sapiens KIAA0792 gene product (KIAA0792), mRNA | MR3-HT0487-150200-115-a06 HT0487 Homo saplens cDNA
 | RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA | RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA |
| Top Hit
Database
Source | EST HUMAN | EST_HUMAN | L | EST_HUMAN | EST_HUMAN | EST_HUMAN | LN L | LN | NT
 | NT

 | NT | NT

 | N | LN | N
L | TN
 | N | N | NT | NT | LΝ
 | NT
 | Ť.N. | | -2 | NT
 | NT | NT | EST_HUMAN
 | EST_HUMAN | EST HUMAN |
| Top Hit Acession
No. | AI809994.1 | AA230303.1 | .77566.1 | 41497807.1 | 41497807.1 | 4A282955.1 | 5031668 | 4757723 | 4B032369.1
 | AB032369.1

 | AJ000052.1 | AB037715.1

 | AB037715.1 | M74099.1 | M74099.1 | (59841.1
 | (59841.1 | AF153715.1 | 11525964 | 11525964 | 11526319
 | 11526319
 | 4500466 | 4302100 | /เลบยวธ. T | 8923899
 | 7662307 | 7662307 | 3E166034.1
 | 3E071796.1 | 3.0E-70 BE071796.1 |
| Most Similar
(Top) Hit
BLAST E
Value | 1.0E-69 | 8.0E-70 | 8.0E-70 | 7.0E-70 | 7.0E-70 | 7.0E-70 | 7.0E-70 | 7.0E-70 | 7.0E-70
 | 7.0E-70

 | 7.0E-70 | 7.0E-70

 | 7.0E-70 | 7.0E-70 | 7.0E-70 | 7.0E-70
 | 7.0E-70 | 7.0E-70 | 7.0E-70 | 7.0E-70 | 7.0E-70
 | 7.0E-70
 | 02. 20 | 0.01-70 | 0.05-70 | 6.0E-70
 | 5.0E-70 | 5.0E-70 | 5.0E-70
 | 3.0E-70 | 3.0E-70 E |
| Expression
Signal | 2.32 | 1.52 | 2.16 | 1.93 | 1.93 | 1.63 | 3.57 | 3.86 | 5.28
 | 5.28

 | 1.89 | 2.36

 | 2.36 | 3.98 | 3.98 | 3.72
 | 3.72 | 3.13 | 1.56 | 1.56 | 1.78
 | 1.78
 | 1 03 | 20.1 | 05. | 0.99
 | 1.83 | 1.83 | 1.73
 | 0.89 | 0.89 |
| ORF SEQ
ID NO: | | 22065 | 23954 | 21547 | 21548 | 21660 | | 23807 | 25124
 | 25125

 | 26120 | 26980

 | 26981 | 27131 | 27132 | 27357
 | 27358 | 26627 | 26648 | 26649 | 28978
 | 28979
 | 20630 | 24074 | 41017 | 22232
 | 22268 | 22269 |
 | 21332 | 21333 |
| Exon
SEQ ID
NO: | 19124 | 12717 | 14176 | 11670 | 11670 | 11784 | 11909 | 14032 | 15289
 | 15289

 | 15985 | 16788

 | 16788 | 16940 | 16940 | 17159
 | 17159 | 16441 | 16457 | 16457 | 18687
 | 18687
 | 10780 | 11070 | 9/8 | 12338
 | 12723 | 12723 | 18879
 | 11475 | 11475 |
| Probe
SEQ ID
NO: | 9510 | 2284 | 4277 | 1771 | 1771 | 1888 | 2018 | 4132 | 5369
 | 5369

 | 6138 | 6910

 | 6910 | £90 <i>1</i> | 7063 | 7283
 | 7283 | 7428 | 7445 | 7445 | 8875
 | 8875
 | 853 | 2000 | 2030 | 2461
 | 2505 | 2505 | 9116
 | 1571 | 1571 |
| | Exon ORF SEQ Expression (Top) Hit Top Hit Acession No. Signal Value Source | Exon SEQ ID NO: Signal BLASTE No. Signal Value 19124 2.32 1.0E-69 Al809994.1 EST HUMAN | Exon SEQ ID ID NO: CRF SEQ Signal NO: Expression Signal NO: (Top) Hit Acession Signal Alabase Top Hit Acession No: Top Hit Acession Source No: Top Hit Acession Source Nature 19124 2.32 1.0E-69 Al809994.1 EST HUMAN 12717 22065 1.52 8.0E-70 AA230303.1 EST HUMAN | Exon
SEQ ID
NO: ORF SEQ
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Signal (Top) Hit
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Source 19124 2.32 1.0E-69 Al809994.1 EST_HUMAN
EST_HUMAN 12717 22065 1.52 8.0E-70 AA2330303.1 EST_HUMAN
EST_HUMAN 14176 23954 2.16 8.0E-70 L77566.1 NT | Exon SEQ ID NO: CRF SEQ Signal No: Rost Similar (Top) Hit Acession Signal No: Top Hit Acession No: Top Hit Acession Signal No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top 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Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate Plate</td><td>Exon NO:- CRF SEQ ID ID NO:- Expression Signal No:- Most Similar No:- Top Hit Acession No:- Top Hit Acession Signal No:- Top Hit Acession No:- Top Hit Acession No:- Top Hit Acession No:- Top Hit Acession No:- Top Hit Acession No:- 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Table 4
Single Exon Probes Expressed in Heart

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Single Lyon Flores Expressed III Heart	Top Hit Descriptor	602141561F1 NIH MGC 46 Homo sabiens cDNA clope IMAGE: 4302808 F.	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 57	y07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P29286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECIPSOR	907410.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5 inniar to SW:D3Hi RAT P29268 3-HYDROXYISORI ITYRATE DEHYDROCENAGE BELGING IN CO.	qx51h01x1 NC CGAP Pan1 Homo sapiens cDNA clone IMAGE: วกกลดาล ล่	Homo sapiens hypothetical protein FLJ20758 (FLJ20758) mRNA	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA	Homo sapiens KIAA0193 gene product (KIAA01931 mRNA	hz64c12x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGF:3212758 31	Homo sapiens chromosome 21 segment HS21C002	2/48g04.r1 Soares refina N2b4HR Homo sapiens cONA clone IMAGE:380214 5' similar to SW:GAG_HTL1A P03345 GAG POI YPROTEIN	Human nonmuscle myosin heavy chain-B (MYH10) mRNA nartial cris	H.saplens gene for schwannomin (CS8)	H.sapiens gene for schwannomin (CS8)	Homo sapiens NALP1 mRNA, complete cds	Human mRNA for NF1 protein Isoform (neurofibromin Isoform), complete cds	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete chs	Homo sepiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds	Homo sapiens sialytransferase 6 (N-acetylacosaminide albha 2 3-sialytransferase) (<10.15) mbn/n	Human guanine nucleotide-binding protein elpha-subunit gene (G-s-ainha) avens a sand s	Homo sapiens calcium-binding transporter mRNA, partial cds	Homo sapiens hypothetical protein FLJ20450 (FLJ20450) mRNA	Homo sapiens hypothetical protein FLJ20450 (FLJ20450) mRNA	Homo sapiens eukaryotic translatior initiation factor 3 subunit 6 (48kD) (FIF33S) mBNA	Homo sapiens low density lipoprotein-related protein 2 (1 RP2) mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2) mRNA	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamytransferase) (TGM3) mRNA	Zv54c03.r1 Soares testis NHT Homo saniens cDNA clone IMAGE-757444 F	AV738538 CB Homo sapiens cDNA clone CBLBGB10 5
gie Exori Pio	Top Hit Database Source	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	LN	LN	NT	EST HUMAN	TN	EST HUMAN	N	NT LN	NT	N	N FN	LN	LN LN	N TN	닏	IN	N-	TN	LN LN	FZ	L	Į.	EST HUMAN	EST_HUMAN
	Top Hit Acession No.	3.0E-70 BF685233.1	3.0E-70 BF685233.1	2.0E-70 N42161.1	2.0E-70 N42161.1	2.0E-70 AI246899.1	8923669 NT	7661983 NT	7661983 NT	2.0E-70 BE467311.1	2.0E-70 AL163202.2	2.0E-70 AA054010.1		2.0E-70 X72662.1	2.0E-70 X72662.1	2.0E-70 AF310105.1	2.0E-70 D12625.1	7.	2.0E-70 AF123074.1	11422642 NT	2.0E-70 M21741.1	2.0E-70 AF123303.1	8923420 NT	B923420 NT	4503520 NT	11430460 NT	11430460 NT	4507476 NT	1.0E-70 AA442292.1	
	Most Similar (Top) Hit BLAST E Value	3.0E-70	3.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	1.0E-70	1.0E-70	1.0E-70
	Expression Signal	3.88	3.88	13.15	13.15	2.01	1.7	1.95	1.95	0.97	2.09	3.62	3.95	8.05	8.05	1.42	1.88	9.83	9.83	1.69	7.67	1.3	3.19	3.19	5.82	2.58	2.58	2.97	2.57	13.73
	ORF SEQ ID NO:	25865	25866	20426	20427	20449	20766		20925		21479		23648	25156	25157	25780	26028	26042	26043	24853	26685	27930	28550	28551	29010	25289	25290			28429
	Exon SEQ ID NO:	15751		10608	10608	10622	10922	11079	11079	11292	11609	12156	13870	15304	15304	15673	15904	15915	15915	15134	16498	17685	18296	18296	18716	19114	19114	13267	17492	18182
	Probe SEQ ID NO:	5845	5845	674	674	689	1004	1167	1167	1387	1708	2272	3963	5385	5385	5766	5999	6010	6010	6177	6618	7835	8422	8422	8908	9499	9499	3347	7642	8305

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5621	15536	25621	6.04	9.0E-71	9.0E-71 AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045 O14045 PHOSPHOTRANSFERASE.;
5621	15536	25622	6.04	9.0E-71	9.0E-71 AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045 O14045 PHOSPHOTRANSFERASE.;
6192	16077	26226	1.88	9.0E-71	9.0E-71 AI654903.1	EST_HUMAN	wb52c05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE.2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.
8811	16077	26226	4.65	9.0E-71	9.0E-71 AI654903.1	EST_HUMAN	wb52c05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.
7245	17122		1.97	8.0E-71	8.0E-71 AA171451.1	EST_HUMAN	zp21d11.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610101 5' similar to TR:G1143061 G1143061 STRAIN XA34 POL;
6363	16226	26386	7.91	7.0E-71	7.0E-71 AA442230.1	EST_HUMAN	zv60h06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:758075 5'
7037	16914	27103	1.52	7.0E-71		EST_HUMAN	zj91a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'
8643	18507	28786	4.18	7.0E-71		LN	Homo sapiens chromosome 21 segment HS21C010
2163	12050		3.45	5.0E-71		TN	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4030	13933			5.0E-71	τ	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo saplens cDNA
5144	15011	24782	3.2	5.0E-71	AI829496.1	EST_HUMAN	w18h10.x1 NCi_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2425315 3'
5586	15501	25577	2.14	5.0E-71	4502740 NT	LN	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6434	16295	26457	1.59	5.0E-71		TN	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
6548	16406	26585	19.78	5.0E-71	5.0E-71 AF072810.1	L	Homo sapiens transcription factor WSTF mRNA, complete cds
7702	17552		2.26	5.0E-71	5.0E-71 X13467.1	N	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
8378	18225	77786	0	5 OE_74	11436514	F	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective
8528	18400	28668		5.0E-71		NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC63325), mRNA
2906	18848		1.84	5.0E-71		NT	Homo saplens calcineurin binding protein 1 (KlAA0330), mRNA
9411	19063		1.62	5.0E-71	11418039 NT	NT	Homo sapiens RNA binding motif protein 9 (RBM9), mRNA
97	10082	19899	1.13	4.0E-71	4507592 NT	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
347	10306	20123	115.63	4.0E-71	4.0E-71 AF157626.1	LN	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
347	10306	20124	115.63	4.0E-71	4.0E-71 AF157626.1	LN	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2850	12778		0.88	4.0E-71		NT	Homo sapiens hook1 protein (HOOK1), mRNA
2850	12778		0.88	4.0E-71		NT	Homo saplens hook1 protein (HOOK1), mRNA
2857	12785	22575	1.63	4.0E-71		NT	Homo sapiens plasminogen (PLG) mRNA
4330	14227	24009			AF056322.1	LN L	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4913	14792	24567	4.99	4.0E-71	7657602 NT	LN	Homo sapiens putative heme-binding protein (SOUL), mRNA

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Exon No: 1700 CRF SEQ Expression No: 1700 Most Similar Top Hit Accession No: 1700 Top Hit Accession Source No: 1710 Top Hit Accession No: 1710 Top Hit Accession Source No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 Top Hit Accession No: 1710 No: 1710 No: 1710 No: 1710 No: 1710 No: 1710 No: 1710 No: 1710 No: 1710 No: 1710 No: 1710 No: 1710 No: 1710 No: 1710 No: 1710 No: 1710 <td>Des Expressed in Heart</td> <td>Top Hit Descriptor</td> <td>nI45h10.s1 NOI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5</td> <td>Homo sabiens chromosome 21 segment HS21Chais</td> <td>Human mRNA for KIAA0272 gene partial rds</td> <td>Human mRNA for KIAA0272 gene, partial cds</td> <td>Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds</td> <td>Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds.</td> <td>bb81a06.y1 NIH_MGC_10 Home sapiens cDNA clone IMACE:3048754 s' similar to SW:R23B_HUMAN P547271 IV EXCISION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXCISION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATT</td> <td>W443409 of Society fatel lives relieve to the Library HVMULOG B</td> <td>ovideous, 1 Source, senescent, fibroblasts, NbHSF Homo sapiens cDNA clone IMAGE:120520 5' contains 1 OPA to 1 ODA</td> <td>Homo sapiens perional cell death, related material (1005/2016)</td> <td>Homo saplens disabled 2 nene avvns 2 through 15 mg.</td> <td>Homo sabiens phosphaticulary 4 kings 200 (1147,000) This</td> <td>Homo sapiens PMS21 16 mRNA partial cds</td> <td>Homo saplens PMS2 16 mRNA partial cds</td> <td>Homo sapiens hair/enhancer-of-snilt related with VRDM motif ill. (UCVI)</td> <td>Homo sapiens inorganic ovrophosphatase mRNA complete and</td> <td>Homo saplens SNARE protein kinase SNAK mRNA complete cds</td> <td>Homo sapiens SNARE protein kinase SNAK mRNA, complete cds</td> <td>02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19</td> <td>02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA</td> <td>Homo sapiens, affractin precinsor (A TRN) some action</td> <td>Human mRNA for KIAA0045 dene complete etc.</td> <td>Homo saniens GONS (nances) control of emine and</td> <td>Homo saniens, CAGI 79 mRNA partial cata</td> <td>Homo sapiens myomesin (M-profein) 2 (165kh) (MXOMA)DNA</td> <td>Homo sapiens hypothetical profein FLJ10998 (FLJ10998), mRNA</td>	Des Expressed in Heart	Top Hit Descriptor	nI45h10.s1 NOI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5	Homo sabiens chromosome 21 segment HS21Chais	Human mRNA for KIAA0272 gene partial rds	Human mRNA for KIAA0272 gene, partial cds	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds.	bb81a06.y1 NIH_MGC_10 Home sapiens cDNA clone IMACE:3048754 s' similar to SW:R23B_HUMAN P547271 IV EXCISION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXCISION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY IN EXPENSION REDAID BEATEIN BEATEIN BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATTERN PARTY BATT	W443409 of Society fatel lives relieve to the Library HVMULOG B	ovideous, 1 Source, senescent, fibroblasts, NbHSF Homo sapiens cDNA clone IMAGE:120520 5' contains 1 OPA to 1 ODA	Homo sapiens perional cell death, related material (1005/2016)	Homo saplens disabled 2 nene avvns 2 through 15 mg.	Homo sabiens phosphaticulary 4 kings 200 (1147,000) This	Homo sapiens PMS21 16 mRNA partial cds	Homo saplens PMS2 16 mRNA partial cds	Homo sapiens hair/enhancer-of-snilt related with VRDM motif ill. (UCVI)	Homo sapiens inorganic ovrophosphatase mRNA complete and	Homo saplens SNARE protein kinase SNAK mRNA complete cds	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA	Homo sapiens, affractin precinsor (A TRN) some action	Human mRNA for KIAA0045 dene complete etc.	Homo saniens GONS (nances) control of emine and	Homo saniens, CAGI 79 mRNA partial cata	Homo sapiens myomesin (M-profein) 2 (165kh) (MXOMA)DNA	Homo sapiens hypothetical profein FLJ10998 (FLJ10998), mRNA
Exon ORF SEQ Expression Signal (Top) Hit Top Hit Accession No. Most Similar Value No. 17968 28216 3.32 3.0E-71 AA557693.1 No. 11119 20968 2.52 2.0E-71 AL163206.2 15181 24957 6.96 2.0E-71 AP095703.1 17872 28114 2.56 2.0E-71 AF095703.1 10559 2.0371 2.56 2.0E-71 AF095703.1 10851 28219 2.3 2.0E-71 AF095703.1 10850 2.0371 2.11 7.06-71 AF095703.1 10851 2.06-71 AF095703.1 7.06-71 AF095703.1 10852 2.0E-71 AF095703.1 7.06-71 AF095703.1 10851 2.08-71 AF095703.1 7.06-71 AF095703.1 11020 20841 4.01 1.0E-71 AF095703.1 11020 20841 4.01 1.0E-71 AF246219.1 11927 21822 2.0E-71 AF095703.1 11927 21822 2.0E-71 AF095703.1 11927 21822 2.0E-71 AF095703.1 11927 21822	JIE EXOII PIO	Top Hit Database Source			TN	LN	TN	LN ⊢N	EST HUMAN	FST HIMAN	EST HIMAN	L	N-	N	Z-	N	N-	LY.										
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Exon NO: ORF SEQ ID NO: Express Signe 17968 28218 5igne 11119 20968 11119 11119 20968 11119 15181 24957 28216 17872 28115 17872 17872 28116 1182 10851 20871 11822 11000 20841 11 11224 21080 11 11927 21822 11 11927 21821 11 11927 21822 11 13462 23256 1 13511 23298 0 13511 23298 0 13552 2355 1 14266 24050 1 16189 26079 1 16794 26936 6 16794 26986 6		Most Similar (Top) Hit BLAST E Value	3.0E-71	2.0E-71	2.0E-71	2.0E-71	2.0E-71	2.0E-71	2.0E-71	2.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71
Exon ORF SEQ ID ID NO: 17968 11119 15181 15181 17870 10851 11000 11224 11927 11927 11927 11927 11927 11927 11927 11927 11966 13595 1659 1659 1659		Expression Signal	3.32	2.52	6.96	96.9	2.56	2.56	2.3	6.22	2.11	1.93	4.01	10.59	1.23	1.23	4.85	1.17	4.73	4.73	0.94	0.94	1.87	1.86	1.4	10.62	96.9	4.18
		ORF SEQ ID NO:			24957	24958			28219		20371	20699	20841	21080	21821	21822	22416	23179	23256	23257	23298	23299	23381	24050	26079	26351	26816	26986
Probe SEQ ID NO: 8077 1210 5259 5259 8022 8022 8022 8022 926 1084 1317 2036 2036 2036 2036 3546 3546 3597 3597 3597 3597 6044 6044 6044 6050 6916		Exon SEQ ID NO:								18920	10559	10851	11000	11224	11927	11927	12528	13373	13462	13462	13511	13511	13595	14266	15947	16189	16629	16794
		Probe SEQ ID NO:	8077	1210	5259	5259	8022	8022	8079	9181	622	926	1084	1317	2036	2036	2661	3457	3546	3546	3597	3597	3681	4370	6044	6326	6750	6916

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Table 4
Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart

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חושל האלון וספס באלון הפספת הווים במתו	Top Hit Descriptor	Homo sapiens hypothetical protein dJ1057B20.2 (DJ1057B20.2), mRNA	Homo sapiens hect domain and RLD 2 (HERC2), mRNA	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA	yı.28a03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:235084 5'	yd29d09.s1 Soares fetal liver spleen 1NFLS Homo sapions cDNA clone IMACE:109649 3'	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor	ah63a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1310290 3'	Human chondroltin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA	TCR V delta 2-C alpha =T-cell receptor delta and C alpha fusion gene {alternatively spliced, splice junction}	Inuman, precursor B-cell line KEH, mKNA Partial, 211 nt	Home sapiens hypothetical protein (FLJ 11127), mRNA	wb31a08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307254 3	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5	Homo sapiens mRNA for KIAA1081 protein, partial cds	Homo sapiens mRNA for KIAA1081 protein, partial cds	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naib) and survival motor neuron protein (smn) genes, complete cds	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds	Homo sapiens gene for AF-6, complete cds	aj28b09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391609 3' similar to gb:X02067 H sapiens	IIINAA IO 10L NA pseudogere (hovan),	Rattus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds	ai83d02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387395 3	Homo sapiens vacuclar protein sorting 41 (yeast homolog) (VPS41), mRNA	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
TO LIOUS OIL	Top Hit Database Source	ΝΤ	NT	NT	EST_HUMAN	EST_HUMAN		EST_HUMAN	Z	NT	NT	ZI	ļ	Į.		T_HUMAN	NT	NT	LN L	NT	NT	Ł	L	L	IN	TOT.	EG TOWAN	LN	EST_HUMAN	NT	L'N
5	Top Hit Acession No.	11034844 NT	5729867 NT	8923669 NT				3.0E-72 AA723823.1			3.0E-72 AJ229043.1	8923548 NT		S77589.1	1416196	_		۲.		3.0E-72 AB029004.1	4826987 NT		5031892 NT		3.0E-72 AB011399.1		Z.UE-12 AA169211.1		AA846225.1	~ 1	11321578 NT
-	Most Similar (Top) Hit BLAST E Value	4.0E-72	4.0E-72	4.0E-72	4.0E-72 H79421.1	4.0E-72 T81910.1	4.0E-72	3.0E-72	3.0E-72 U16306.1	3.0E-72 U16306.1	3.0E-72	3.0E-72	L	_	3.0E-72	3.0E-72 AI654337	3.0E-72 AF073367	3.0E-72	3.0E-72 AB029004	3.0E-72	3.0E-72	3.0E-72 U80017.1	3.0E-72	3.0E-72	3.0E-72	70.0	Z.UE-12/	2.0E-72 /		1.0E-72	1.0E-72
	Expression Signal	1.06	1.4	1.42	7.32	2.76	4.2	4.88	90.9	90'9	10.51	2.63	i	2.51	3.22	0.94	2.4	2.4	4.35	4.35	3.02	2.32	1.26	1.3	1.85	- 4	4.40	3.74	2.61	3.15	19.78
	ORF SEQ ID NO:		26402	27705	28917	29030	25249		20894	20895	22759	22963		23445	24129	24500	25643	25644	25758	25759	26016	26501	26822	28051	25262	11000	/0797	25246	21812	25506	25976
	Exon SEQ ID NO:	14602	16242	17484		18737	19185	10811	11053	11053	12965	13164						15552		15651	15893	16334		17810	19129						15854
	Probe SEQ ID NO:	4716	6380	7633	8815	8929	9603	882	1139	1139	3037	3241		3750	4445	4835	5639	5639	5743	5743	5988	6475	6755	2960	9516	0	77 0	9600	2030	5524	5949

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Table 4

Single Exon Probes Expressed in Heart

	1	-	$\overline{}$	$\overline{}$	Т	-			-		_				-,-					т.		1	-	_		-			
, Top Hit Descriptor	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13) mRNA	RC4-HT0578-170300-012-q02 HT0578 Homo sapiens cDNA	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA complete cds	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds	MRO-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA	Homo sapiens ribosomal protein L13a (RPL13A), mRNA	ws55c06.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR:Q59050 Q59050 HYPOTHETICAL PROTEIN MJ1656	ov39h08.x1 Soares testis NHT Homo seniens cDNA clone IMAGE 1630743 3	Homo sapiens Ivsozyme homolog (LOC57151) mRNA	Homo sapiens vacuolar ATPase isoform VA68 mRNA complete cde	bb62a06.yf NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb.X04098_cds1 ACTIN, CYTOPI ASMIC 2 (HIMAN): nh:M91405 Maries extechded annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells annual cells an	Homo sapiens interleukin 12 recentor heta 1 (II 12RA1) mRNA	Homo sapiens interleukin 12 recentor, beta 1 (II 19RR1) mRNA	Homo sapiens DNA for Human P2XM complete cds	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA	Homo saplens chromosome 21 segment HS21C006	Homo sapiens chromosome 21 segment HS21C082	Homo sapiens chromosome 21 segment HS21C018	QV0-HT0494-020300-137-d03 HT0494 Homo sapiens cDNA	Homo sapiens HELG protein (FAM4A1), mRNA	Homo sapiens heme-binding protein (HEBP), mRNA	Homo sapiens heme-binding protein (HEBP), mRNA	Homo sapiens BASS1 (BASS1) mRNA, partial cds	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA	Human beta globin region on chromosome 11	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASPR) mRNA	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
 Top Hit Database Source	LN L	EST HUMAN	EST HUMAN	N _T	LN	EST HUMAN	F	EST HUMAN	EST HUMAN	LN LN	LN	EST HUMAN	LZ	NT	NT	FN	NT	NT	NT	NT	EST_HUMAN	FZ	N⊤	LN	LN	EST_HUMAN	NT	N	L
Top Hit Acession No.	11321578 NT	1.0E-72 BE175434.1	1.0E-72 BE175434.1	1.0E-72 AF222742.1	1.0E-72 AF222742.1	9.0E-73 AW374968.1	11424099 NT	AW071755.1	Al024877.1		8.0E-73 AF113129.1	BE019900.1	11526037 NT	11526037 NT	8.0E-73 AB002059.1	11418189 NT	8923290 NT		2.2	8.2	4.1	11422159 NT	11435913 NT	11435913 NT		31.1		4502582 NT	7669539 NT
Most Similar (Top) Hit BLAST E Value	1.0E-72	1.0E-72	1.0E-72	1.0E-72	1.0E-72	9.0E-73	9.0E-73	8.0E-73 AW0717	8.0E-73 AI02487	8.0E-73	8.0E-73	8.0E-73.BE01990	8.0E-73	8.0E-73	8.0E-73	8.0E-73	7.0E-73	7.0E-73 AL16320	7.0E-73 /	6.0E-73 AL16321	6.0E-73 BE16657	4.0E-73	3.0E-73	3.0E-73	2.0E-73 AF13989	2.0E-73	2.0E-73 U01317.1	2.0E-73	2.0E-73
Expression Signal	19.78	3.82	3.82	90.9	90.9	1.23	23.9	1.03	3.06	4.6	2	15.88	222	2.22	2.12	2.69	0.78	1.06	1.62	2.37	3.36	2.05	0.99	0.99	1.75	1.48	1.1	3.48	96.0
ORF SEQ ID NO:		26533	26534		27595			20782	21163	25986	26785	27459	27682	27683	25282	25235	20875	22983			26274	24832	21595	21596	20610			22869	23221
Exon SEQ ID NO:		16360	16360	17383		11348	18197	10939	11304	15864	16595	17254	17465	17465	19081	19217	11033	13184	14743	10126	16121	15138	11715	11715	10760	11798	12135	13069	13420
Probe SEQ ID NO:	5949	6501	6501	7532	7532	1443	8320	1022	1399	5959	6715	7385	7614	7614	9446	9654	1118	3261	4863	152	6255	5215	1818	1818	833	1902	2251	3144	3503

Page 274 of 413 Table 4 Single Exon Probes Expressed in Heart

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Single Exon Plopes Expressed in Reart	Top I-lit Descriptor	Homo sapiens Parkinson diseasc (autosomal recessive, juvonile) 2, parkin (PARK2), transcript variant 3, mRNA	Homo sapiens mRNA for KIAA1591 protein, partial cds	Homo sapiens interleukin 4 receptor (IL4R), mRNA	Homo sapiens interleukin 4 receptor (IL4R), mRNA	Homo sapiens glutathione synthetase (GSS) mRNA	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA	Homo sapiens KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 (KIAA1080), mRNA	Homo sapiens galactosyteeramidase (Krabbe disease) (GALC), mRNA	Homo sapiens galactosylcerarnidase (Krabbe disease) (GALC), mRNA	Homo sapiens mRNA for KIAA1059 protein, partial cds	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	gg61b07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839637 5' similar to contains element MER22 repetitive element:	601276071F1 NIH MGC 20 Homo sapiens cDNA clone IMAGE 3617105 5	Homo sapiens CD39-like 4 (CD39L4) mRNA	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]	Homo sapiens NKG2D gene, exon 10	Homo sapiens chromosome 21 segment HS21C046	601649284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932997 5'	601191927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535855 5'	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds	xn78g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700636.31	601283521F1 NIH MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE 3605453 5'	UI-H-BI0-aah-h-03-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE-2709365 3'	UI-H-BI0-aah-h-03-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'	ht54e11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332.3'
JIE EXOII PIO	Top Hit Database Source	Į.	F	F	NT	LN L	NT	TN	N	N F	NT	LN	EST HUMAN	EST_HUMAN	LN	EST HUMAN	EST HUMAN	Ί	LN	Z	NT	LN	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN
) III O	Top Hit Acession No.	7669539 NT	2.0E-73 AB046811.1	11431471 NT	11431471 NT	4504168 NT	11496980 NT	11496980 NT	11431598 NT	4557612 NT	4557612 NT	2.0E-73 AB028982.1	2.0E-73 AW898081.1	1.0E-73 AU121585.1	-	1.0E-73 AI147427.1		57428			1	2	1	7	-	۲.	+	1	6.0E-74 AW014039.1	1.	-
	Most Similar (Top) Hit BLAST E Value	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73 A	2.0E-73	1.0E-73	1.0E-73 AF198349	1.0E-73	1.0E-73 E	8.0E-74	8.0E-74 S83194.1	8.0E-74 S83194.1	7.0E-74 AJ001689.	7.0E-74 AL163246.	7.0E-74 BE967432	7.0E-74 BE266305.	6.0E-74 AF109907.	6.0E-74 AW263177	6.0E-74 BE388260.	6.0E-74 BE388260.	6.0E-74 A	6.0E-74	6.0E-74 BE048846.
	Expression Signal	96.0	7.6	1.35	1.35	1.34	2.45	2.45	4.14	3.79	3.79	1.78	1.72	1.57	0.93	1.36	2.67	1.39	1.84	1.84	3.01	0.99	2	2.81	2.58	1.03	96.6	96.6	1.39	1.39	2.63
	ORF SEQ ID NO:	23222	25933	26058	26059	28048	28085	28086	28272	28537	28538	28562		21512	22207	27534	28140	20485	25602	25603	21679	23007	27432	25234	20865	21373	22050	22051	22553	22554	23352
	Exon SEQ ID NO:	13420	15808	15927	15927	17806	17843	17843	18026	18284	18284	18306	11798	11644	12311	17329	17896	10655	15521	15521	11801	13207	17231	19216	11022	11514	12152	12152	12762	12762	13566
	Probe SEQ ID NO:	3503	5902	6023	6023	7956	7993	7993	8138	8408	8408	8432	9447	1743	2434	7469	8747	723	9099	2606	1906	3286	7327	9653	1106	1609	2268	2268	2834	2834	3652

Page 275 of 413
Table 4
Single Exon Probes Expressed in Heart

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| Top Hit Descriptor | hr54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:31323323' | Homo sapiens actin filament associated protein (AFAP), mRNA | df17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5 | PM0-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA | Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
 | H.sapiens mRNA for TPCR16 protein | Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, | and translated products

 | Homo saplens interleukin 4 receptor (IL4R), mRNA | Homo sapiens interleukin 4 receptor (IL4R), mRNA
 | Homo sapiens KIAA0716 gene product (KIAA0716), mRNA | Homo saplens hypothetical protein FLJ13222 (FLJ13222), mRNA | H.saplens mRNA for HIP-I | H.sapiens mRNA for HIP-I | Homo sapiens DNA for amyloid precursor protein, complete cds

 | Homo sapiens mRNA for KIAA1019 protein, partial cds | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, | complete cds) | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,

 | complete cas) | Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA

 | Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA | Homo sapiens mRNA for KIAA1168 protein, partial cds | Homo sapiens PLP gene

 | Homo sapiens PLP gene | Homo sapiens chromosome 21 segment HS21C010
 | Homo sapiens chromosome 21 segment HS21C047 | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA | Homo sapiens mRNA for transmebrane receptor protein | Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHR) mRNA | Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
 | EST13131 Thymus tumor III Homo saplens cDNA 5' end similar to similar to ribosomal protein 1.37 |
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| Expression
Signal | 2.63 | 2.49 | 2.58 | 5.19 | 2.15
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 | 1.85 | 1.85
 | 3.73 | 2.69 | 1.88 | 1.88 | 1.89

 | 4.95 | | 2.44 | -

 | 2.44 | 4.34

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 | 4.44 | 0.93
 | 1.31 | 1.57 | 0.82 | 3.76 | 3.76
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Page 276 of 413 Table 4 Single Exon Probes Expressed in Heart

Single Exult Probes Expressed in near	Top Hit Descriptor	EST01132 Subtracted Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCPF91	no17g05.s1 NCI_CGAP_Phet Homo sapiens cDNA clone IMAGE:1100984 3'	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA	Human endogenous retrovirus HERV-K-T47D	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204.3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;contains element MER22 repetitive element;	Homo saplens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA	PT2.1_15_G11.r tumor2 Homo sapiens cDNA 3'	Novel human gene mapping to charnosome 22	Novel human gene mapping to chomosome 22	Human platelet glycoprotein IIb mRNA, 3' end	RC6-HT0678-220500-011-C03 HT0678 Homo sapiens cDNA	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA	601557524F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827549 5'	Homo sapiens mRNA for KIAA1395 protein, partial cds	Homo sapiens chromosome 21 segment HS21C004	zp96a06.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'	602121428F1 NIH_MGC_56 Homo sapiens cDNA clone IMACE:4278559 5	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA	QV4-ST0234-181199-037-f05 ST0234 Homo saplens cDNA	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA	Homo sapiens bela 2 gene	Homo saplens zinc finger protein 259 (ZNF259) mRNA	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens DNA for Human P2XM, complete cds	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
IE EXUIT PIODE	Top Hit Database Source	EST_HUMAN ES	EST_HUMAN no			LN H	EST_HUMAN Q			EST HUMAN P	LN	ĽN ⊢N	도 도	EST_HUMAN R					EST HUMAN 60		NT HA	HUMAN	EST_HUMAN 60		T_HUMAN		NT H		NT Ho		
Billo	Top Hit Acession No.	3.0E-74 M78984.1	3.0E-74 AA601493.1	7669491 NT	7669491 NT	2.0E-74 AF020092.1	2.0E-74 Al950528.1	4885198 NT	4885198 NT	2.0E-74 AI557280.1	2.0E-74 AL355092.1	2.0E-74 AL355092.1		2.0E-74 BE711134.1	11439587	11439587 NT	11439587	11439587 NT	2.0E-74 BF030788.1	1	2		2.0E-74 BF666568.1	7657334 NT	1.0E-74 AW816405.1	8922829 NT		4508020 NT		1.0E-74 AB002059.1	4758697 NT
	Most Similar (Top) Hit BLAST E Value	3.0E-74	3.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74 J02963.1	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74 /	2.0E-74	2.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74 X02344.1	1.0E-74	1.0E-74 /	1.0E-74 /	1.0E-74
	Expression Signal	2.42	2.22	126.24	126.24	1.01	1.15	2.94	2.94	1.09	1.95	1.95	1.89	1.64	1.98	1.98	2.57	2.57	1.55	1.43	6.54	1.46	1.26	0.97	3.6	1.19	2.7	1.35	2.17	6.19	5.96
	ORF SEQ ID NO:	27519	28010	20714	20715	20916	20986	21340	21341	22323	24582	24583	24588	25530	25584	25585	25584	25585	26235	26700	27523		25196	19841	20108	20247	20252	20331	20751	21968	22822
	Exon SEQ ID NO:	17312	177771	10867	10867	11071	11132	11481	11481	12430	14815	14815	14820	19446	19448	19448	19448	19448	16085	16511	17316	19047	19380	10035	10293	10434	10439	10524	10906	12066	13026
	Probe SEQ ID NO:	7394	7921	942	945	1158	1224	1577	1577	2558	4937	4937	4942	5543	5594	5594	5629	5629	6218	6631	7398	9387	9903	47	334	491	497	586	983	2179	3100

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Single Exon Probes Expressed in Heart	Top Hit Database Top Hit Descriptor	NT Homo sapiens chromosome 21 segment HS21C068	EST_HUMAN RC2-BT0642-270300-019-106 BT0642 Homo sapiens cDNA	HUMAN	NT Homo sapiens DCRR1 mRNA, partial cds	HUMAN	Т				7856 NT Homo sapiens glutathione S-transferase theta 2 (GST12), mRNA	NT Homo sapiens DNA for Human P2XM, complete cds			N1 Homo saplens DNA cytosine-5 methytransferase 38 (DNMT3B) mRNA, complete cds		wk38a08.x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb.M14123_cds4 EST_HUMAN RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);		T	T	EST_HUMAN 60218601611 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'	#31c12.x1 NCI_CGAP_GC6 Homo sepiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361 FST HIMAN HYPOTHETICAL 20.1 KD PROTEIN	Τ	Г	EST_HUMAN CM0-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA	EST_HUMAN						NT Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
sed in Heart	7	ns chromosome 21 segment HS210	2-270300-019-f06 BT0642 Homo s	NCI_CGAP_Lu24 Homo sapiens cl	is DCRR1 mRNA, partial cds	1 NIH_MGC_12 Homo sapiens cD	1 NIH_MGC_12 Homo sapiens cD	s tracheal epithelium enriched prot	s hypothetical protein FLJ10783 (F	ns glutathione S-transferase theta 2	is glutathione S-transferase theta 2	is DNA for Human P2XM, complete	ns glutathione S-transferase theta 2	lete ods	is DNA cytosine-5 methyltransferas	is chromosome 21 segment HS210	NCI_CGAP_Pr22 Homo sapiens d JS-RELATED POL POLYPROTEII	oares_testis_NHT Homo sapiens o	OME RIVA RECOGNITION MOTIF	0-080600-006-g06 SN0040 Homo	1 NIH_MGC_49 Homo sapiens cD	CL CGAP GC6 Homo sapiens cDI	2-210200-079-e02 BT0632 Home s	cares melanocyte 2NbHM Homo s	7-150400-335-a11 NN0057 Homo	1 NIH_MGC_21 Homo sapiens cDI	is eukaryotic translation initiation fac	is NIPSNAP, C. elegans, homolog	is NIPSNAP, C. elegans, homolog	s myosin, heavy polypeptide 1, skel	is HTRA serine protease (PRSS11)	s HTRA serine protease (PRSS11)
opes Expres		Homo sapier	Π		T	П	Т		Homo sapier	Homo sapier	Homo sapier	Homo sapier	Homo sapien	genes, comp	Homo saplen	Homo sapien	wk38a08.x1 RETROVIRU	aj28c06.s1 S	CHROMOS	MK0-SN004(602186616T		Т	yx90h08.r1 S	CMO-NN005	601303866F	Homo sapien	Homo sapien	Homo sapien	' Homo sapien	Homo sapien	Homo sapien
gie Exon Pr	Top Hit Database Source	N L		EST HUMAN	Z	EST_HUMAN	EST_HUMAN	N	Ŗ	N L	뇐	NT	ļ	L I	N	L	EST_HUMAN	1	ES HOMAN	EST HOMAN	EST_HUMAN	H.ST HIMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST	NT	N-I	NT	IN	된	NT
uic	Top Hit Acession No.	1.0E-74 AL163268.2	1.0E-74 BE083080.1	1.0E-74 BE467769.1	1.0E-74 D83327.1	1.0E-74 BE549105.1	1.0E-74 BE549105.1	1.0E-74 AF214562.1	11420549 NT	11417856 NT	11417856 NT	1.0E-74 AB002059.1		1.0E-74 AF240786.1	8.0E-75 AF176228.1	8.0E-75 AL163202.2	6.0E-75 AI817415.1		0.UE-73 AA769263.1	5.0E-75 BE841305.1	BF690254.1	5.0E-75 A1638623 1	4.0E-75 BE081333.1	4.0E-75 N36757.1	4.0E-75 AW897230.1	BE40946	5579457	11417946 NT	11417946 NT	7669505	3.0E-75 AF157623.1	3.0E-75 AF157623.1
	Most Similar (Top) Hit BLAST E Value	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	l c	1.0E-74	8.0E-75	8.0E-75	6.0E-75	1	0.05-7.0	5.05-75	5.0E-75	5.05-75	4.0E-75	4.0E-75	4.0E-75		4.0E-75	4.0E-75	4.0E-75	4.0E-75	3.0E-75	3.05-75
	Expression Signal	4.56	6.0	6.0	1.19	1.83	1.83	3.92	1.31	1.6	2.83	4.14		1.36	4.07	1.67	0.88	o c	00.0	40.1	1.22	5	1.05	1.23	1.5	4.65	4.29	1.56	1.56	8.72	2.91	2.25
	ORF SEQ ID NO:		23656	23845	24754	26765	26766	27182		29108		21968					22055		0,1,0	24/46	27520	27969	19903		21498	22540	25806	26084	26085	28214	20754	20754
	Exon SEQ ID NO:	13798	13881	14070	14980	16574	16574	16989	17838	18818	18873	12066	7000	19261	124/5	19059	12157	44005	14990	14970	17313	17726	10088	10395	11629	12747	15698	15953	15953	17963	10909	10909
	Probe SEQ ID NO:	3887	3974	4170	5112	6694	6694	7112	7988	9024	9106	9249	9	97.20	7007	9406	2273	64.70	0170	7016	7395	7876	107	451	1728	2818	5792	6052	6052	8072	986	987

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Table 4
Single Exon Probes Expressed in Heart

Ongle Even Topics Expressed in region	Top Hit Descriptor	Homo sapiens mRNA for KIAA0581 protein, partial cds	Homo sapiens synaptojanin 1 (SYNJ1), mRNA	Homo sapiens synaptosomal-associated protein, 29kD (SNAP29) mRNA	Homo sapiens chromosome 21 segment HS21C001	Homo sapiens mRNA for KIAA0581 protein, partial cds	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds	Homo saplens DNA for amyloid precursor protein, complete cds	Homo sapiens KIAA0971 protein (KIAA0971), mRNA	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA	Homo sapiens Oncogene TIM (TIM) mRNA	Homo sapiens Oncogene TIM (TIM) mRNA	Homo sapiens snail 1 (drosophila homolog), zinc finger protein (SNAI1), mRNA	7734680 cdA Homo sapiens cDNA done cdABED02 5'	qo81e02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POL/ENV GENE ;	xg60d02.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2632/07 3' similar to contains PTR7 t1 PTR7 renetitive element	H.sapiens ERCC2 gene, exons 1 & 2 (partial)	2157h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726485 3' similar to gb:M13932 40S	KIBOSOWAL PROTEIN STV (HOMAN);	601900294F1 NIH_MGC_19 Homo septens cDNA clone IMAGE:4129678 5	601900294F1 NiH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5	ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5	wb30b10.x1 NCI_CGAP_GC6 Horno sepiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
I LAUIT I UDE	Top Hit Database Source	NT																EST_HUMAN A	EST_HUMAN P	XC WIMAN D	Τ		\neg	ヿ		EST_HUMAN a	H IS	EST_HUMAN 6	EST_HUMAN_T
Billo	Top Hit Acession No.	3.0E-75 AB011153.1	4507334 NT	4759153 NT	3.0E-75 AL163201.2	3.0E-75 AB011153.1				7662421 NT	11526319 NT	11526319 NT	7662209 NT	7662209 NT	4885632 NT	4885632 NT	11420804 NT	2.0E-75 AV734680.1	2.0E-75 Al311783.1	4 OF 75 AM 468495 4	T		_	1	1.0E-75 BF313645.1	1.0E-75 AA664377.1	1.0E-75 AF223391.1	1.0E-75 BE894192.1	
	Most Similar (Top) Hit BLAST E Value	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75 M72393.1	3.0E-75 M72393.1	3.0E-75 D87675.1	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	2.0E-75	2.0E-75	1 07	1.0E-75 X52221.1		1.0E-75 /	1.0E-75	1.0E-75	1.0E-75	1.0E-751	1.0E-75	9.0E-76
	Expression Signal	1.98	1.05	3.66	1.19	1.33	1.01	1.01	1.42	96.0	1.53	1.53	3.83	3.83	2.92	2:92	123	1.5	1.73	ŭ	3.17		4.13	3.73	3.73	3.99	2.6	1.86	1.45
	ORF SEQ ID NO:	21569	21852	22144	22711	22877	23030	23031	23759	24015	26183	26184	26248	26249	26522		27259		27152	10000			_	27499	27500		28573		
	Exan SEQ ID NO:	11693	11955	12253	12916	13077	13227	13227	13979	14233	16041	16041	16100	16100	16353	16353	17070	15400	16959	1	12843	1	16781	17290	17290	18137	18315	L	10026
	Probe SEQ ID NO:	1795	2065	2373	2988	3152	3306	3306	4077	4336	6058	6058	6234	6234	6494	6494	7193	5480	7082	000	2916		6903	7423	7423	8257	8441	9299	38

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Table 4
Single Exon Probes Expressed in Heart

		1	-		1		-		,	_	,			_		_	_		_	1	_	_		-	•	τ .	_		,	т	
Single EXUIT FLODES EXPLESSED III HEALT	Top Hit Descriptor	wb30b10.x1 NCI_CGAP_GC6 Hcmo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;	2/85b07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:447541 3'	Human ferritin Heavy subunit mRNA, complete cds	Homo sapiens H factor 1 (complement) (HF1) mRNA	Homo sapiens H factor 1 (complement) (HF1) mRNA	Homo sapiens mediator (Sur2), mRNA	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA	Homo sapiens serine/threonine kinase 2 (STK2), mRNA	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds	Homo saplens lymphocyte antigen 75 (LY75) mRNA, and translated products	Homo sapiens core-binding factor, runt domain, aipha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA	601312019F1 NIH_MGC_44 Hamo sapiens cDNA clone IMAGE:3658757 5'	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506029 5'	Human mRNA for HMG-1, complete cds	Human mRNA for HMG-1, complete cds	Human mRNA for HMG-1, complete cds	HUM178G01B Human fetal brain (TFujiwara) Homo sapiens cDNA clone GEN-178G01 5	HUM178G01B Human fetal brain (TFujiwara) Homo sapiens cDNA clone GEN-178G01 5'	UI-H-BW 1-anz-b-04-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'	UI-H-BW1-anz-b-04-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA	RC5-ST0300-180100-033-A03 ST0300 Homo saplens cDNA	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA	HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zqd04 3'
gie EXUII FIU	Top Hit Database Source	EST_HUMAN	EST_HUMAN	NT	NT	NT	NT	NT	NT	LN⊤	NT	, Z	N.	Z	LΝ	LZ	N	EST HUMAN	EST_HUMAN	LN	NT	LN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN
JIIO	Top Hit Acession No.	N652648.1	9.0E-76 AA702415.1	112937.1	4504374 NT	4504374 NT	7706724 NT	11421442 NT	11435215 NT	10442821 NT	11417862 NT	5016092 NT	NF056490.1	4505052 NT	4757915 NT	4507184 NT	4507184 NT	6.0E-76 BE396253.1	3E273201.1	063874.1	063874.1	063874.1	081625.1	081625.1	3F516262.1	3F516262.1	4503476 NT	4503476 NT	3.0E-76 BF375689.1	3.0E-76 BF375689.1	241314.1
	Most Similar (Top) Hit BLAST E Value	9.0E-76 AI652648.	9.0E-76	9.0E-76 M12937.1	8.0E-76	8.0E-76	8.0E-76	8.0E-76	8.0E-76	8.0E-76	8.0E-76	7.0E-76	7.0E-76 AF056490	7.0E-76	7.0E-76	7.0E-76	7.0E-76	6.0E-76	6.0E-76 BE273201	5.0E-76 D63874.1	5.0E-76 D63874.1	5.0E-76 D63874.1	4.0E-76 D81625.1	4.0E-76 D81625.1	3.0E-76 BF516262	3.0E-76 BF516262	3.0E-76	3.0E-76	3.0E-76	3.0E-76	3.0E-76 Z41314.1
	Expression Signal	1.45	1.16	23.8	1.69	1.69	1.06	5.38	1.3	6.44	1.44	4.12	2.64	7.08	1.1	4.3	4.3	19.65	2.69	3.69	3.69	3.69	5.6	5.6	1.78	1.78	2.78	2.78	4.18	4.18	9.13
	ORF SEQ ID NO:	19826		27770	20695	20696	22603	25760	26443	28198		20527	22975	22982	23017	23951	23952		28154	21673	21674	21675	27834	27835	20359	20360		21346	23099	23100	29104
	Exon SEQ ID NO:	10026		17547	10848	10848	12807	15652	16282	17948	19207	10689		13183	13215	14174	14174	11122	17910		11795	11795	17609	17609	10549	10549	11485	11485			15084
	Probe SEQ ID NO:	38	2364	7697	923	923	2880	5744	6421	8057	9636	692	3254	3260	3293	4275	4275	1214	8761	1899	1899	1899	7759	7759	613	613	1581	1581	3382	3382	5204

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Single Exon Probes Expressed in Heart

Single Exon Propes Expressed in Heart	Top Hit Descriptor	Homo sapiens angiostatin binding protein 1 mRNA, complete cds	y/20g10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:271842.5	xs49h01x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2773009 3	zv54d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5	zv54d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5	EST380059 MAGE resequences, MAGJ Homo saplens cDNA	EST368525 MAGE resequences, MAGD Homo sapiens cDNA	Human mRNA for possible protein TPRDII, complete cds	Human mRNA for possible protein TPRDII, complete cds	Human mRNA for possible protein TPRDII, complete cds	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA	Homo sapiens glucagon (GCG) mRNA	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA	zs60h11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE: 701925.3'	OLFACTORY RECEPTOR-LIKE PROTEIN F5	zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.	zw64e02.s1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN RETA-5 SIIRI INIT DECRIDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE	Human mRNA for possible protein TPRDII complete cds	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3). mRNA	Homo sapiens mRNA for KIAA1081 protein, partial cds	Homo sapiens TPCR86 protein (HSTPCR86P), mRNA	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63150), mRNA	Homo sapiens HIRA interacting protein 4 (dnaJ-like) (HIRIP4), mRNA	Human mRNA for HMG-1, complete cds	Human mRNA for HMG-1, complete cds	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'	601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5	601866926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
ie Exon Piope	Top Hit Database Source	TN	П		П		Г	EST_HUMAN E		TZ LZ	LN L						T HUMAN	Γ	EST_HUMAN F	· · · ·	LZ	Т		T.				N			EST_HUMAN 6	EST_HUMAN 6
Suic	Top Hit Acession No.	3.0E-76 AF286598.1		3.0E-76 AW299353.1	3.0E-76 AA442309.1		3.0E-76 AW967984.1	3.0E-76 AW956455.1				4557662 NT	4503944 NT	4758053 NT	4504028 NT	4504028 NT	2.0E-76 AA253954.1		2.0E-76 AA445992.1	2.0E-76 AA445992 1		18.1	5031660 NT	2.0E-76 AB029004.1	11427410 NT	11437211 NT	7549807 NT			.1	.1	1
	Most Similar (Top) Hit BLAST E Value	3.0E-76	3.0E-76 N42671.1	3.0E-76	3.0E-76	3.0E-76	3.0E-76	3.0E-76	2.0E-76 D84295.1	2.0E-76 D84295.1	2.0E-76 D84295.1	2.0E-76	2.0E-76	2.0E-76	2.0E-76	2.0E-76	2.0E-76	2.0E-76 P23266	2.0E-76	2.0E-76	2.0E-76 D84295.1	2.0E-76	2.0E-76	2.0E-76	2.0E-76	2.0E-76	2.0E-76	1.0E-76 D63874.1	1.0E-76 D63874.1	1.0E-76 BE796537	9.0E-77	8.0E-77 BF205181
	Expression Signal	7.85	1.92	3.2	1.32	1.32	2.13	3.75	1.22	3.68	3.66	2.17	1.07	1.03	1.53	1.53	1.43	2.83	2.01	2.01	0.94	6.33	1.25	4.74	1.79	3.28	2.76	2.18	2.18	5.29	3.98	1.65
	ORF SEQ ID NO:	25861	26806	27667	27684		25062		20065	20112	20113		20320	20778	21281	21282	21658	22536	22979	22980	20065	24527	24710	25432	26554	27988	28416	23881	23882	25093	26119	24101
	Exon SEQ ID NO:	15748	16616	17453	17466	17466	19537	19745	10245	10298	10298	10397	10513	10932	11423	11423	11782	12740	13180	13180	10245	14747	14938	15374	16377	17748	18172	14100	14100	15266	15984	14315
	Probe SEQ ID NO:	5842	6737	7602	7615	7615	9014	9120	280	339	339	453	575	1014	1518	1518	1886	2811	3257	3257	4043	4867	5068	5453	6518	7898	8293	4200	4200	5345	6137	4421

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Single Exon Probes Expressed in Heart

ſ			Г	Т	ß	Т	T	Т		Τ	Τ	<u> </u>	Γ	Τ	Τ		Г	1	T	- 1200 4 3"	Ť,		Γ.	T	Ť	Γ	<u> </u>	T	i –	1		12.00
	Top Hit Descriptor	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7) mRNA	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5	ye69f04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE.123007 3' similar to contains MFR10 renatitive element.	zu91g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE.745392 3'	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA	EST369823 MAGE resequences, MAGE Homo sapiens cDNA	qe77h12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745063 3'	7 Homo sapiens glucokinase (GCK) gene, exon 2	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA	Homo sapiens cullin 1 (CUL1) mRNA	Homo sapiens EGF-like repeats and discoidin Lilke domains 3 (EDIL3), mRNA	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA	DKFZp434G1728_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G1728 5'	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA	Homo sapiens sorting nexin 5 (SNX5), mRNA	Homo sapiens sorting nexin 5 (SNX5), mRNA	Human mRNA for KIAA0299 gene, partial cds	Human mRNA for KIAA0299 gene, partial cds	Homo saplens SET domain and mariner transposase fusion gene (SETMAR) mRNA	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	PM3-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA	AV764617 MDS Homo sapiens cDNA clone MDSBTF10 5'	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA	Homo sapiens CYP17 gene, 5' end	Horno sapiens CGI-79 protein (LOC51634), mRNA	Homo sapiens mRNA for KIAA1415 protein, partial cds	Homo sapiens mRNA for KIAA1415 protein, partial cds
מון וומען מול	Top Hit Database Source	LN	EST_HUMAN	EST_HUMAN	TOTAL TOTAL	EST HUMAN	N	LN LN	NT	EST_HUMAN	EST_HUMAN	IN	NT	LN	NT	NT	EST_HUMAN	NT	LN	LN	NT	IN	NT	LN	N ⊢N	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	NT	N
5	Top Hit Acession No.	4506230 NT	AA019770.1	8.0E-77 AA019770.1	200245 1	7.0E-77 AA625755.1	4505944 NT	4505944 NT	4504600 NT	AW957753.1	Al204066.1	AF041015.1	4557250 NT	4503160 NT	5031660 NT	5031660 NT	5.0E-77 AL043953.1	11428849 NT	11428849 NT	11421928 NT	11421928 NT	AB002297.1	AB002297.1	5730038 NT	5730038 NT	3.0E-77 BF359917.1	2.0E-77 AV764617.1	2.0E-77 AW997712.1	2.0E-77 L41825.1	7706315 NT	2.0E-77 AB037836.1	2.0E-77 AB037836.1
	Most Similar (Top) Hit BLAST E Value	8.0E-77	8.0E-77	8.0E-77	2 OF 77 B00245 1	7.0E-77	77.9E-77	7.0E-77	6.0E-77	6.0E-77	6.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	2.0E-77	5.0E-77	3.0E-77	3.0E-77	3.0E-77	2.0E-77	2.0E-77	2.0E-77	2.0E-77	2.0E-77	2.0E-77
	Expression Signal	2.46	2.12	2.12	70.7	3,28	2.1	2.1	4.29	6.0	17.64	1.78	1.16	76.0	2.02	2.02	2.05	1.39	1.39	2.55	2.55	1.96	1.96	1.12	1.12	3.31	1.7.1	1.73	0.84	2.64	2.02	2.02
	ORF SEQ ID NO:	25095	28861	28862	0.000				20043	20882	21287	20973	21101	22492	24280	24281	24514	26947	26948	27543	27544	28080	28081	21705	21706	28377	21093	21185	21830			22313
	Exon SEQ ID NO:	15268	18578	18578	0000	11783	12240	12240	10227	11040	11429	11124	11243	12598	14493	14493	14733	16752	16752	17338	17338	17840	17840	11824	11824	18129	11237	11320	11935	11946	12724	12724
	Probe SEQ ID NO:	5347	8691	8691	0774	1887	2360	2360	262	1125	1524	1216	1337	2736	4605	4605	4853	6873	6873	7519	7519	7990	7990	1929	1929	8249	1330	1414	2044	2056	2549	2549

Page 282 of 413 Table 4 Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	hc43b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN	tw22g02.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:C65245 O65245 F21E10.7 PROTEIN	WZZG02.x1 NOL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE.2260466 3' similar to TR.O65245 O65245 F21E10.7 PROTEIN.	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA	ns68g12.s1 NCL_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29_f11 contains element MSP1 reportition element.	601119852F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE 3029436 51	601476802F1 NIH MGC 68 Homo sapiens cDNA clone IMAGE:3879505 5	at74a09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311 Q13311 TAX1-BINDING PROTEIN TXBP151, [1]:	Human protein kinase C substrate 80K-H (PRKCSH) gene. exon 7	Human protein kinase C substrate 80K-H (PRKCSH) gene. exon 7	Homo sapiens mRNA for KIAA1276 protein, partial cds	Homo sapiens mRNA for KIAA1276 protein, partial cds	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimcr disease) (APP), mRNA	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II Atzhæimer diseasea) (ADD) m.DNA	Homo sapiens mRNA for KiAA1101 protein, complete cds	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1) mRNA	Homo sapiens CGI-60 protein (LOC51626), mRNA	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21a22: segment 1/3	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5
gle Exon Pro	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	⊢N	N FN	L	LN⊤	N	N	LN	N	NT	NT	NT	L	NT	EST_HUMAN
N. CID	Top Hit Acession No.	2.0E-77 BE044316.1	2.0E-77 Al613519.1	2.0E-77 Al613519.1	4504068 NT	2.0E-77 AA653025.1	2.0E-77 BE298940.1			2.0E-77 U50321.1	2.0E-77 U50321.1	1.0E-77 AB033102.1	1.0E-77 AB033102.1	4502166 NT	4502166 NT	4502166 NT	4502166 NT	AB029024.1	4503300 NT	T706299 NT	1.0E-77 AJ229041.1	6552322 NT	1.0E-77 AW755254.1
	Most Similar (Top) Hit BLAST E Value	2.0E-77	2.0E-77	2.0E-77	2.0E-77	2.0E-77	2.0E-77	2.0E-77	2.0E-77	2.0E-77	2.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77
	Expression Signal	1.33	0.89	0.89	3.48	3.58	1.8	1.34	12.74	4.99	4.99	0.97	26.0	1.87	1.87	4.95	4.95	1.22	2.82	2.99	14.73	1.95	2.89
	ORF SEQ ID NO:	23629	23995	23996		24334	25629	25761	26276	27564	27565	19821	19822	20054	20055	20635	20636	22168	22727	23930	24103	24229	24810
	Exon SEQ ID NO:	13855	14212	14212	14386	14546	15540	15653	16123	17359	17359	10024	10024	10237	10237	12679	12679	12272	12935	14155	14317	14445	15043
	Probe SEQ ID NO.	3947	4315	4315	4492	4659	5625	5745	6257	7489	7489	37	37	271	271	857	857	2394	3007	4256	4423	4552	5179

Page 283 of 413 Table 4 Single Exon Probes Expressed in Heart

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Single Extra Frodes Expressed in real	Top Hit Descriptor	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28	Human von Willebrand factor gene, exon 20	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA	Homo sapiens hu-GlcAT-P mRNA for glucuronytransferase, complete cds	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds	RC3-CT0254-280999-011-b05 CT0254 Homo sapiens cDNA	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA	RC2-ET0023-080500-012-e05 ET0023 Homo saplens cDNA	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'	Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP:Y48B6A.6	CE22121 ;	Human collagenase type IV (CLG4) gene, exon 6	Homo sapiens Best's macular dystrophy related protein mRNA, partial cds	Homo saplens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA	EST365190 MAGE resequences, MAGB Homo sapiens cDNA	Human lysosomal alpha-mannosidase (manB) gene, exon 7	601648061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:393188? 5'	Novel human gene mapping to chomosome 22	wr97b12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMACE:2495615 3' similar to SW:WAP_PIG 046655 WHEY ACIDIC PROTEIN PRECURSOR;	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds	Homo sapiens syncytin (LOC30816), mRNA	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sapiens s-CaBP1 (CABP1) mRNA, complete cds	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)	Homo sapiens gene for AF-6, complete cds	Homo sapiens eRF1 gene, complete cds
ale Exuli Fron	Top Hit Database Source	NT	NT	NT	NT	NT	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT		EST_HUMAN	LN	NT	NT	EST_HUMAN	NT	EST_HUMAN	IN	EST_HUMAN	Z	Z	NT	NT	NT	LN	NT	N	TN	NT
TIO .	Top Hit Acession No.	AF086944.1	AF086944.1		5881412 NT	1.0E-77 AB029396.1	1.0E-77 AB029396.1			8.0E-78 AW947061.1	6.0E-78 AU118789.1	6.0E-78 AU118789.1	11432710 NT	11422486 NT		5.0E-78 AW673424.1	M55586.1	5.0E-78 AF038536.1	11416585 NT	AW953120.1	J60889.1	5.0E-78 BE960836.1	4.0E-78 AL355841.1	4.0E-78 AI985094.1	4.0E-78 AF107405.1	7656876 NT	4505806 NT	4505806 NT	11560151 NT	11560151 NT	4.0E-78 AF169148.1	X05844.1	4.0E-78 AB011399.1	3.0E-78 AF095901.1
	Most Similar (Top) Hit BLAST E Value	1.0E-77	1.0E-77	1.0E-77 M25844.	1.0E-77	1.0E-77	1.0E-77	9.0E-78	8.0E-78	8.0E-78	6.0E-78	6.0E-78	6.0E-78	5.0E-78		5.0E-78	5.0E-78 M55586.	5.0E-78	5.0E-78	5.0E-78 AW9531	5.0E-78 U60889.	5.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78 X05844.	4.0E-78	3.0E-78
	Expression Signal	1.93	1.93	1.56	11.39	1.22	122	2.53	2.97	2.97	1.83	1.83	2.51	1.1		4.1	3.81	2.39	9.35	2.17	6.5	3.75	1.6	1.53	2.21	1.39	1.27	1.27	1.94	1.94	1.97	3	2.85	1.6
	ORF SEQ ID NO:	25607	25608	25698	26089	28093	28094	28109	25907	25908	19881	19882		19996		22281	23066	25048	25396	26262	27318	27319	21265	21393	22053	23899	24340	24341	28058	28059	28822	28944		19944
	Exon SEQ ID NO:	15525	15525	15597	15957	17852	17852	17863	15786	15786	10064	10064	15855	10182	ļ		13259	15243	15343	16110	17125	17126	11406	11533	12154	14125	14550	14550	17817	17817	18538	18656	19224	10129
	Probe SEQ ID NO:	5610	5610	5688	6197	8002	8002	8013	5880	5880	80	80	9950	211		2515	3339	5323	5422	6244	7248	7249	1502	1629	2270	4227	4664	4664	7967	7967	8721	8844	9664	155

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Table 4
Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	Exon EQ ID ID NO:CRF SEQ SignalExpression ASIGNATop Hit Acession No.Top Hit Acession SourceTop Hit Descriptor SourceNo:Signal ValueValueSource	10129 19845 1.6 3.0E-78 AF095901.1 NT Homo sapiens eRF1 gene, complete cds	0.91 3.0E-78 4507164 NT	0.93 3.0E-78 4507334 NT	5.56 3.0E-78 BE144758.1 EST_HUMAN	28478 5.52 3.0E-78 BE156318.1 EST_HUMAN	2.22 2.0E-78 U04489.1 NT	1.68 2.0E-78 AA311872.1 EST_HUMAN	26435 1.46 2.0E-78 AW402306.1 EST_HUMAN	26436 1.46 2.0E-78 AW 402306.1 EST HUMAN	26584 3.88 2.0E-78 BF689800.1 EST HUMAN	26761 2.73 2.0E-78 AV714177.1 EST HUMAN	EST HUMAN	EST_HUMAN	28559 4.5 2.0E-78 A197837.1 EST HUMAN	28605 3.28 2.0E-78 N66951.7	15170 24943 2.9 1.0E-78 11417304 NT Homo sapiens GAP-like protein (LOC51305). mRNA		25350 5.14 1.0E-78 11430460 NT	18986 25327 1 26 1 0E-78 11443E002 NIT	24274 4 4B 9 0F-79	24431 2.48 9.0E-79 BE000837.1 EST HUMAN	25078 12.03 9.0E-79 AB028070.1 NT	25844 2.18 9.0E-79 5454145 NT	27315 4.99 9.0E-79 J02853.1 NT	27316 4.99 9.0E-79 J02853.1 NT	28042 1.31 9.0E-79 AF062346.1 NT	28043 1.31 9.0E-79 AF062346.1 NT	28547 1.82 9.0E-79 AY008273.1 NT	28906 2.82 9.0E-79 11423827 NT	28907 2.82 9.0E-79 11423827 NT	1.49 9.0E-79 11417877 NT
-	_ Q	10129					13010	13841										16622	18924				15255	15733		17120		17803				
	Probe SEQ ID NO:	155	3178	4015	7902	8349	3083	3932	6412	6412	6547	6687	6921	6921	8429	8467	5247	6743	9189	9284	4600	4758	5335	5827	7243	7243	7953	7953	8419	8802	8802	9854

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Table 4
Single Exon Probes Expressed in Heart

	sscriptor				RNA	MAGE:38756573'	sapiens cDNA clone IMAGE:462558 3' similar to		MENA	1 MAGE-4101245 5'	omplete cds	cer protein I/Cin) gene complete ada	or process (Carry gene, carrypiete cus	V						MAGE 3511107 E		MAGE:21186853'	d, alpha (PDE6A), mRNA	d. alpha (PDE6A), mRNA	af1 gene)	en 88 (HCA88) mRNA complete cdc	mplete cds	af1 dene)		P6) transcript variant 4 mRNA	P6) transcript variant 4 mDNA	MRNA	id mRNA 3011 mtl	id, mRNA, 3011 nt]
Single Exoll Plobes Expressed in Heart	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C010	Human mRNA for KIAA0045 gene, complete cds	Human mRNA for KIAA0045 gene, complete cds	Homo sapiens period (Drosophila) homolog 3 (PER3) mRNA	601472766T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE 3875657 3	294e04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to TR:Q15408 Q15408 NEUTRAL PROTFASE LARGE STRINITT.	Homo sapiens chromosome 21 segment HS21C082	Homo saplens hypothetical protein FL 110283 (Fl. 110283) mRNA	601874522F1 NIH MGC 54 Homo sapiens cDNA clone IMAGE-4101245 5	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds	Homo sapiens cell-line tsA201a chloride ion current inducer protein I/Cin) gene complete add	Human zinc finger protein ZNF131 mRNA, partial cds	Homo sapiens MSTP016 (MST016) mRNA complete cds	Homo saplens mRNA for KIAA0892 protein, partial cds	Homo sapiens netrin 1 (NTN1), mRNA	Homo sapiens netrin 1 (NTN1), mRNA	Homo sapiens mRNA for KIAA0620 protein partial cds	Homo sapiens mRNA for KIAA0620 protein partial cds	601159415F2 NIH MGC 53 Homo sepiens CDNA close IMACE 35111107 5	Homo sapiens BCL2-like 2 (BCL2L2) mRNA	th18h07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE-2118685 3	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A) mRNA	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)	Homo sapiens hepatocellular carcinoma associated antigen 88 (HCA88) mRNA complete and	Homo sapiens chloride channel CLC4 (CIC4) mRNA, complete cds	Homo sapiens mRNA for Fas-associated factor. FAF1 (Faf1 gene)	Homo sapiens chromosome 21 segment HS21C006	Homo sapiens Rho GTP ase activating protein 6 (ARHGAP6) transcript variant 4 mRNA	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6) transcript variant 4 minut	Homo sapiens hypothetical protein FL J11006 (FL J11006) mBNA	H4(D10S170)=putative cytoskeletal protein ihuman thyroid mRNA 3011 nil	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
gie Exoli Pio	Top Hit Database Source	N	LZ LZ	NT	NT	EST_HUMAN	EST HUMAN	N	N	EST HUMAN	NT	IN	LN	LN	LN	LN LN	NT	NT	LN.	EST HUMAN	1	EST HUMAN	NT	TN	L	ΙN	LN	NT	LN	77	LZ	トフ	NT	NT
IIO	Top Hit Acession No.	8.0E-79 AL163210.2	8.0E-79 D28476.1	8.0E-79 D28476.1	8567387 NT	7.0E-79 BE619648.1	6.0E-79 AA699829.1	5.0E-79 AL163282.2		4.0E-79 BF210869.1	3.0E-79 AF114488.1	3.0E-79 AF232708.1	3.0E-79 U09410.1	3.0E-79 AF110322.1	3.0E-79 AB020699.1	11426770 NT	11426770 NT	0.1	1.7	1.0	4757841 NT	+	35863	2.0E-79 4585863 NT					2.0E-79 AL163206.2	7382479 NT	7382479 NT	11427428 NT		
	Most Similar (Top) Hit BLAST E Value	8.0E-79	8.0E-79	8.0E-79	8.0E-79	7.0E-79	6.0E-79	5.0E-79	4.0E-79	4.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79 AB014520	3.0E-79 AB01452(2.0E-79 BE379926	2.0E-79	2.0E-79 AI523747	2.0E-79	2.0E-79	2.0E-79	2.0E-79 /	2.0E-79 /	2.0E-79	2.0E-79 /	2.0E-79	2.0E-79	2.0E-79	2.0E-79 S72869.1	2.0E-79 S72869.1
	Expression Signal	1.2	0.94	0.94	1.4	6.85	1.29	4.15	1.12	1.33	1.4	2.68	1.36	4.52	1.71	3.47	3.47	3.28	3.28	1.05	1.14	1.43	14.14	14.14	0.99	1.54	0.86	1.17	0.96	1.83	1.83	2.6	1.44	1.44
	ORF SEQ ID NO:	23382	24069	24070	24889	22941		28891		24590	20091	20733	22778	25012	25486	25507	25508	26091	26092	20367	20685		21888	21889	21931	22049	23542	23755	24265	26270	26271	27029	27896	27897
	Exon SEQ ID NO:	13596	14287	14287		13138	18827	18601						_		15442	15442	15960	15960	10555	10836	10937	11990	11990	12034	12149	13749	13976	14478	16117	16117	16834	17658	17658
	Probe SEQ ID NO:	3682	4391	4391	9107	3214	9040	8786	3139	4946	310	362	3060	5291	5506	5525	5525	6200	6200	618	912	1019	2101	2101	2146	2265	3838	4074	4590	6251	6251	9269	7808	7808

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Single Exon Probes Expressed in riear	Top Hit Descriptor	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA	Homo sapiens KIAA0879 protein (KIAA0879), mRNA	Homo sapiens mRNA for KIAA0833 protein, partial cds	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA	MR0-NN0087-260600-017-b10 NN0087 Homo sapiens cDNA	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA	al 23e05.s1 Soares testis NHT Homo sapiens cDNA clone 1343648 3'	ar23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'	601581652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936061 5	Homo saplens solute carrier femily 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA	Homo sablens Y chromosome spermatorenesis candidate protein (RRM) neaudonene mRNA nartial ede	Home sarione KIAA0724 name product (KIAA024) mBNA	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA	Home conjugate triple framed dense in 1910 Elektronia (TDIO) and A	Homo sapiens upbe functional domain (PTPRF interacting) (TRIO), mRNA Homo sapiens trible functional domain (PTPRF interacting) (TRIO) mRNA	#58d02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN	LICENSOLVANDI FUDINZUINOINE, CALUCANOLIANE SUNDI SUBDINI I PRECURSUR,	Home satisfies mRNA for KIA41155 moteln partial cds	Homo sapiens mRNA for KIAA1155 protein, partial cds	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)	Homo sapiens tubby like protein 3 (TULP3), mRNA	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA	Homo saplens chromosome 21 segment HS21C101	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
Jie Exon Proc	Top Hit Database Source	EST_HUMAN	EST HUMAN	NT	LN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	N		TIN		N17		H C C	TIST TOWNER	F2	Z	LN	N	NT	N-	LN	NT	IN	⊢Z.
SUIS	Top Hit Acession No.		2.0E-79 BE064386.1	7662357 NT	2.0E-79 AB020640.1	11418322 NT		3F087405.1	9.0E-80 AA725848.1	9.0E-80 AA725848.1	9.0E-80 BE798603.1	11433924 NT	11433924 NT		44400E47	11422647 NT	700000	IN 1265009	4 704004	-			1462	AJ404468.1	11436736 NT	11526464 NT	11526464 NT	1.2		11427366 NT
}	Most Similar (Top) Hit BLAST E Value	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79	1.0E-79 BF36307	1.0E-79	9.0E-80 /	9.0E-80	9.0E-80	9.0E-80	9.0E-80	8 0F-80 1194387	00 10 0	8.0F-80	20 10 0	8.0E-80	L	0.0E-00 A1422197	0.00-10.0 08-10.0	6.0E-80	6.0E-80		6.0E-80	6.0E-80	6.0E-80	6.0E-80	6.0E-80 U20211.1	6.0E-80
	Expression Signal	4.22	4.22	2.6	4.23	1.96	2.78	2.74	3.79	3.79	1.28	11.05	11.05	0.05	200	2.63	2 4	1.19		2.34	50.7	1.09	4.01	2.56	3.84	3.07	3.07	1.74	1.68	2.91
	ORF SEQ ID NO:	28516	28517	24888	25341	25307		28998	22828	22829	27824	28735	28736			26513		27482		76007	73865	23866	25532	25712			27192	27281	27748	28437
	Exon SEQ ID NO:	18267	18267	15096	18907	19050	19456	18704		13033	17601	18464	18464	<u> </u>	1	-	1	17276	1	LUGUS			1		15683		17000			18188
	Probe SEQ ID NO:	8391	8391	9078	9161	9391	5971	8894	3107	3107	7751	8597	8597	3551	2000	6485	1400	7409	CCC	700,	4188	4188	5545	5702	5776	7123	7123	7214	7672	8311

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Single Exon Probes Expressed in Heart Top Hit Database Source Top Hit Descriptor	nn01f12.x5 NC]_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR t1 OFR repetitive element:	4A) mRNA complete cds	gment HS21C078	iens cDNA clone IMAGE:3615433 5'	gene exons 1-54, complete cds	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA	clone IMAGE:2472206 3'	ane IMAGE: 2472206 3'	SIGNR mRNA complete ode	SIGNR mRNA complete cos	conduction of the second			1 (MN1), mRNA			IMAGE:1854296 3'	IMAGE:1854296 3'	3632070 5	100 IMAGE: 299918 3	3352840 F	Der 3 (ABCA3) mBNA	er 3 (ABCA3) mRNA		294601 5'	4294601 5'	3345480 5'				
pes	nn01f12.x5 NCI_CGAI	Homo sapiens cullin 4A (CUL 4A) mRNA complete cds	Homo sapiens chromosome 21 segment HS21C078	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615433 5	Human pro-alpha1 type II collagen (COL 2A1) gene exons 1-54, complete cds	Homo sapiens malate dehydrogenase 2, NAD (mit protein, mRNA	wq25c05.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE 2472288 3	wq25c05x1 NCL CGAP Kid11 Homo sapiens cDNA clone IMAGE: 2472296 3	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA complete and	Homo saplens probable mannose binding C-type lectin DC-SiGNR mRNA complete cus	Homo sapiens mRNA for KIAA0145 protein, partial cds	Homo sapiens similar to rat myomegalin (LOC64182), mRNA	Homo sapiens similar to rat myomegalin (LOC64182), mRNA	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA	Homo sapiens mRNA for KIAA0833 protein, partial cds	Homo sapiens gene for AF-6, complete cds	qn90gu5.x1 Soares_NFL_1_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3	Histograms States Incl. GBC S1 Home sepiens cDNA clone IMAGE:1854296 3'	za91c08.x5 Soares fetal linn NhH 10M Home conjunctions (100 x5)	601111970F1 NIH MGC 16 Homp septems CINA clone IMAGE 3352840 E	601111970F1 NIH MGC 16 Homo sapiens cDNA clone IMAGE 3352840 F	Homo sapiens ATP-binding cassette, sub-family A (ABC1) member 3 (ABC43) mRNA	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABC43), mBNA	EST69129 Fetal lung II Homo sapiens cDNA 5' end	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5	Homo sapiens mRNA for KIAA0454 protein, partial cds	Homo sapiens mRNA for KIAA0454 protein, partial cds	Homo sapiens hypothetical protein (FLJ11045), mRNA	Homo sapiens CRP2 binding protein mRNA, partial cds
Top Hit Database Source	EST HUMAN	NT	NT	EST HUMAN	NT	LN LN	EST_HUMAN	EST_HUMAN	N	NT	NT	NT	NT	NT	LN	NI TOT	EST HUMAN	EST HIMAN	EST HUMAN	EST HUMAN	EST_HUMAN	NT	NT	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LU	N	LZ	- L
Top Hit Acession	1.0E-80 AI732656.1	1.0E-80 AF077188.1	1.0E-80 AL163278.2	1.0E-80 BE386615.1	1.0E-80 L10347.1	5174540 NT	Al948731.1	Al948731.1	1.0E-80 AF245219.1	AF245219.1	D63479.2	11641276 NT	11641276 NT	11417901 NT	AB020640.1	4DO 11399.1	8.0E-81 AI251752 1	8.0E-81 BE394525 1	7.0E-81 AI822115.1	3E256829.1	9.1	4501848 NT	1848	7.1		1			5.0E-81 AB007923.1	3506634	-
Most Similar (Top) Hit BLAST E Value	1.0E-80	1.0E-80	1.0E-80	1.0E-80	1.0E-80	1.0E-80	1.0E-80 AI948731	1.0E-80 AI94873	1.0E-80	1.0E-80 AF24521	1.0E-80 D63479.	1.0E-80	1.0E-80	1.0E-80	1.0E-80 AB02064	8 OE 84 A 1264 752	8.0E-81	8.0E-81	7.0E-81	6.0E-81 BE256829	6.0E-81 BE25682	6.0E-81	6.0E-81	6.0E-81 AA36001	6.0E-81 E	6.0E-81 BF679022	5.0E-81 BE268042	5.0E-81	5.0E-81/	5.0E-81	4.0E-81 AF 252257
Expression Signal	3.13	96.0	76.0	5.63	6.41	1.6	2.68	2.68	1.23	123	1.19	7.42	7.42	1.45	1.80	233	2.33	4.95	3.06	4.84	4.84	1.93	1.93	1.34	1.82	1.82	3.14	3.47	3.47	2.51	0.07
ORF SEQ ID NO:			24819		25635	25947	26496	26497	27417	27418	28049	28183	28184	25281	00707	28212	28213	28631	26321	23971	23972	24920	24921	27401	25269	25270	21960	26974	26975	10008	13880
Exon SEQ ID NO:	11806	l			15547	[16329	17218	17218	17807	17935	1/935	19079	192791	17962	17962	18367	16164	14188	14188	15153	15153	17201	19.100	19166	12057	16/80	18/80	10185	ומומו
Probe SEQ ID NO:	1911	4358	5192	5285	5633	5916	6470	6470	7350	7350	7957	8044	8044	9443	9670	8071	8071	8494	6300	4290	4230	5229	2228	325	6/06	95/9	0/17	0901	0801 8865	214	17.7

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1779	11678	21556	66.0		4.0E-81 AW779612.1	EST_HUMAN	hn98d02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW:COPG_BOVIN P53620 COATOMER GAMMA SUBUNIT;
3134	13059	22858	3.79		4.0E-81 AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
3576	13490	23280	1.18			EST_HUMAN	ws90h03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:C43815 O43815 STRIATIN.;
4068		L	2.14	4.0E-81	4.0E-81 AF263306.1	IN	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4068	13970	23747	2.14		4.0E-81 AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
6821	16700	26893	2.15		4.0E-81 X06989.1	NT	Human mRNA for amyloid A4(751) protein
6973	16850		3.4		4.0E-81 U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
6973	16850	27042	3.4		4.0E-81 U20197.1	N	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
7320	17196	27396	59.65		4.0E-81 AB018001.1	L	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
7816	17666	27906	1.49	4.0E-81	11425281 NT	. LN	Homo sapiens ligase I, DNA, ATP-dependent(LIG1), mRNA
8522	18394		2.24	4.0E-81	4759085 NT	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
8522		28659	2.24	4.0E-81	4759085 NT	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
6906	19627	25007	3.81	4.0E-81	11417862 NT	NT	Homo sapiens calcineurIn binding protein 1 (KIAA0330), mRNA
8069	19627	25008	3.81	4.0E-81	11417862 NT	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9612	19191		2.52	4.0E-81	11417871 NT	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
9612	19191		2.52	4.0E-81	11	NT	Homo sapiens beta-ureldopropionase (LOC51733), mRNA
9750	19275	25228			_	LN	Homo sapiens transcobalamin II, macrocytic anemia (TCN2), mRNA
1246	11153	21000			Y18000.1	NT	Homo sapiens NF2 gene
1246	11153	21001	98.6		3.0E-81 Y18000.1	NT	Homo sapiens NF2 gene
2320	12201	22100	1.7		3.0E-81 AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2961	12888	22685	5.12	3.0E-81	4506280 NT	L	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2961	12888	22686			3.0E-81 4506280 NT	۲	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
4933	L	L	0.87	3.0E-81	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2802	12732	22530	1.77		2.0E-81 BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2802	l		1.77		2.0E-81 BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5
3707	13620		0.98		2.0E-81 AW611542.1	EST_HUMAN	hg85c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
4579	14469		0.85		5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mRNA
9888	13620		1.74		2.0E-81 AW611542.1	EST_HUMAN	hg85c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
9898	19375				8567387 NT	l. I	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1403	11308	21169	3.32		1.0E-81 W26539.1	EST_HUMAN	33f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
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Julius Lyon Flores Lypressed III heart	Top Hit Descriptor	EST372729 MAGE resequences, MAGF Homo sapiens cDNA	2k45h09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to	PTK:S5Z437 S5Z437 CDP-diacylglycerol synthase - fruit fly ;	t245c04.y1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291526 5'	Human aconitate hydratase (ACO2) gene, exon 3	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds	602137864F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5'	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 57	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'	601577339F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3838280 5	CM3-NN0059-140400-147-a12 NN0059 Homo sapiens cDNA	MR0-CT0006-250599-019 CT0006 Homo sapiens cDNA	MR0-C10006-250599-019 C10006 Homo saplens cDNA	EST372729 MAGE resequences, MAGF Homo sapiens cDNA	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'	Homo saplens phorbolin (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA	Homo sapiens HSPC288 mRNA, partial cds	Homo sapiens HSPC288 mRNA, partial ods	Human CRFB4 gene, partial cds	Human CRFB4 gene, partial cds	Human CRFB4 gene, partial cds	Homo sapiens mRNA for KIAA1327 protein, partial cds	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2.	mRNA	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'	Inf69e11.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:925196 3'
אופ רייחוו ב וחי	Top Hit Database Source	EST_HUMAN		ESI_HUMAN	EST_HUMAN	NT	IN	IN	NT	N	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Z	NT	LN	TN	NT	N L	TN		NT	NT	EST HUMAN	EST HUMAN	
	Top Hit Acession No.	AW960658.1			6.1	J87928.1	11432966 NT	11432966 NT	U52351.1	1.0E-81 U52351.1	1.0E-81 BF674641.1	11432966 NT	3E958278.1	3E958278.1	3E564367.1	3E744545.1	3E744545.1	1.0E-81 AW897550.1	1.0E-81 AW844986.1	1.0E-81 AW844986.1	1.0E-81 AW960658.1	1.0E-81 BF204253.1	11418138 NT	8.0E-82 AF161406.1	8.0E-82 AF161406.1				8.0E-82 AB037748.1		6715601 NT	8923432 NT	3F035327.1	0.1	2.1
	Most Similar (Top) Hit BLAST E Value	1.0E-81 AW9606	10	1.0E-81 AA04037	1.0E-81	1.0E-81 U87928.	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81 BE95827	1.0E-81 BE95827	1.0E-81 BE56436	1.0E-81 BE74454	1.0E-81 BE74454	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	8.0E-82	8.0E-82	8.0E-82 U08988.1	8.0E-82 U08988.1	8.0E-82 U08988.1	8.0E-82		8.0E-82	8.0E-82	7.0E-82 BF035327	7.0E-82	5.0E-82 AA51551
	Expression Signal	2		3.07	7.85	9.03	4.01	4.01	3.54	3.54	3:15	6.4	2.62	2.62	4.81	2.93	2.93	1.46	1.96	1.96	2.42	1.96	3.62	1.87	1.26	1.66	2.17	1.11	1.12		1.24	0.81	1.27	1.82	0.81
	ORF SEQ ID NO:	23304			24222	29103		24983	25449	25450	25750	26606	27702	27703	27799	27909	27910	28091	28568	28569	23304	28915	25325	19789	19789	20044	20566	20645	21244		21400	23825		22495	23713
	Exon SEQ ID NO:	13516		_	14439	15083	15206	15206	15388	15388	15645	16425	17482	17482	17576	17669	17669	17850	18312	18312	13516	18624	18981	9998	8666	10228	10726	10795	11380		11540	14050	11339	12601	13937
	Probe SEQ ID NO:	3602	7 7 7	4414	4546	5203	5284	5284	5468	5468	5737	6567	7631	7631	7726	7819	7819	8000	8438	8438	8594	8810	9278	12	101	263	797	869	1475		1636	4150	1434	2739	4034

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Oligie Evoll Flores Expressed III real	Top Hit Descriptor	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds	wp75e09x1 NOI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR:075276 075276 PKD1 ;	Homo sapiens presenilin-1 gene, exons 1 and 2	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA	RC2-BN0120-010400-013-f02 BN0120 Homo sapiens cDNA	Homo sapiens transforming growth factor beta-activated kinase binding protein 1 (TAB1), mRNA	Homo sapiens amykold beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA	ai 23e 05.s1 Soares_testis_NHT Homo capiens cDNA clone 1343648 3'	RC6-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA	Homo saplens chromosome 21 segment HS21C085	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type I (ADCYAP1R1) mRNA	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA	z193b04.r1 Stratagene lung carcinoma 937218 Homo saplens cDNA clone IMAGE:565711 5' similar to SW:PAGT_BOVIN Q07537 POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE;	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA	Homo sapiens mRNA for KIAA1077 protein, partial cds	Homo sapiens mRNA for KIAA1077 protein, partial cds	Homo sapiens mRNA for KIAA0999 protein, partial cds	Homo sapiens mRNA for KIAA0999 protein, partial cds	DKFZp434M117_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M117 5'	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA	Homo sapiens mRNA for KIAA1096 protein, partial cds	Homo sapiens mRNA for KIAA1096 protein, partial cds	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and	replication factor C subunit 2 (RFC2) gene, complete cds	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
ווכ באטוו ז וטט	Top Hit Database Source	LZ.	EST_HUMAN	NT	TN	EST_HUMAN	LN	LZ.	EST_HUMAN	EST HUMAN	LZ.	EST_HUMAN	N	LN	EST_HUMAN	LN	LN	LN	LN	LN	EST_HUMAN	NT	LN	NT	LN		N⊤	レス	LZ
300	Top Hit Acession No.	4.0E-82 AF081484.1	4.0E-82 AI937300.1	4.0E-82 AF029701.2	4502165 NT	3.0E-82 BE005705.1	5174702 NT	4502166 NT	3.0E-82 AA725848.1	3.0E-82 AW875073.1	3.0E-82 AL163285.2		4501922 NT	5453811 NT	3.0E-82 AA135979.1	11425206 NT	3.0E-82 AB029000.1	3.0E-82 AB029000.1	2.0E-82 AB023216.1	2.0E-82 AB023216.1	2.0E-82 AL046390.1		4504116 NT	2.0E-82 AB029019.1	2.0E-82 AB029019.1		2.0E-82 AF045555.1	4507580 NT	4507580 NT
	Most Similar (Top) Hit BLAST E Value	4.0E-82	4.0E-82	4.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	3.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82 D87675.1	2.0E-82	2.0E-82	2.0E-82		2.0E-82	2.0E-82	2.0E-82
	Expression Signal	6.51	6.47	6.19	13.75	2.19	4.44	3.22	13.76	5.47	2.03	1.82	6.0	2.06	0.91	2.84	3.79	3.79	1.92	1.92	1.75	1.14	1.14	0.98	0.98		3.18	1.66	1.66
	ORF SEQ ID NO:	21412	29054		20061	20446	20539	20629		21098	21219	21630	21744		24501	26807	27728	27729	20326	20327	21428	23466	23815	24143	24144		24441	24653	24654
	Exon SEQ ID NO:	11551	18761	19130	10242	10620	10700	10779	10963	11240	11355	11755	11855	13158	14718	16617	17504	17504	10520	10520	11562	13684	14040	14352	14352		j	14887	14887
	Probe SEQ ID NO:	1647	8954	9519	278	289	770	852	1045	1333	1450	1859	1961	3234	4836	6738	7654	7654	285	282	1660	3772	4140	4458	4458		4768	5013	5013

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Table 4
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Slight Event Flores Expressed III real.	Top Hit Descriptor	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA	ab14e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains	THR.t2 THR repetitive element ,	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	genes, complete cds	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds	Novel human gene mapping to chomosome X	Homo sapiens catalase (CAT) mRNA	Homo sapiens catalase (CAT) mRNA	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 11	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquilin-conjugating enzyme E2D 3	(UBE2D3) genes, complete cds	601511580F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913195 5	EST79542 Placenta I Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9	np87c07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR.t2 THR	repetitive element ;	ot64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0218.;	ot64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592.3' similar to TR:092614	Q92614 MYELOBLAST KIAA0216.;	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'	RC6-ET0046-280600-013-H12 ET0046 Homo sapiens cDNA	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA	Homo sapiens chromosome 21 segment HS21C002	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds	Rattus norvegicus densin-180 mRNA, complete cds	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
JIE EXUII LIU	Top Hit Database Source	LN		EST_HUMAN		LN	NT	LN	NT	NT	LN	IN		L	EST_HUMAN	EST HUMAN		EST HUMAN	EST_HUMAN		EST_HUMAN		EST_HUMAN	NT	NT	LN	IN	LN	NT	NT	님	LN	N-	LN L
SIIO	Top Hit Acession No.	4505314 NT		6.0E-83 AA486105.1		6.0E-83 AF240786.1		5.0E-83 AF006305.1	5.0E-83 AL133207.2	4557013 NT	4557013 NT	5.0E-83 AF083827.1		4.0E-83 AF224669.1	4.0E-83 BE888078.1	3.0E-83 AA368311.1		AA632654.1	2.0E-83 AA993492.1		2.0E-83 AA993492.1	V66951.1	2.0E-83 BE828694.1	11430834 NT	2.0E-83 AL163202.2	2.0E-83 AF202879.1	7706398 NT	7706398 NT	11024711 NT	11024711 NT	2.0E-83 AF129533.1	2.0E-83 U66707.1	2.0E-83 AF011920.1	2.0E-83 AF011920.1
	Most Similar (Top) Hit BLAST E Value	6.0E-83		6.0E-83		6.0E-83	5.0E-83 U17883.1	5.0E-83	5.0E-83	5.0E-83	5.0E-83	5.0E-83		4.0E-83 /	4.0E-83	3.0E-83		3.0E-83 /	2.0E-83		2.0E-83 /	2.0E-83 N66951.1	2.0∈-83	2.0∈-83	2.0E-83	2.0E-83	2.0E-83	2.0E-83	2.0E-83	2.0E-83	2.0E-83	2.0E-83	2.0E-83	2.0E-83
	Expression Signal	6.77		6.32		3.11	4.14	2.1	0.92	10.99	10.99	0.86		1.47	96.0	4.5		1.82	<u>.</u>		1.9	2.23	1.11	1.82	1	4.47	8.13	8.13	23.35	23.35	5.9	1.52	2.56	2.56
	ORF SEQ ID NO:	27644							23289	24651		24739	-	20373	23190				21529		21530	21654	22542			23915	24230		25109	25110	26419		26911	26912
	Exon SEQ ID NO:	17430		18630		18834	10856	12649	13500	14885	14885	14964		10561	13385	10904		12612	11658		11658	11779	12750	13155	L.	14140	14446	14446	15279	15279	16258		16718	16718
	Probe SEQ ID . NO:	7579		8817		9050	931	2004	3586	5011	5011	5094		624	3469	981		2750	1759		1759	1883	2821	3231	3708	4241	4553	4553	5359	5359	6396	6659	6833	6839

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Single Exon Probes Expressed in Heart	Most Similar Top Hit Acession (Top) Hit Descriptor Top Hit Descriptor Source Value	32 2.0E-83 M22094.1 INT Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end	2.0E-83 M22094.1 NT	2.0E-83 AU117659.1 EST_HUMAN	2.0E-83 11436448 NT	2.0E-83 AL134452.1 EST_HUMAN	2,0E-83 AL134452.1 EST_HUMAN	2.0E-83 AB011399.1 NT	Homo saplens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydrotase (trifunctional protein), beta subunit (HADHB) mRNA	Homo sepiens hydroxyacyl-Coenzyme A dehydrogenasa/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein). bota subunit (HADHR) mRNA	1.0E-83 BE883690.1 EST HUMAN	1.0E-83 7662349 NT	1.0E-83 AF053768.1 NT	1.0E-83 Z25822.1 NT	1.0E-83 4502168 NT	1.0E-83 A1027614.1 EST HUMAN	7.0E-84 BE901209.1 EST HUMAN	6.0E-84 BE838864.1 EST HUMAN	6.0E-84 BE838864.1 EST_HUMAN	6.0E-84 AA776574.1 EST_HUMAN	6.0E-84 AL042863.2 EST_HUMAN	R OF 84 AA807230 1 ECT III IMANI	6.0E-84 BE810371.1 FST HIMAN	6.0E-84 BE770199.1 EST HUMAN	6.0E-84 AW369812.1 EST HUMAN	5.0E-84 AA382811.1 EST HUMAN	5.0E-84 AF109718.1 NT	5.0E-84 11428740 NT	4.0E-84 AB037735.1 NT
		2.0E-83 M2209	2.0E-83 M2209	2.0E-83/AU11	2.0E-83	2.0E-83 AL134	2.0E-83 AL134	2.0E-83 AB011	1.0E-83	1.0E-83	1.0E-83 BE883	1.0E-83	1.0E-83 AF053	1.0E-83 Z2582	1.0E-83	1.0E-83 AI0276	7.0E-84 BE901	6.0E-84 BE838	6.0E-84 BE838	6.0E-84 AA776	6.0E-84 AL042	B OF BA AABO7	6.0E-84 BE810	6.0E-84 BE770	6.0E-84 AW36	5.0E-84 AA382	5.0E-84 AF109	5.0E-84	4.0E-84 AB037
	Expression Signal	3.32	3.32	1.21	3.7	1.82	1.82	3.48	16.57	16.57	1.6	0.84	3.55	2.22	1.36	1.75	2.82	4.21	4.21	4.76	6.24	7	3.17	1.9	1.94	1.06	1.01	2.76	1.08
	ORF SEQ ID NO:	27845	27846	27920	28358	28422	28423		21152	21153	22378	22872	23491	23826	24461	26057	23425	21028	21029	22125		25160	26440	26774		20456		28926	21116
	Exon SEQ ID NO:	17617	17617	17676	18105	18177	18177	19226	11295	11295	12488	13071	13705	14051	14674	15926	13639	11180	11180	12228	15085	15307	16277	16586	18634	10630	12908	18643	11260
	Proba SEQ ID NO:	7767	7767	7826	8223	8238	8298	1996	1390	1390	2620	3146	3793	4151	4789	6022	3727	1273	1273	2348	5206	5388	6415	90/9	8821	697	2981	8830	1354

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יישט בייטור באלו סלילים וו ויסמור	Top Hit Descriptor	wa76c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC HUMAN 043847 NARDII YSIN PRECI IRSOR.	Homo sapiens myosin light chain kinase Isoform 2 (MI CK) mRNA complete catc	Human 2,4-dienoyl-CoA reductase gene exons 3 and 4	Homo sapiens protein tyrosine phosphataso, recentor type, G /PTPRG), mRN to	Homo sapiens protein tyrosine phosphalase, receptor type (3 (PTPRG) mRNA	Homo saplens histone deacetylase 3 (HDAC3) gene. complete cds	Homo sapiens KIAA0783 gene product (KIAA0783) mRNA	Homo sapiens mRNA for KJAA (130 protein, partial cds	Homo sapiens Bach1 protein homolog mRNA, partial cds	Homo sapiens chondroitin sulfate proteodiycan 2 (versican) (CSPG2) mRNA	Homo saciens pericentriolar material 1 (PCM4) m RNA	Novel human mRNA containing Zinc finger C2H2 has domains	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRS1) mRNA complete cds	wu20d05.x1 Soares_Dieckgracfe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to db:L05093 60S RIBOSOMAI PROTEIN 148 6 JUINAAN.	CM1-BT0795-190600-272-b08 RT0705 Home serions about	CM1-BT0795-190600-272-b08 RT0705 Home content cDNA	Homo sapiens myelin transcription factor 1-like (MYT1-I) mRNIA complete add	H.sapiens DNA for endogenous retroviral like element	601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE 4121727 F	601887664F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE 4121727 F	qm87c09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895728.3'	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756C23.1:	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:09UGS3 Ogi IGS3 D.I.YAG223 1	Homo sapiens intersectin short isoform (ITSN) mRNA complete ods	Homo sapiens tyrosine 3-monocxygenase/tryptophan 5-monocxygenase activation protein, zeta polypeptide (YWHAZ) mRNA	Homo sabiens complement component 5 (CE) mRN A	am85b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629885 3'
	Top Hit Datebase Source	EST HUMAN	N-	된	Ę	닏	FZ	NT	٦	N-	TN	ĮN	N _T	1	LN	NT	EST HUMAN	EST HUMAN	EST HUMAN	11	LZ.	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	N	L	2	T HUMAN
	Top Hit Acession No.	4.0E-84 AI685321.1	4.0E-84 AF069601.2	U94982.1	4.0E-84 11386168 NT	11386168 NT	4.0E-84 AF059650.1	11421326 NT	4.0E-84 AB032956.1	3.0E-84 AF026200.1	4758081 NT	5453855 NT	3.0E-84 AL096880.1		3.0E-84 AB026898.1	3.0E-84 AF014459.1	3.0E-84 AI983801.1	2.0E-84 BE695397.1	2.0E-84 BE695397.1	2.0E-84 AF036943.1	2.0E-84 X89211.1	2.0E-84 BF308518.1	2.0E-84 BF308518.1	2.0E-84 Al298674.1	2.0E-84 BF448000.1	2.0E-84 BF448000.1	1.0E-84 AF114488.1	4507952 NT	11427631 NT	1.0E-84 AA984379.1
	Most Similar (Top) Hit BLAST E Value	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	3.0E-84	3.0E-84	3.0E-84	3.0E-84	100	3.0⊏-84	3.0E-84	3.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84 /	2.0E-84	2.0E-84 F	1.0E-84/	1.0E-84	1.0E-84	1.0E-84 /
	Expression Signal	4.03	1.76	1.27	1.31	1.31	2.35	12.15	6.56	1.36	0.89	1.15	3.03	0	1.18	4.11	7.8	5.89	5.89	9.55	0.93	1.11	1.11	1.67	1.89	1.89	1.53	5.2	0.99	1.92
	ORF SEQ ID NO:	21151	24529			25389	25805	26543	28413	20094	20891	21690	21745	03054	10707	23389	-	21845	21846	22640	22659	24364	24365		25334	25335	20090	20290		21026
	Exon SEQ ID NO:	11294	14749	14930	15336	15336	15697	16366	18169	10275	11051	11812	11856	13/58	13430	13602	18133	11948	11948	12840	12859	14568	14568	16575	19003	19003	10271	10478	10636	11178
	Probe SEQ ID NO:	1389	4869	2060	5416	5416	5791	6507	8290	313	1137	1917	1962	3540	24.00	3689	8253	2058	2058	2913	2932	4682	4682	6695	9308	9308	309	537	203	1271

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Single Exon Probes Expressed

Exan ORF SEQ NO: NO: NO: NO: NO: 11900 21790 21790 12063 21964 14489 24276 14489 24276 14216 23998 146007 26144 16007 26144 16007 26144 16007 26144 16007 26144 16007 26144 16007 26144 16007 26144 16007 26149 16007 26149 16007 26149 16007 26149 16007 26149 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 26160 16007 16007 26160 16007 16007 26160 16007 26160 16007 26160 16007 16007 26160 16007 16007 26160 16007 16007 26160 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16007 16	Signal 3.11 Signal 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00			Top Hit Database Source Source ST HUMAN ST HUMAN ST HUMAN	Single Exon Probes Expressed in Heart Top Hit Descriptor Source Source Source Source EST_HUMAN Homo saplens percentiada meteral i (PCMI) mIRNA EST_HUMAN Homo saplens percentiada meteral i (PCMI) mIRNA EST_HUMAN Homo saplens percentiada meteral i (PCMI) mIRNA EST_HUMAN Homo saplens percentiada meteral i (PCMI) mIRNA EST_HUMAN Homo saplens percentiada meteral i (PCMI) mIRNA EST_HUMAN MYZPG-SANO322_11 434 (synonym: Hess) Homo saplens cDNA chore MCRE-563400323 5 Homo saplens percentiada meteral i (PCMI) mIRNA NT Novel human gene meteral between AM.1 and CBR1 on chromosome 21q22; segment 1/3 NT Novel human gene meteral between AM.1 and CBR1 on chromosome 21q22; segment 1/3 NT Novel human gene meteral between AM.1 and CBR1 on chromosome 21q22; segment 1/3 NT Novel human gene meteral between AM.1 and CBR1 on chromosome 21q22; segment 1/3 NT Novel human gene meteral between AM.1 and CBR1 on chromosome 21q22; segment 1/3 NT Novel human gene meteral between AM.1 and CBR1 on chromosome 21q22; segment 1/3 NT Novel human gene meteral between AM.1 and CBR1 on chromosome 21q22; segment 1/3 NOVEL human gene meteral between AM.1 and CBR1 on chromosome 21q22; segment 1/3 NT Novel human gene meteral between AM.1 and CBR1 on chromosome 21q22; segment 1/3 NT Homo saplens between AM.1 and CBR1 between AM.1 and CBR1 him NA.1 Homo saplens butter specific protein (1/6/E24 percent) 1/6/E24 percental protein 1/6/E24 percental protein 1/6/E24 percental protein 1/6/E24 percental protein 1/6/E24 percental protein 1/6/E24 percental protein 1/6/E24 percental protein 1/6/E24 percental protein 1/6/E24 percental protein 1/6/E244 percental protein 1/6/E244 percental protein 1/6/E244 percental protein 1/6/E244 percental protein 1/6/E244 percental protein 1/6/E244 percental protein 1/6/E244 percental protein 1/6/E244 percental protein 1/6/E244 percental protein 1/6/E244 percental protein 1/6/E244 percental protein 1/6/E244 percental protein 1/6/E244 percental protein 1/6/E244 percental protein 1/6/E244 percenta
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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens DEAD/H (Asp-Clu-Ala-Asp/His) box polynentide 10 (RNA holingso) (DDX10)	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	Homo sapiens T-type calcium charnel alphat subrunit Alphatta isoform (CACNIA4I)	602084730F1 NIH MGC 83 Homp seniens CDNA clans IMAGE 4040007 E1	602084730F1 NIH MGC 83 Homo septemb CDNA clane IMAGE 4243067 51	RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA	HSDHEGC03 Stratagene cDNA library Human heart cattoacone Homoscope	Homo sablens protein phosphatase 24 BR damma submit and over 6	ye53g09.r1 Soares fetal liver spleen 1NFLS Homo senions CONA Chara INACE 2025 2	601189704F2 NJH MGC 7 Homo septiems cDNA charal MACE 3423646 E	Homo sapiens F-box only protein 24 (FBXO24) mRNA	Homo sapiens F-box only protein 24 (FBXO24) mRNA	Homo sapiens mRNA for KIAA1563 protein, partial cds	Homo sapiens olfactory receptor, family 12, subfamily D. member 2 (OR1202), mBNA	Homo sapiens KIAA0793 gene product (KIAA0793) mRNA	Homo sapiens KIAA0793 gene product (KIAA0793) mRNA	Homo sapiens mRNA for dynein heavy chain (DNA H9 mene)	Homo sapiens DENN mRNA, complete cds	Homo sapiens phospholipase C, epsilon (PLCE), mRNA	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (FD)[3] mRNA	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	Homo sapiens KIAA0929 profein Msv2 interacting professional and the sapiens KIAA0929 professional and the sapiens KIAA0929 professional and the sapient statements and the sapients of the sapients of the sapients and the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sapients of the sa	Homo sapiens Intersectin 2 (SH3D18) mRNA complete cde	Homo sabiens apolipoprotein C-II (APOC2) mPNA	Homo sapiens apolipoprotein C-II (APOCS) mRNA	Human DNA polymerase beta dene exons 12 and 13	Homo sapiens similar to rat integral membrane divoporotein POM121 (POM1211 1) mRNA	Homo sapiens plasminogen (PLG) mRNA
gle Exon Prol	Top Hit Database Source	TN	L	NT	LN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	NT	EST HUMAN	EST HUMAN	NT	LN	N	NT	NI	7	NT	NT					N			IN		
Sin	Top Hit Acession No.	11438573 NT	AL 163284.2	5.0E-85 AF224669.1	4F211189.1	4.0E-85 BF677910.1	3F677910.1	4.0E-85 BE079263.1	218867.1	1		3.0E-85 BE267189.1	11024695 NT	11024695 NT	3.1	7363442 NT	7662309 NT	7662309 NT	1.7		11430889 NT	5031660 NT	11418177 NT	7657266 NT	Γ	5174775 NT	2.0E-85 5174775 NT		7657468	4505880 NT
	Most Similar (Top) Hit BLAST E Value	6.0E-85	5.0E-85 AL16328	5.0E-85	5.0E-85	4.0E-85	4.0E-85 BF67791	4.0E-85	4.0E-85	3.0E-85 AF096157.	3.0E-85 T97495.1	3.0E-85	3.0E-85	3.0E-85	3.0E-85 AB04678	3.0E-85	3.0E-85	3.0E-85	3.0E-85	3.0E-85 U44953.1	3.0E-85	3.0E-85	3.0E-85	2.0E-85	2.0E-85 A	2.0E-85	2.0E-85	2.0E-85 U10525.1	2.0E-85	2.0E-85
	Expression Signal	2.56	1.21	6.1	2.45	1.66	1.66	1.68	1.97	1.15	3.37	0.94	1.73	1.73	8.66	0.94	6.94	6.94	7.04	1.61	4.06	2.28	2.66	0.87	1.85	7.1	7.1	2.12	4.24	5.42
	ORF SEQ ID NO:	28820	22066	28598		25751	25752			21035	21509	23894	24475	24476	24523	24540	25739	25740		26663	27256	28901		20719	20786	21164	21165	21972		23913
	Exon SEQ ID NO:	18535	12168	18335	15094	15646	15646	17867	19549	11185	11642	14117	14689	14689	14744	14764	15636	15636	16025	16474	17067	18610	19298	10871	10942	11305	11305	12070	11222	14138
	Probe SEQ ID NO:	8718	2285	8462	9886	5738	5738	8017	9237	1277	1741	4219	4805	4805	4864	4883	5729	5729	6152	6594	/190	8796	9788	947	1024	1400	1400	2183	2793	4239

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Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C084	wi67h08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element MSR1 repetitive element	601591416F1 NIH MGC 7 Homo saniens CDNA clone MACE 2006640 51	601462817F1 NIH MGC 67 Home saniens cDNA clone IMA CE 2862021 E	601462817F1 NIH MGC 67 Homo saciens cDNA clone IMAGE 386603 6	601109738F1 NIH MGC 16 Homo sapiens cDNA clone IMA CE 7350552 5	245f03.s1 Soares fetal liver spleen 1NFLS S1 Home sanions CNM clara MAACE 452345 51	245f03.s1 Soares fetal liver spleen 1NFI S St Home senions CDNA close INA CEL 152245 5	601897003F1 NIH MGC 19 Homo sapiens cDNA clone IMAGE-4108446 5	601897003F1 NIH MGC 19 Homo sapiens cDNA clone IMAGE:4128440 5	Homo sapiens calcineurin binding protein 1 (KIAA0330) mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330) mRNA	601120778F1 NIH MGC 20 Homo saniens cDNA clone IMAGE: JORZEGO E	Homo sapiens KIAA0680 gene product (KIAA0680) mRNA	aj88f08.s1 Soares parathyroid tumor NbHPA Homo saniens CDNA clone IMACE-14の3を50つ	aj88f08.s1 Soares, parathyroid fumor NbHPA Homo sapiens cDNA clone IMAGE: 1403450.2	Homo sapians Tax1 (human T-cell leukemia virus tope I) binding profein 1 (TAX18P1)	Homo sapiens galactocerebrosidase (GALC) gene exm 15	Homo sapiens RAN binding profein 7 (RANBP7) mRNA	Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6) mRNA	Homo sapiens similar to transcription factor CA150 (H sariens V) (CR33.73) (FINAL)	Homo sapiens similar to transcription factor CA150 (H. sapiens) (I OC63170) mRNA	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH) mRNA	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5	601176865F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531953 5	801072694F1 NIH MGC 12 Homo sapiens cDNA clone IMAGE 3468830 F	x392h12.x1 NCI CGAP Lu24 Homo sabiens cDNA clone IMAGE: 2871749 3'	601509696F1 NIH MGC 71 Homo sapiens CDNA cinne IMAGE 301303 F	601509696F1 NIH MGC 71 Home sabiens cDNA clone IMACE 2011303 F	tu18b02.x1 NCI CGAP Pr28 Hamo saniens cDNA clone IMA GE-20543243	601302333F1 NIH MGC 21 Horno saniens of NA Alara MA CE 2626262 5	EST177232 Jurkat T-cells VI Homo seniens CONA 5 and	Horno sapiens chromosome 21 segment HS210003
gle Exon Pro	Top Hit Database Source	NT	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LN	LN	EST HUMAN	Ί.	EST_HUMAN	EST_HUMAN	LN ⊢N	LN T	FZ	Z	M	NT	LN T	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LN L
us	Top Hit Acession No.	2.0E-85 AL163284.2	AI760820.1			1.0E-85 BE618392.1		35.1		1.0E-85 BF311552.1	1.0E-85 BF311552.1	11417862 NT	11417862 NT	3E274217.1	7662247 NT	7.0E-86 AA860801.1	7.0E-86 AA860801.1	11421737 NT	L38557.1	5453997 NT	11526307 NT	11417012 NT	11417012 NT	4505492	3.1	3.1			Г					
	Most Similar (Top) Hit BLAST E Value	2.0E-85	2.0E-85 AI76082	1.0E-85 BE7943	1.0E-85	1.0E-85	1.0E-85 BE25791	1.0E-85	1.0E-85	1.0E-85	1.0E-85	1.0E-85	1.0E-85	9.0E-86 BE2742	7.0E-86	7.0E-86	7.0E-86		7.0E-86	7.0E-86	7.0E-86	7.0E-86	7.0E-86	6.0E-86	4.0E-86 BE54717	4.0E-86 BE29584;	4.0E-86 BE54717	3.0E-86	3.0E-86	3.0E-86	3.0E-86 A	3.0E-86 B	2.0E-86 A	2.0E-86 AL163203
	Expression Signal	1.3	1.29	2.44	8.09	8.09	2.06	2.56	2.56	2.28	2.28	2.7	3.43	7.66	1.3	1.33	1.33	6.91	2.91	1.63	2.35	2.15	2.15	9.33	1.48	10.18	1.9	6.02	3.31	3.31	9.01	2.02	1.33	1.67
	ORF SEQ ID NO:	24489	27408		22121	22122	27704	28419	28420	28492	28493	25283	25283		20001	20691	20692	24865	27148		27696	28455	28456	21027	19993	25686	19993	25411	27963	27964	28125		20046	
	Exon SEQ ID NO:	14705	17209	12125	12224	12224	17483	18175	18175	18242	18242	19082	19082	11315	10190	10845	10845	15121	16955	17444	17475	18206	18206	11179	10175	15586	10175	15355	17718	177/18	17883	19560	10231	10354
	Probe SEQ ID NO:	4822	7341	2241	2344	2344	7632	8296	8296	8365	8365	9194	9448	1410	220	921	921	6164	7078	7593	7624	8329	8329	1272	204	2/99	8567	5435	7868	7868	8734	9163	266	408

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Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	yz19a08.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE.283478 5'	Human endogenous retrovirus, complete genome	Homo sapiens mRNA for KIAA1277 protein, partial cds	EST378215 MAGE resequences, MAGI Homo sapiens cDNA	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds	hd87g08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2916542 3'	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds	H.sapiens mRNA encoding phospholipase c	H.sapiens mRNA encoding phospholipase c	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase)	Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L) mRNA	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA	Homo sapiens gene for AF-6, complete cds	Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), mRNA	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase)	(NDOEST) MIKNYA Homo sanjans filvijin 5/EBI NIS) mBNJA	Human gamma-glutamy transpentidasa mRNA complete ode	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens hypothetical protein (LOC51318), mRNA	Homo sapiens hypothetical protein (LOC51318), mRNA	Homo sapiens chromosome 21 segment HS21C100	Homo sapiens FK506-binding protein FKB23 isoform mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C084	qb77c09.x1 Soares_fetal_heart_NbHH19W Homo saplens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10;
le Exon Pro	Top Hit Database Source	EST_HUMAN	L	N⊤	EST_HUMAN	LX	⊥N	EST_HUMAN	LN	LN	LN L	5		17	トラ	- - -	トラ	Ę	N	누	Ŀ		L L	NT	NT	L N	ラ	Ę	TN	NT	EST_HUMAN
Sing	Top Hit Acession No.	N58977.1 EST	9635487				2.0E-86 AF156776.1	2.1	2.0E-86 AF056490.1			11437135 NT	11437135 NT	11422084	11545846 NT	11545846 NT	4759051 NT	11418189 NT	2.0E-86 AB011399.1	11417883 NT	1100000	TN 626853 N 1	20492.1	9.2	1.0E-86 AL163209.2	706161	7706161 NT	1.0E-86 AL163300.2			9.0E-87 AI150703.1
	Most Similar (Top) Hit BLAST E Value	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86 Z16411.1	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	L	1.0E-86	1.0E-86 20492.1	1.0E-86	1.0E-86	1.0E-86	1.0E-86	1.0E-86	1.0E-86	1.0E-86/	9.0E-87
	Expression Signal	2.18	2.37	1.12	1.43	2.16	2.16	2.42	2.8	1.53	1.53	2.22	2.22	1.95	2.69	2.69	1.83	2.4	1.81	1.47		2.06	2.42	1.32	1.32	11.48	11.48	5.76	1.11	2.15	1.47
	ORF SEQ ID NO:	20929	21930	22011	23087	23385	23386		24360	25571	25572	27057	27058	27446	28061	28062	28397	25250		25139	07070	27847	22927	22977	22978	23568	23569	23842	24497	25378	
	Exon SEQ ID NO:	11085			13288	13599	13599		_ {		15495	16864	16864	17241	17819	17819	18156	19187	19290	19520	4		13122	13179	13179	13775	13775	14067	14714	15328	15209
	Probe SEQ ID NO:	1173	2144	2222	3369	3686	3686	3954	4679	5580	5580	6987	6987	7372	7969	2967	8276	9096	9772	9955	4570	3125	3197	3256	3256	3864	3864	4167	4832	8882	5287

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Single Exon Probes Expressed in Heart

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Single Exori Probes Expressed in near	Top Hit Descriptor	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA	O.cuniculus mRNA for elongation factor 1 alpha	7h85f02.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3	7h85f02.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3	IL3-HT0619-060700-198-D10 HT0619 Homo sapiens cDNA	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo saplens mRNA for KIAA1081 protein, partial cds	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA	EST96094 Testis I Homo sapiens cDNA 5' end	EST96094 Testis I Homo sapiens cDNA 5' end	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens mRNA for KIAA144 protein, partial cds	yi80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;	Homo sapiens mRNA for KIAA0456 protein, partial cds	Homo sapiens CGI-60 protein (LOC51626), mRNA	Homo sapiens CGI-60 protein (LOC51626), mRNA	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Horno sapiens cDNA clone TCBAP4051	Human von Willebrand factor pseudogene corresponding to exons 23 through 34	Homo sapiens similar to heat shock 70kD protein 98 (mortalin-2) (H. sapiens) (LOC63184), mRNA	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA	AU116935 HEMBA1 Homo sapiens cDNA done HEMBA1000307 5'	CM0-TN0038-150900-552-h08 TN0038 Homo sapiens cDNA
Jie Exori Proc	Top Hit Database Source	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	TN	L	LΝ	EST_HUMAN	EST_HUMAN	IN	TN	EST HUMAN	L	Z	NT	LN	SWISSPROT	EST_HUMAN	LN	TN	NT	NT	EST_HUMAN	EST HUMAN
SIIIC	Top Hit Acession No.	4757721 NT	4757721 NT	(62245.1	3F063211.1	3F063211.1	7.0E-87 BF352776.1	.2	7.0E-87 AL043314.2	(03002.1	(03002.1	7657213 NT	6.0E-87 AB029004.1	11432444 NT	A382811.1		4.0E-87 AL163210.2	4.0E-87 AB037835.1	778133.1	AB007925.1	7706299 NT	7706299 NT	5174574 NT	000321	3E247284.1	M60676.1	11417339 NT	11417812 NT	35420	5	2.0E-87 BF376311.1
	Most Similar (Top) Hit BLAST E Value	9.0E-87	9.0E-87	8.0E-87 X62245.1	7.0E-87 BF063211	7.0E-87 BF063211	7.0E-87	7.0E-87	7.0E-87	7.0E-87 K03002.1	7.0E-87 K03002.1	6.0E-87	6.0E-87	6.0E-87	5.0E-87 AA38281	5.0E-87 AA382811	4.0E-87	4.0E-87	4.0E-87 R78133.1	4.0E-87 AB00792	4.0E-87	4.0E-87	4.0E-87	4.0E-87	4.0E-87 BE24728	4.0E-87 M60676.1	4.0E-87	4.0E-87	2.0E-87	2.0E-87	2.0E-87
	Expression Signal	2	2	14.17	2.74	2.74	2.67	3.38	3.38	10.88	10.88	0.87	1.73	3.52	1.69	1.53	1.33	10.54	0.86	0.92	1.07	1.07	2.19	6.47	4.36	4.35	2.13	14.77	2.99	0.89	1.17
	ORF SEQ ID NO:	26424	26425	20233	22031	22032	26829	27877	27878	28384	28385	23203	25893	<u> </u>	20898	20898	20721	20912	21179	21771	22142	22143	23140	25090	25696	28644	29091		22502	23414	24492
-	Exon SEQ ID NO:	16264	16264	10414	12134	12134	16642	17644	17644	18144	18144	13398	15774	17997	11056	11056	10874	11068	11316	11878	12252	12252	13336		15595	18378	18798			13629	14708
	Probe SEQ ID NO:	6403	6403	471	2250	2250	6763	7794	7794	8264	8264	3482	5868	8107	1142	9450	950	1155	1411	1985	2372	2372	3419	5343	5686	8505	8994	9692	2749	3717	4826

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Single Exon Probes Expressed in

December Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Composition Com					Т	\neg	T	T		Т	1		1	- 1			-		-	T-	-	_	í –	7000	T .	_		- 27	<u></u>	, ;			<u>_</u>	1000	3,000 -000	,
Single Exon Pro Signal	es Expressed in Heart	Top Hit Descriptor	RC5-HT0580-200300-031-G04 HT0580 Home contains contains	601569041F1 NIH MGC 21 Homo saniens cDNA close IMA CE 2042720 El	601569041F1 NIH MGC 21 Homo sanlens china close IMACE:3343730 5	601341383F1 NIH MGC 53 Homo saniens cDNA close [MA/CE-3692246]	601176032F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE 353146 5	W21e07.r1 Soares fetal liver sniden 1NFI S. Homer springs. Chord Long 1MACE charges and	W21e07.r1 Soares fetal liver spleen 1NFLS Homo saniens CDNA clone IMA CE: 243396 5	Human cyclophilin gene for exclophilin (FC 5 21 8)	801278315F1 NIH MGC 39 Homo saniens cDNA clore IMAGE 3840520 5	Homo saplens butative olympia in professional of OCEACL SO 10339 3	PM2-CT0265-141099-001-004 CT0265 Home Seniors CANA	PM2-CT0265-141099-001-004 CT0265 Home Senior CNN	Human mRNA for T-cell cyclophilin	Homo engines non-con III Ala VAIO	Raffils provedicis faste hid records made: TD 644 /TD 643	removements around fortier concepts the profit (18 041) gene, complete cds	Home sequence grown receptor-bound protein 10 (SKB10) gene, exon 8	Hours septens growth factor receptor-bound protein 10 (GRB10) gene, exon 8	Homo captura protein intase C, beta 1 (P'KKCB1), mKNA	Hours septiens underlied epithelium enriched protein (PLUNC) gene, complete cds	Homo septens minna for alpha 2,3-stalytransterase ST3Ga VI, complete cds	One Bulgate of other April 2012 and the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the stat	SC6-BN0276-0307/03-0 12-E02 BN0276 Homo sapiens cDNA	Iomo saniens hect domain and BI D 2 (HEDCS). This	Homo sapiens RGH1 gene retrogging live along at	dino capiens culforteneferate solution and activity of in TVA	form captoins agree asserted by the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the	domo saniens mRNA for K1AA1300 models.	domo sanians mRNA for KIAA1200 protesti, per tel cus	domo sanione chromocoxus 24 socioses i LECASOSOS	Asaniens FCF-1 dene (even 0)	Sapiens ECF-1 dene (evon 9)	Homo septiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	
Exon No: ORF SEQ Expression Signal Most Similar (Top) Ht Aces: Most Similar (Top) Ht Aces: No. 14760 24537 0.8 2.0E-87 BE175478.1 No. 15393 25457 7.87 2.0E-87 BE774790.1 No. 16726 24537 0.8 2.0E-87 BE754790.1 No. 16726 25458 7.87 2.0E-87 BE754790.1 No. 16726 25458 7.87 2.0E-87 BE754390.1 No. 16726 26564 28.31 2.0E-87 BE531490.1 No. 16771 26965 28.31 2.0E-87 BE531430.1 No. 17485 26564 28.31 2.0E-87 BE531430.1 No. 17485 26564 28.31 2.0E-87 BE531430.1 No. 17485 26564 28.31 2.0E-87 BE531430.1 No. 17581 27182 0.94 1.0E-87 AW361977.1 No. 13563 23349 1.0E-87 AW361977.1 No. 1.0E-87 AW361977.1 14927 24699 1.04 1.0E-87 AW3	jle Exon Pro	Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	NT	EST HUMAN	Ί.	EST HUMAN	EST HUMAN	N	NT.	L Z	L	17	FZ				HI MAANI	HIMAN		- -									
Exon No: ORF SEQ ID ID NO: Signal Signal Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO: Mos Signal ID NO:	Sinc		BE1754	BE734190.1			32.1	_	-	1		5683		ļ	-	4758827	1	711		1500	AF214562 1	» 1			T	29867	_	7657632	F167465.1						1.6	
Exon SEQ ID ORF SEQ Expression Signal Seq ID NO: 14760 24537 7 15393 25457 7 15393 25458 7 16284 28 7 16285 26275 1 16286 26543 3 16287 2 2 16286 26564 28 16385 26564 28 16386 26564 28 16386 26564 28 16387 26564 28 16386 26564 28 16386 26564 28 16386 26564 28 16387 23349 3 16804 26589 1 16804 26783 1 16804 26783 1 16804 26783 1 17405 27234 1 17405 27621 2 17405 27621		Most Similar (Top) Hit BLAST E Value	2.0E-87	2.0E-87	2.0E-87	2.0E-87	2.0E-87	2.0E-87	2.0E-87	2.0E-87	2.0E-87	1.0E-87	1.0E-87	1.0E-87	1.0E-87	1.0E-87	1.0E-87	1.0E-87	1.0F-87	1.0E-87	1 0F-87	1 0F-87	1.0F-87	1 0F-87 F	1.0E-87		1.0E-87	1.0E-87	9.0E-88	9.0E-88	9.0E-88	9.0E-88	9.0E-88	9.0E-88	9.0E-88 AB026898	
Exon SEQ ID ORI NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:		Expression Signal	0.8	7.87	78.7	6.27	1.51	32.21	28.31	3.81	5.11	2.33	0.94	0.94	3.18	2.47	1.04	3.39	3.39	1.6	13.13	1.19	1.19	2.77	2.77	2.06	1.78	2.02	7.39	2	2	1.13	2.64	2.64	1.23	
		ORF SEQ ID NO:												21182	23349	23374	24699	25788	25789	26398	26793	27233	27234	27620	27621	28249			20847	21090	21091	23279	23847	23848	24580	
Probe SEQ ID NO: 4880 5473 5819 6626 6626 6626 6626 6626 6626 6626 66		Exon SEQ ID NO:		15393	15393	15725	16122	16268	16385	16771	17485	12645	11318	11318	13563	13587	14927	15681	15681	16238	16604	17042	17042	17405	17405	18003	18244	19761	11006	11234	11234	13488	14072	14072	14812	
		Probe SEQ ID NO:	4880	5473	5473	5819	6256	6407	6526	6892	7634	1165	1413	1413	3649	3673	5057	5774	5774	6376	6724	7165	7165	7554	7554	8114	8367	9539	1090	1327	1327	3574	4172	4172	4934	

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Single Exon Probes Expressed in Deari	Top Hit Descriptor	Homo sapiens X-linked anhidroilic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	regions	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC	FINGER PROTEIN HZF1	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	wd68h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE.2336799 3' similar to contains Alu	repetitive element; contains element MER22 MER22 repetitive element;	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	ym06b10.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:47129 5	Homo sapiens chromosome 21 segment HS21C084	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA	Homo saplens KIAA0152 gene product (KIAA0152), mRNA	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA	Homo saplens zinc finger protein 259 (ZNF259) mRNA	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA	Homo sapiens a disIntegrin and metalloprotelnase domain 23 (ADAM23) mRNA	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA	Homo sapiens valosin-containing protein (VCP), mRNA	Homo sapiens polycythemia rubra vera 1, cell surface receptor (PRV1), mRNA	Homo sapiens v-ral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA	Homo sapiens putative anion transporter 1 mRNA, complete cds	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA	Homo sapiens growth differentiation factor 5 (cartilage derived morphogenetic protein 1) (GDF5), mRNA
lle Exon Prop	Top Hit Database Source			NŢ		T_HUMAN	NT	LN	LN		T HUMAN	TN	L	EST_HUMAN			EST_HUMAN	LN	L			NT		EST_HUMAN	LN	L	NT	NT	LN	NT	NT	NT	
SILIC	Top Hit Acession No.		AF003528.1	7661887 NT				5.0E-88 AF114488.1	5.0E-88 AF114488.1		41693217.1	5.0E-88 AF114488.1	5.0E-88 AF114488.1	110932.1	5.0E-88 AL163284.2	3F091229.1	3F091229.1	11416585 NT	4502694 NT	7661947 NT	7661947 NT	11545800 NT	4508020 NT	V66951.1	4501912	4501912 NT	11429300 NT	11429567 NT	9966888 NT	11420697 NT	3.0E-88 AF279265.1	11436400 NT	11421726 NT
	Most Similar (Top) Hit BLAST E Value		6.0E-88	5.0E-88		5.0E-88	5.0E-88	5.0E-88	5.0E-88		5.0E-88 AI693	5.0E-88	5.0E-88	5.0E-88 H1090	5.0E-88	4.0E-88 BF091	4.0E-88 BF09	4.0E-88	4.0E-88	4.0E-88	4.0E-88	3.0E-88	3.0E-88	3.0E-88 N669	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88
	Expression Signal		3.69	1.19		ဇ	0.92	0.94	0.94		2.31	0.91	0.87	2.64	1.84	1.64	1.64	1.93	2.84	2.1	2.1	0.93	4.77	4.31	1.21	1.21	3.17	4.09	3.84	3.39	12.03	99:9	8.52
	ORF SEQ ID NO:		27284			22366		22704	22705			23212	24310	26185	26694	21070	21071	26316	28402	28883	28884	20475			23819	23820		24937	25403	25480	26098	26479	26688
	Exon SEQ ID NO:		17093	11685		12470	12897	12905	12905		13263	13407	14519	16042	16507	11214	11214	16159	18160	<u>'</u>	18595	10647	11669	12845	14047	14047	14276	15166	15349	15417	15964	16313	16500
	Probe SEQ ID NO:		7216	1787		2602	2970	2978	2978		3343	3491	4631	6909	6627	1307	1307	6295	8281	8780	8780	715	1770	2918	4147	4147	4380	5242	5429	5498	6204	6452	6620

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Table 4
Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein C mRNA, complete cds	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA	Homo sapiens Calsenilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA	UI-H-BI1-aea-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'	UI-H-BI1-aea-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'	Homo sapiens KIAA0417 mRNA, complete cds	Homo sapiens KIAA0417 mRNA, complete cds	aa54a11.51 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:80272.2	EUUODI,	UKF.Zp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5	os91g03.s1 NCL_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612756 3' similar to gb:M16342 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens transgelin 2 (TAGLN2), mRNA	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5'	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA	DKFZp434E246_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E246 5	H.sapiens CLN3 gene, complete CDS	H.sapiens CLN3 gene, complete CDS	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA	H.sapiens Wee1 hu gene	H.sapiens Wee1 hu gene	Homo saplens mRNA for KIAA0823 protein, partial cds	Homo sapiens mRNA for KIAA0823 protein, partial cds	Human aconitate hydratase (ACO2) gene, exon 2	Homo saplens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA
le Exon Probe	Top Hit Database Source	TN T					LN T			THUMAN	NT	TN TN		7	寸		L L		T HUMAN				T_HUMAN	NT				l NT	NT TN	NT I			
Sing	Top Hit Acession No.	74.1	11526262 NT	11417974 NT	7305198 NT	9.1	9.1	5031666 NT			17.7	1.7.1	4 00 00 4 4 4 00 00 4 4		14.2	79.1	16.2	11421238 NT	57.1	7657213 NT	7657213 NT	4557390 NT	18.1	1	1	11420754 NT	.1			7.0E-89 AB020630.1	.1	5803114 NT	4506124 NT
	Most Similar (Top) Hit BLAST E Value	3.0E-88 AF0343	3.0E-88	3.0E-88	2.0E-88	2.0E-88 AF2462	2.0E-88 AF24621	2.0E-88	1.0E-88	1.0E-88	1.0E-88	1.0E-88 AB0078	90 10	1.0E-88	1.0E-88 AL0433	1.0E-88 AA9914	1.0E-88 AL1632	9.0E-89	8.0E-89 BE3115	7.0E-89	7.0E-89	7.0E-89	7.0E-89 AL04574	7.0E-89 X99832.	7.0E-89 X99832.	7.0E-89	7.0E-89 X62048	7.0E-89 X62048.	7.0E-89	7.0E-89	7.0E-89 U87927	6.0E-89	6.0E-89
	Expression Signal	1.41	2.12	4.78	1.42	0.93	4.19	1.93	4.98	4.98	17.59	17.59	90 1	4.00	2.95	2.27	2.98	4.12	1.41	1.35	1.35	2.94	5.14	1.35	1.35	1.78	1.42	1.42	1.17	1.17	3.07	1.07	1.12
	ORF SEQ ID NO:	26836	26626		20780	21372	21486	24007	25597	25598	26033	26034	00000	70707	2/584	28135		28447	22459	20194	20195	24457	24511	25076	25077	26450	28097	28098	28107	28108		20768	21954
	Exon SEQ ID NO:	16648	16440	18988	10938	11512	11617	14225	15518	15518	15909	15909	0.70	10170	1/3/5	17891	19117	18198	12568	10371	10371	14670	14728	15254	15254	16289	17856	17856	17862	17862	19393	10924	12053
	Probe SEQ ID NO:	6929	7427	9286	1020	1607	1716	4328	5604	5604	6004	6004	6000	0203	/524	8742	9502	8321	2705	426	426	4785	4847	5334	5334	6428	8008	8008	8012	8012	9920	1006	2166

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Top Hit Descriptor	hr81d09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN ;	hr81d09.x1 NCI_CGAP_KId11 Homo sapiens cDNA clone IMAGE:3134897.3' similar to TR.O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN :	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	7e36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3	7e36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	ai63d08.s1 Soares testis NHT Homo sapiens cDNA clone 1375503.	601655837R1 NIH MGC 66 Homo sapiens cDNA clone IMAGE 3855824 3	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3	yr86e04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C11C: HI IMAN P11586 C-1.TETRAHYDROFOLIATE CYNTHAGE CYTODIAGAIN.	y 86604.51 Soares fetal liver spleen 1NFLS Homo sabiens CDNA clone IMAGE 212190 31 cimilar to	SP.C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC,	H.sapiens ECE-1 gene (exon 6)	H.sapiens ECE-1 gene (exon 6)	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA	Homo sapiens HsGCN1 mRNA, partial cds	Homo sapiens HsGCN1 mRNA, partial cds	Homo saplens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA	Homo sapiens TCL6 gene, exon 1-10b	Human gamma-aminobutyric acid transamlnase mRNA, partial cds	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds	Homo sapiens pregnancy-zone protein (PZP) mRNA	z/82g10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4614423'	z/82g10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4614423	DKFZp762P1616_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762P1616 5'
Top Hit Database Source	EST_HUMAN	EST HUMAN	NT	N	LN L	۲	EST_HUMAN	EST_HUMAN	⊢ N	EST HUMAN	EST HUMAN	EST HUMAN	EST HIMAN		EST_HUMAN	ĹΝ	LN	LN	NT	NT	NT	NT	LN	IN	LN	NT	ΝΤ	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	1.0E-89 BF196052.1	1.0E-89 BF196052.1	9.0E-90 AL163246.2	9.0E-90 AL163246.2	8.0E-90 AL163246.2	8.0E-90 AL163246.2	8.0E-90 BE670561.1	8.0E-90 BE670561.1	7.0E-90 AF223391.1	7.0E-90 AA782977.1	2	2	168849 1		168849.1	(91926.1	K91926.1	TN 8922398 NT	10 8922398 NT	J77700.1	U77700.1	4504794 NT	4504794 NT	5.0E-90 AB035344.1	J80226.1	5.0E-90 AF114487.1	4506354 NT	1	5.0E-90 AA705222,1	NL135549.1
Most Similar (Top) Hit BLAST E Value	1.0E-89	1.0E-89	9.0E-90	9.0E-90	8.0E-90	8.0E-90	8.0E-90	8.0E-90	7.0E-90	7.0E-90 /	7.0E-90	7.0E-90	7.0E-90 H68849 1		7.0E-90 H68849.1	6.0E-90 X91926.1	6.0E-90 X91926.1	6.0E-90	6.0E-90	6.0E-90 U77700.1	6.0E-901	6.0E-90	6.0E-90	5.0E-90 /	5.0E-90 U80226.1	5.0E-90 /	5.0E-90	5.0E-90	5.0E-90	5.0E-90/
Expression Signal	6.12	6.12	1.16	1.16	1.62	2.93	5.28	5.28	2.65	1.91	1.88	1.88	1.98		1.98	1.14	1.14	7.33	7.33	3.54	3.54	3.25	3.25	10.5	1.55	2.19	3.08	1.07	1.07	0.98
ORF SEQ ID NO:	28960	28961	26859			20806	21072	21073			27250		27927		27928	22749	22750	23809	23810	25646		ı	26919		20931	22273	24124			24251
Exon SEQ ID NO:	18672	18672	16668	16668	10965	10965	12690	12690	10746	16785	17060	17060	17683		17683	12957	12957	14034	14034	15554	15554	16725	16725	10123	11087	12382	14334	14400	14400	14463
Probe SEQ ID NO:	8860	8860	6289	6289	1047	1048	1308	1308	818	2069	7183	7183	7833		7833	3029	3029	4134	4134	5641	5641	6846	6846	149	1175	2508	4440	4507	4507	4571

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Single Exon Probes Expressed in Heart

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Ongle Event Topics Expressed in Team	Top Hit Descriptor	H.sapiens mRNA encoding phospholipase c	H.sapiens mRNA encoding phospholipase c	Homo saplens anglopoietin 4 (ANG4) mRNA, partial cds	Homo sapiens angiopoietin 4 (ANG4) mRNA, partial cds	Homo sapiens adenylate cyclase 9 (ADCY9) mRNA	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA	Homo sapiens gene for AF-6, complete cds	ar 78h05.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE.2128761 3'	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens myosin phosphalase, target subunit 1 (MYPT1), mRNA	H.sapiens gene encoding discoidin receptor tyrosine kinase, exon 16	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens mRNA for KIAA1244 protein, partial cds	Human prohormone converting enzyme (NEC2) gene, exon 8	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'	Homo saplens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA	qc54c02.x1 Soares_placenta_8tc9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:17;3410.3' similar to SW:0LF3_MOUSE P23275 OLFACTORY RECEPTOR OR3.;	Homo sapiens mRNA for KIAA0289 gene, partial cds	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA	be49d05.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2899881 5' similar to TR:O75208 O75208 HYPOTHETICAL 35.5 KD PROTEIN.;	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
וב רעמווו ומם	Top Hit Database Source	NT	NT	NT	NT	NT	NT	N⊤	L	LN	EST_HUMAN	NT	NT	TN	NT	NT	NT	LN	EST_HUMAN	EST_HUMAN	N	NT	EST_HUMAN	LN	LN	EST_HUMAN	LN.	LN	EST_HUMAN
Silo I	Top Hit Acession No.			5.0E-90 AF113708.1	5.0E-90 AF113708.1	4557258 NT	11345483 NT	11419429 NT	11433721 NT	5.0E-90 AB011399.1	5.0E-90 AI523386.1	1	4.0E-90 AF231920.1	4505316 NT).1		1	2.0E-90 BE537913.1	5031748 NT	5031748 NT	2.0E-90 AI138213.1	2.0E-90 AB006627.1	5729855 NT	2.0E-90 AW672686.1	11427320 NT	127320	2.0E-90[AU118985.1
	Most Similar (Top) Hit BLAST E Value	5.0E-90 Z16411.1	5.0E-90 Z16411.1	5.0E-90 ₽	5.0E-90 /	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	4.0E-90	4.0E-90	4.0E-90	4.0E-90 X99033.1	4.0E-90 D87675.1	4.0E-90	4.0E-90 M95967.1	3.0E-90 E	2.0E-90 E	2.0E-90	2.0E-90	2.0E-90	2.0E-90 /	2.0E-90	2.0E-90	2.0E-90	2.0E-90	2.0E-90[/
	Expression Signal	2.52	2.13	2.26	2.26	7.93	4.66	1.24	15.41	2.16	2.37	1.85	1.85	2.94	9.22	4.07	1.97	1.9	103.62	4.28	3.65	3.65	2.81	1.13	8.33	4.34	2.9	2.9	1.56
	ORF SEQ ID NO:	25409	25409	26302	26303	26489	26899	27646	28060			20083	20084	20829	21432	24235	24372	24385	29004	19995	20913	20914	23465		24488	25519	27708	27709	27796
	Exon SEQ ID NO:	15353	15353	16147	16147	16323	16704	17432	17818	19306	19299	10263	10263	10986	11565	14449	14577	14599	18709	10178	11069	11069	13683	14476	14703	15451	17489	17489	17572
	Probe SEQ ID NO:	5433	5523	6283	6283	6464	6825	7581	7968	9744	9789	299	299	1070	1663	4557	4691	4713	8901	207	1156	1156	3771	4588	4820	5534	7638	2638	7722

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA	Homo sapiens amyloid beta (A4) precursor profein (profease nexin-II Alzheimer disease) (ADD) - MDNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA	Homo sapiens protein phosphatase 2A BR gamma suhimit gene evon 3	Homo sapiens protein phosphatase 2A BR gamma subunit gene expn 3	601159563F2 NIH MGC 53 Homo sapiens cDNA clone IMAGE 3511118 5	Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57167) mRNA	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2) mRNA	Homo sapiens mRNA for KIAA0903 protein, partial cds	Homo saplens mRNA for KIAA0903 protein, partial cds	Homo saplens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9	end complete cds, alternatively spliced	Homo sapiens mRNA for KIAA0633 protein, partial cds	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2) mRNA	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively solited	Homo sapiens CGI-15 protein (LOC51006), mRNA	Homo sapiens CGI-15 protein (LOC51006), mRNA	Homo saplens DNA for Human P2XM, complete cds	Homo sapiens DNA for Human P2XM, complete cds	HUM000S381 Liver HepG2 cell line, Homo sapiens cDNA clone s381 3'	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA nartial cds	Homo sapiens makorin, ring finger protein, 1 (MKRN1), mRNA	zi90b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE: 448015.3'	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
JIB EXON Proc	Top Hit Database Source	EST_HUMAN	N-	Ę	NT	LN	LN LN	LN LN	NT	N⊤	N-	N	LN	EST HUMAN	1	LN	LN	NT	Ļ	2	LZ	F	トフ	NT	5	17	NT	N	EST_HUMAN	NT		1	EST_HUMAN
	Top Hit Acession No.	AU118985.1	11024711 NT	4502166 NT	5.1	5.1	2.1	1.0E-90 AJ237589.1		1.0E-90 AF264750.1	4507828 NT			1.1	1420514	6005720 NT	1.0E-90 AB020710.1	1.0E-90 AB020710.1		-		11426758 NT	11422086 NT	1.0E-90 AF163864.1	11422109 NT	11422109 NT		1.0E-90 AB002059.1		7.0E-91 AF053768.1	419234	.1	5.0E-91 AU143539.1
	Most Similar (Top) Hit BLAST E Value	2.0E-90	2.0E-90	1.0E-90	1.0E-90 AF23192	1.0E-90 AF23192	1.0E-90 AJ237589	1.0E-90 /	1.0E-90/	1.0E-90/	1.0E-90	1.0E-90 /	1.0E-90	1.0E-90 BE379884	1.0E-90	1.0E-90	1.0E-90 /	1.0E-90/	1 00	1.05-90.1	1.0E-90 AB01453	1.0E-90	1.0E-90	1.0E-90 A	1.0E-90	1.0E-90	1.0E-90	1.0E-90	8.0E-91 D12234.1	7.0E-91 A	7.0E-91	5.0E-91 AA702794	5.0E-91 A
	Expression Signal	1.56	49.27	3.39	1.21	1.04	2.03	2.03	7.71	7.71	2.45	3.47	3.47	4.02	4.98	8.4	1.18	1.18	•	- 0	7.7	2.85	3.78	1.22	1.72	1.72	1.89	1.89	5.48	0.88	2.05	1.47	1.05
	ORF SEQ ID NO:		28159	20060	20148	20148	20435	20436	20472	20473		21044	21045		21631	22545	23473	23474	24005	24003	73404	26558	27189		27444	27445	25225	25226	23780	21199	26907	23151	24092
	Exon SEQ ID NO:	Li	17914	10241	12639	12639	10613	!		10645	11010	11192	11192	11548	11756	12752	13689	13689	14223	15404	1.040.1	16380	16998	17224	17240	17240	19268	19268	14001	11333	16714	13346	14309
	Probe SEQ ID NO:	7722	8765	275	370	371	089	680	713	713	1094	1284	1284	1644	1860	2823	3777	3777	4326	1020	3401	6521	7121	7356	7371	7371	9732	9732	4101	1428	6835	3429	4415

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Oligie Exoli Todos Expressed II Todi.	Top Hit Descriptor	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'	AV649878 GLC Horno sapiens cDNA clone GLCBYF08 3'	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds	Homo sapiens lysophosphatidic acid acytransferase-delta (LPAAT-delta) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C084	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to	Ketrovirus-related gag polyprotein	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6	Homo sapiens chromosome 21 segment HS21C083	Homo sapiens mRNA for KIAA1278 protein, partial cds	Homo sapiens mRNA for KIAA1278 protein, partial cds	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds	Human Ku (p70/p80) subunit mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C085	Homo sapiens chromosome 21 segment HS21C085	Homo sapiens epididymal secretory protein (19.5kD) (HE1), mRNA	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11	Human mRNA for very low density lipoprotein receptor, complete cds	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	
JIE LAUII I IUL	Top Hit Database Source	EST_HUMAN	LN	L	EST_HUMAN	EST HUMAN	LN	LN	NT	141041111111111111111111111111111111111	EST_HUMAN	EST HUMAN	١.	N	NT	NT	NT	TN	NT	LN	LN	NT	LN	LNT	NT	LZ	LN.	۲	님	NT	NT	
	Top Hit Acession No.	AU143539.1	7110634 NT	7110634 NT	5.0E-91 AV649878.1	5.0E-91 AV649878.1	4.0E-91 AF156776.1	4.0E-91 AF156776.1	4.0E-91 AL163284.2		4.0E-91 M77994.1	M77994.1	11430193 NT	11430193 NT	3.0E-91 AF169555.1	3.0E-91 AF169555.1	3.0E-91 AL163283.2	3.0E-91 AB033104.1	3.0E-91 AB033104.1	3.0E-91 AF084530.1	3.0E-91 M30938.1	3.0E-91 AL163285.2	3.0E-91 AL163285.2	11434964 NT	4502740 NT	11497611 NT	11497611 NT	U86959.1	3.0E-91 U86959.1	3.0E-91 D16494.1	3.0E-91 AF240786.1	
	Most Similar (Top) Hit BLAST E Value	5.0E-91	5.0E-91	5.0E-91	5.0E-91	5.0E-91	4.0E-91	4.0E-91	4.0E-91	1	4.0E-91	4.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	3.0E-91	
	Expression Signal	1.05	0.82	0.82	1.34	1.34	1.3	1.3	3.13		1.67	1.67	5.12	5.12	66.0	0.99	1.77	2.96	2.96	0.83	4.02	1.2	1.2	1.45	2.39	4.11	4.11	4.4	4.4	3.31	1.45	
	ORF SEQ ID NO:	24093	24379	24380	27157	27158	22895	22896	28427		25314	25360	21366	21367	22382	22383	23020		23137		24168	24560	24561	25470		25996		26535	26536		25286	
	Exan SEQ ID NO:	14309	14589	14589	16964	16964	13091	13091	18180		18954	18954	11506	11506	12492	12492	13219	13333	13333	13632	14381	14785	14785	15407	15712	15872	15872	16361	16361	16970	19104	
	Probe SEQ ID NO:	4415	4703	4703	7087	7087	3166	3166	8301		9239	9239	1601	1601	2624	2624	3297	3416	3416	3720	4487	4905	4905	5488	5807	5967	5967	6502	6502	7093	9480	

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Single Exoli Flobes Explessed III near	Top Hit Descriptor	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6	Homo saplens beta-ureidopropionase (BUP1) gene, exon 6	Homo sapiens chromosome 21 segment HS21C084	UI-H-BI3-aks-d-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'	602022088F1 NCL_CGAP_Brn67 Horno sapiens cDNA clone IMAGE:4157804 5'	602022088F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'	ym30e03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:49587 5'	Homo sapiens NKG2D gene, exon 10	Homo sapiens NKG2D gene, exon 10	Human Na+,K+ ATPase alpha-subunit mRNA, partial cds	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA	Homo sapiens NALP1 mRNA, complete cds	Homo sapiens mRNA for KIAA1512 protein, partial cds	Homo sapiens mRNA for KIAA1512 protein, partial cds	Homo sapiens brefeldin A-Inhibited guanlhe nucleotide-exchange protein 2 (BIG2), mRNA	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5	Homo sapiens diacylglycerol khase, gamma (90kD) (DGKG), mRNA	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA	Homo sapiens MCP-4 gene	Human lens membrane protein (mp19) gene, exon 11	Human lens membrane protein (mp19) gene, exon 11	Homo sapiens mRNA for KIAA0611 protein, partial cds	Homo sapiens mRNA for MBNL protein	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds	Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA	Homo equippe fracile Y mental retardation authoromal homology (EYD4) mDMA	There is a Milk beard of after an indicator and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second	Turidar Vol. Williams a secundarie con espanding to exans 23 miougn 54	Homo sapiens mRNA for KIAA0758 protein, partial cds	Homo sapiens mRNA for KIAA0758 protein, partial cds	Homo sapiens cytoplasmic Seprase truncated isoform mRNA, complete cds	Homo sapiens B-cell CLUlymphoma 7b (BCL7B) mRNA
JIO EXON PIO	Top Hit Database Source	TN	IN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	LN	NT	IN	NT	LN	IN	IN	N⊺	EST_HUMAN	EST_HUMAN	NT	⊥N	LN	LN	NT	ΙN	⊥N	LN	F	L	- L	2	LN L	NT	N	N.
Silic	Top Hit Acession No.			1.0E-91 AL163284.2	1.0E-91 AW 449746.1	3F348182.1	3F348182.1	115212.1		3.1		11427149 NT	9.0E-92 AF310105.1	\B040945.1	9.0E-92 AB040945.1	11422086 NT	V26367.1	8.0E-92 BE386363.1	11434722 NT	11434722 NT	8.0E-92 AJ000979.1	L04193.1	.04193.1	\B014511.1	/13829.1	AF074393.1	4503340 NT	T1434704			Ţ.	1.1	4F007822.1	4502384 NT
	Most Similar (Top) Hit BLAST E Value	3.0E-91	3.0E-91	1.0E-91	1.0E-91	1.0E-91 BF348182	1.0E-91 BF348182	1.0E-91 H15212.1	9.0E-92	9.0E-92	9.0E-92 J03007.1	9.0E-92	9.0E-92	9.0E-92 AB04094	9.0E-92	9.0E-92	8.0E-92 W26367.1	8.0E-92	8.0E-92	8.0E-92	8.0E-92	8.0E-92	8.0E-92 L04193.1	8.0E-92 AB01451	8.0E-92	8.0E-92 AF074393	8.0F-92	8 OF 02	7 00 14 60 676 4	1.05-92.1	7.0E-92 /	7.0E-92 AB01830	7.0E-92 AF007822	7.0E-92
	Expression Signal	3.03	3.03	3.02	3.58	1.7	1.7	2.42	8.41	8.41	3.56	1.75	3.22	19.33	19.33	1.66	2.02	5.9	1.29	1.29	1.29	3.61	3.61	2.61	1.31	4.53	3.21	4 43	25.1	2.04	2.51	2.51	1.25	1.91
	ORF SEQ ID NO:	22382	22383	19833	20987	26175	26176		20981	20982	25103	25418	25911	26954	26955	27409	19887	20068	21554	21555	25973	26978	26979	27314	27836	28316	28841					20021		21017
	Exon SEQ ID NO:	12492	12492	10030	11133	16035	16035	19685	11130	11130	15273	15362	15789	16757	16757	17210	10071	10248	11677	11677	15849	16786	16786	17119	17610	18067	18556	10162	20100	10040	_]	[11166
	Probe SEQ ID NO:	9812	9812	42	1225	0609	0609	8626	1221	1221	5353	5442	5882	8789	6878	7342	87	283	1778	1778	5944	8069	8069	7242	7760	8180	8667	0677	2108	20	236	236	929	1259

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Oligie Lyon Flores Lypiessed III Healt	Top Hit Descriptor	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds	Homo sapiens NRAS-related gene (D1S155E), mRNA	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960	int]	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA	zw66d12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781175.5	601283012F1 NIH MGC 44 Homo sapiens cDNA clone IMAGE 3605018 5	601501242F1 NIH MGC 70 Homo saptiens cDNA clone IMAGE:3902939 5	EST91020 Synovial sarcoma Homo sapiens cDNA 5' end similar to similar to ribosomal protein S13	Human mRNA for alpha-actinin	Human mRNA for alpha-actinin	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA	Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA	Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA	601118337F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:3028304 5'	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'	mrg=mas-related [human, Genomic, 2416 nt]	wk27d07.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN:	wk27407.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTFIN	Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
gie LAUI FIOL	Top Hit Database Source	N	N	LN LN	N	NT	IN	LN TN		NT	TN	Z	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	N	L	NT	N	LN L	EST HUMAN	EST_HUMAN	L	EST_HUMAN	EST HUMAN		LN	LN	LN	
5	Top Hit Acession No.	5031570 NT	5031570 NT	7.0E-92 AF167706.1	6005738 NT	7.0E-92 AB031007.1	4507500 NT	4507500 NT		571824.1	S71824.1	4506118 NT	7.0E-92 AA446206.1	5.0E-92 BE390882.1	3.0E-92 BE909714.1	3.0E-92 AA378336.1	K15804.1		4501898 NT	11422946 NT	11422946 NT	2.0E-92 BE299190.1	2.0E-92 BE299190.1	378653.1	20E-92 Al818119.1	2.0E-92 AI818119.1	4506860	6912457 NT	2.0E-92 AF231919.1		5803180 NT
	Most Similar (Top) Hit BLAST E Value	7.0E-92	7.0E-92	7.0E-92	7.0E-92	7.0E-92	7.0E-92	7.0E-92	i i	7.0E-92 S71824.1	7.0E-92	7.0E-92	7.0E-92	5.0E-92	3.0E-92	3.0E-92	3.0E-92 X15804.1	3.0E-92 X15804.1	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	20E-92	2.0E-92	2.0E-92	2.0E-92	20E-92	2.0E-92/	2.0E-92
	Expression Signal	1.67	1.67	2.32	5.01	1.04	0.92	0.92		1.01	1.61	1.45	4.87	0.93	2.45	3.74	5.7	5.7	1.53	2.83	2.93	1.38	1.38	2.74	1.55	1.55	4.71	37.64	1.02	1.02	4.99
	ORF SEQ ID NO:	21923	21924	22283		22481		23024		24165	24166	24752	24836		22494	25575	28281	28282	19803	19958	19959	20497	20498		21667	21668	21787	22381	23265	23266	23332
	Exon SEQ ID NO:	12027	12027	12391	12558	12586	15068	15068	6	143/8	14378	14978	15142	11473	12600	15498	18034	18034	10010	10143	10143	10664	10664	11588	11789	11789	11895	12491	13478	13476	13545
	Probe SEQ ID NO:	2139	2139	2517	2693	2724	3301	3301	7	4484	4484	5110	5219	1569	2738	2283	8146	8146	23	172	172	732	732	1686	1894	1894	2002	2623	3562	3562	3631

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Table 4
Single Exon Probes Expressed in Heart

Top Hit Descriptor	Human endogenous retroviral DNA (4-1), complete retroviral segment	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds	DKFZp434C0414_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0414 5	Homo sapiens mRNA for KIAA1068 protein, partial cds	Human NPY Y1-like receptor pseudogene mRNA, complete cds	hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR::002711 002711 PRO-POL-DUTPASE POLYPROTEIN ;	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA	Homo sapiens mRNA for KIAA1093 protein, partial cds	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	yi80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'	y80e08.r1 Scares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA	tg01b02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE.2107467 3' similar to SW.PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element	MER17 repetitive element ;	tg01b02x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107457 3' similar to SW PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element	MER17 repetitive element;	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'	EST188414 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds. alternatively	spliced	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'	Homo sapiens ribosomal protein L10a (RPL10A), mRNA	601460521F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863908 5'	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens mRNA for KIAA0611 protein, partial cds	wc09c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314670 3'	wc09c08x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314670 3'	Homo sapiens chromosome 21 segment HS21C001	Human skeletal muscle 1.3 kb mRNA for tropomyosin
Top Hit Database Source	H	NT H	EST_HUMAN D	H	H.	EST HUMAN O		H		EST HUMAN y	EST_HUMAN V		<u>ਨ</u>	EST_HUMAN N	21 O	EST_HUMAN N	EST_HUMAN A	EST HIMANI	T	IN LN	EST_HUMAN 6		EST HUMAN 6	H H	I	EST_HUMAN W	HUMAN	H	H
Top Hit Acessian No.		.1	-	2.0E-92 AB028991.1	2.0E-92 U67780.1	2.0E-92 AW340174.1	134900	2.0E-92 AB029016.1	6912457 NT	R78078.1	R78078.1	450668 NT		1.0E-92 AI380356.1	·	1.0E-92 Al380356.1	9.0E-93 AU121681.1	0 0E-03 4 6316723 1		9.0E-93 AF223391.1	9.0E-93 BE388571.1	11418526 NT	8.0E-93 BF036364.1	7.0E-93 AF231919.1	5.0E-93 AB014511.1	5.0E-93 AI674184.1	1	1.2	5.0E-93 X04201.1
Most Similar (Top) Hit BLAST E Value	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	2.0E-92	1.0E-92	1.0E-92	1.0E-92		1.0E-92		1.0E-92	9.0E-93	0.05.03	23	9.0E-93	9.0E-93	9.0E-93	8.0E-93	7.0E-93	5.0E-93	5.0E-93	5.0E-93	5.0E-93	5.0E-93
Expression Signel	1.02	62'0	2.53	2.49	2.25	1.37	5.91	2.55	26.65	1.11	1.11	34.72		4.04		4.04	3.14	0 21		1.46	96.0	9.6	2.49	6.24	1.25	5.39	5.39	0.95	2.42
ORF SEQ ID NO:	23869	24323		26017		27211	28276	25274	22381	21582	21583	21810		27360		27361	21769				23267		26003	20028	21121	21145	21146		22925
Exon SEQ ID NO:	14091	14534	14801	15894	16273	17018	18030	19172	12491	11704	11704	11919		17162		17162	11876	11800		12478	13477	18719	15879	10212	11265	11290	11290		13120
Probe SEQ ID NO:	4191	4648	4922	5989	6420	7141	8142	9589	6886	1807	1807	2028		7286		7286	1983	1006		2610	3563	8911	5975	246	1359	1385	1385	1459	3195

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product	Homo sapiens secretory nathway component Sec31B 4 mDNA alternation.	Homo sapiens TAR (HIV) RNA-hinding profein 1 (TARRE1) mBNA	Homo sapiens nucleobindin 2 (NI ICR2) mRNA	Homo sapiens gamma-glutamytransferase 1 (GGT1), mRNA	2x50e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE.795588 3' similar to SW.CLPA_RAT P37397 CALPONIN, ACIDIC ISOFORM	Homo sapiens interferon gamma recentor 1 (IENCR1) mRNA	Homo sapiens interferon gamma receptor 1 (TENCEA) mBNA	Homo sapiens pescadillo (zehrafish) homokor 1 containing bor 1 containing bor	Homo sapiens pescadillo (zehrafish) homolog 1, containing DDCT 3, mr. (PES 1), mr.NA	Homo sapiens hypothetical protein FI 120734 (FI 120734) TONA	Homo sabiens dystronhin (DMD) gene deletion breakmaints 4.3 in 11.1.	Homo sabiens chromosome 21 segment HC2/C101	Homo sabiens TNF-inducible profess C3224 (CC324) TDNA	Homo sapiens interleukin 18 recentor 1 (II 19R1) mRNA	yb94c12.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP-A44391 A44391 A44391 SEPLIM PESCONISE ELEMENT CALLETTE CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACT	AV692051 GKC Homo sapiens CDNA class CKCDBEA2 5:	602246554F1 NIH MGC 62 Homo saniers cDNA class (MACE: 4322002) E1	602246554F1 NIH MGC 62 Homo sapiens cDNA clone IMAGE:4332030 5	Homo sapiens tensin mRNA, complete cds	th 29g03.x1 NCI CGAP Brn 25 Homo saniens cDNA clone IMA CE 24soa 22.	th 29g03 x1 NCI_CGAP_Brn25 Homo sepiens cDNA clone IMAGE 216g076 3	Homo sapiens GCN5 (general control of amino-acid synthesis	wb02d05 x1 NCI_CGAP_GC6 Home sanians_CDNA_close_cond_cond_cond_cond_cond_cond_cond_cond	Chlorocebus aethiops mRNA for ribosomal profein S4X complete cds	Chlorocebus aethiops mRNA for ribosomal protein S4X complete cds	Homo sapiens chromosome 21 segment HS21C085	Hómo sapiens chromosome 21 segment HS21C085
le Exon Prot	Top Hit Database Source	L	LN.	L		NT	EST HUMAN	Ί.	7	トフ	7	トラ					HUMAN	Т	HUMAN	T	Z	EST HUMAN			EST HUMAN		LN ⊢N		- LN
Sing	Top Hit Acession No.	5.0E-93 AF067136.1	5.0E-93 AF274863.1	32156	11439599 NT	11417877 NT	4.0E-93 AA459933.1	4557879 NT	4557879 NT	7657454 NT	7657454 NT	8923658 NT	F047677.1	2	7656972 NT	4504654 NT		-				1	1	11426182 NT				2	2
	Most Similar (Top) Hit BLAST E Value	5.0E-93	5.0E-93	5.0E-93	5.0E-93	5.0E-93	4.0E-93	4.0E-93	4.0E-93	4.0E-93	4.0E-93	4.0E-93	4.0E-93 AF047677	4.0E-93 AL163301	4.0E-93	4.0E-93	4.0E-93 T46864.1	4.0E-93 AV692051	3.0E-93 B	3.0E-93 B	3.0E-93 AF225896.1	3.0E-93 AI553853.	3.0E-93 AI553853.	3.0E-93	3.0E-93 AI824829.1	2.0E-93 AB015610.1	2.0E-93 A	2.0E-93 AL163285.	2.0E-93 AL163285.
	Expression Signal	3.67	2.07	1.31	3.01	1.84	4.72	1.75	1.75	1.33	1.33	2.08	5.06	0.84	2.18	1.44	4.81	19.24	5.99	5.99	2.7	1.58	1.58	1.32	4.15	8.31	8.31	69.9	7.68
	ORF SEQ ID NO:	26577	27613	27715	28336	25173		20204	20205	20522	20523	20923	21712	22126	22328	23647	25445	28613	23302	23303		25520	25521	25979	28314	19970	19971	20100	20100
	Exon SEQ ID NO:	16398	17400	17494	18085	19423	10066	10381	10381	10685	10685	11078	11829	12229	12435	13869	15385	18348	13515	13515	14042	15452	15452	15857	18066	10155	10155	10282	10282
	Probe SEQ ID NO:	6540	7549	7644	8200	9487	82	437	437	755	755	1166	1934	2349	2564	3962	5465	8475	3601	3601	4142	5535	5535	5952	8178	183	183	320	321

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				0.5'	3.5'			WAGE:3078329 5'	AGE:1929115 3'	IMAGE:503346 3		3.5.				03 3' similar to TR:Q62384 Q62384					A, complete cds	MDNA Commission (10 III	confidence of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of		5.51	5.5			fron E	tron E	sease, Watson disease) (NF1)	
Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens tensin mRNA, complete cds	Human Clk-associated RS cyclophilin CARS-Cyp mRNA, complete cds	601117586F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3358220 5	601116810F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5	EST376458 MAGE resequences, MAGH Homo sapiens cDNA	Homo sapiens hypothetical protein (LOC51318), mRNA	UI-HF-BN0-aks-g-09-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5	qp78b10.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1929115.3	2/29c10.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503346 3	Homo sapiens CYP17 gene, 5' end	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5	Homo sapiens CTR1 pseudogene	Homo sapiens CTR1 pseudogene	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA	oy84b08.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384 ZINC FINGER PROTEIN.;	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA	Homo sapiens mRNA for KIAA1563 protein, partial cds	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds	Homo sapiens long chain polyunsaturated fatty acid elongation of HELOA (NEW 1907)	Homo sapiens MHC class 1 region	Novel human gene mapping to chomosome 1	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens glucocorticoid receptor (GRL) gene, intron D. exon 5. and intron E	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
Jie Exon Prop	Top Hit Database Source	N	N	EST_HUMAN	EST HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	L	EST_HUMAN	LN	LN	L	EST_HUMAN	LN	LN L	NT	NT	NT	LN	NT	LN	EST_HUMAN	HUMAN	TN	N	NT	IN		NT
SIIS	Top Hit Acession No.	2.0E-93 AF225896.1	2.0E-93 U40763.1	2.0E-93 BE252982.1	2.0E-93 BE253201.1	2.0E-93 AW964385.1	11430039 NT	7.	2.0E-93 AI312025.1	5.1	-41825.1	2.0E-93 BF035327.1	1.0E-93 AF238997.1	AF238997.1	7657016 NT	1.0E-93 AI146755.1	387675.1	8923270 NT	8923270 NT	-	1.0E-93 AF167706.1	1.0E-93 AF231981.1	_	1	1.0E-93 BE297369.1	1		1.0E-93 AL163284.2			4557792 NT	11431590 NT
	Most Similar (Top) Hit BLAST E Value	2.0E-93	2.0E-93	2.0E-93	2.0E-93	2.0E-93 /	2.0E-93	2.0E-93 /	2.0E-93	2.0E-93 /	2.0E-93 L41825.1	2.0E-93	1.0E-93 /	1.0E-93	1.0E-93	1.0E-93	1.0E-93 D87675.1	1.0E-93	1.0E-93	1.0E-93 /	1.0E-93 /	1.0E-93/	1.0E-93	1.0E-93	1.0E-93	1.0E-93	1.0E-93 D87675.1	1.0E-93 /	1.0E-93 U78509.1	1.0E-93 U78509.1	1.0E-93	1.0E-93
	Expression Signal	1.48	1.02	0.89	1.02	4.59	1.52	1.32	2.87	1.52	1.31	2.75	1.64	1.64	2.56	3.75	3.32	6.41	6.41	1.55	1.68	1.01	4.16	1.09	2.69	2.69	4.33	1.44	1.62	1.62	9.15	2.08
	ORF SEQ ID NO:	21363	21868	22210	24732	25049	25442		29093				19897	19898	20262	20330	20631	20974	20975	21083	21085	22070	22190		21030	21031	22627	24010	25391	25392	25604	26197
	Exon SEQ ID NO:	11503	11973	12313	14958	15245	15382	15918	19476	19046	19095	19263	10081	10081	10449	10523	10781	11125	11125	11228	11230	12172	12292	12336	11181	11181	12830	14228	15338	15338	15522	16051
	Probe SEQ ID NO:	1598	2083	2436	5088	5325	5462	6014	8996	9386	9465	9724	96	96	209	585	854	1217	1217	1321	1323	2289	2415	2459	2792	2792	2903	4331	5417	5417	5607	2909

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Table 4
Single Exon Probes Expressed in Heart

Top Hit Descriptor	Human mRNA for NF1 N-isoform-exon11, complete cds	Homo sapiens mRNA for KIAA1411 protein, partial cds	1EMD protein	Homo sapiens protein kinase Inhibitor gamma (PKIG) mRNA, complete cds	Homo sapiens mRNA for KIAA1485 protein, partial cds	form mRNA, complete cds	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)	qm03c12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880758 3' similar to WP:T19B4.4 CE13742 ;	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA	some 21 segment HS21C009	Homo sapiens transcription enhancer factor-5 mRNA, complete cds	Homo saplens mitogen-activated protein kinase 12 (MAPK12), mRNA	Homo sapiens mRNA for KIAA0612 protein, partial cds	Homo sapiens mRNA for KIAA0612 protein, partial cds	zg87g06.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409594 3'	ot83d05.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623369 3'	yd98b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:116239 3'	Homo saplens mRNA for KIAA0027 protein, partial cds	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA	Homo sapiens ribosomal protein L27 mRNA, complete cds	Homo sapiens protein phosphalase 1, regulatory subunit 10 (PPP1R10) mRNA	tw1f10.x1 NCI_CGAP_Brin52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE;	Homo sapiens solute carrier family 22 (organic cation transporter), member 1- ike (SLC22A1L), mRNA	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA	Homo saplens hypothetical protein FLJ12455 (FLJ12455), mRNA	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene	Homo sapiens complement component 5 (C5) mRNA	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
	an mRNA for NF1 N-isoform-e)	sapiens mRNA for KIAA1411	H.sapiens mRNA for MEMD protein	o sapiens protein kinase inhibito	sapiens mRNA for KIAA1485	Homo sapiens Trio isoform mRNA, complete cds	an PreA4 gene for Alzheimer's	an PreA4 gene for Alzhelmer's	qm03c12.x1 NCI_CGAP_Lu5 Homo CE13742;	o sapiens glutathione S-transfe	Homo sapiens chromosome 21 segment HS21C009	o sapiens transcription enhance	o saplens mitogen-activated pro	o sapiens mRNA for KIAA0612	o sapiens mRNA for KIAA0612	g06.s1 Soares_fetal_heart_Nb	105.s1 Soares_total_fetus_Nbz	504.s1 Soares fetal liver spleer	o saplens mRNA for KIAA0027	o sapiens cleavage and polyad	o sapiens ribosomal protein L2	o sapiens protein phosphatase	W11f10.x1 NCI_CGAP_Brn52 Homo sap PROTEIN TYROSINE PHOSPHATASE	o sapiens solute carrier family	o sapiens solute carrier family	io saplens hypothetical protein	o sapiens ASH2L gene, compl	o sapiens complement compor	io saplens cysteine-rich repeat-	o sapiens cysteine-rich repeat-
Top Hit Database Source									EST HUMAN CE1							HUMAN		HUMAN					EST_HUMAN_PRC							Hon
Top Hit Acession No.	742072.1 NT	B037832.1 NT		VF182032.1 NT	\B040918.1 NT	\F091395.1 NT	(13474.1 NT	(13474.1 NT	1 0F-93 AI268262 1 ES	417856			11418351 NT	5.0E-94 AB014512.1 NT	5.0E-94 AB014512.1 NT	5.0E-94 AA722434.1 E	-		725217.2 NT	9558724 NT		4506008 NT	4.0E-94 AI591312.1	11440670 NT	11440670 NT	11545792 NT	4B022785.1	4502506 NT	<u>-</u>	3.0E-94 AF167706.1 N
Most Similar (Top) Hit BLAST E	1.0E-93 D42072.1	1.0E-93 AB037832	1.0E-93 Y10183.1	1.0E-93 AF182032	1.0E-93 AB040918	1.0E-93 AF091395	1.0E-93 X13474.1	1.0E-93 X13474.1	1 0F-93 A	1.0E-93	8.0E-94 AL163209	6.0E-94	6.0E-94	5.0E-94	5.0E-94	5.0E-94	5.0E-94 AI015800.	5.0E-94	5.0E-94 D25217.2	5.0E-94	4.0E-94 L05094.1	4.0E-94		4.0E-94	4.0E-94	4.0E-94	3.0E-94,	3.0E-94		
Expression Signal	4.09	2.04	1.18	1.59	1.8	1.22	4.54	4.54	592	2.33	1 22	1.74	1.67	3.05	3.05	1.72	1.63	4.68	1.27	1.26	4.55	0.86	3.02	1.84	1.84	1.72	1.17	1.17	1.05	1.05
ORF SEQ ID NO:	26320		27039		26640	26643			05130			23579	L	25019			26218					22379	24295	25921	25922	28142		L		21478
Exan SEQ ID NO:	16163	16686	16848	16901	16450	16453	17380	17380	10/07	19257			19331		ł	L	16069		19378	19384	11697	12489	14506	15798	15798	17898	1_		11607	11607
Probe SEQ ID NO:	6288	6807	6971	7024	7437	7440	7529	7529	0054	9716	8025	3880	9830	5296	5296	5689	6183	9361	9901	9907	1799	2621	4618	5892	5892	8749	595	704	1706	1706

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Table 4
Single Exon Probes Expressed in Heart

Oligic Even Forces Expressed II Tealt	Most Similar (Top Hit Acession BLASTE No. Source Source	5 3.0E-94 4557556 NT Homo sapiens E1A binding protein p300 (EP300) mRNA	3.0E-94 AA46480	3.0E-94 11496268 NT	5 3.0E-94 11526228 NT Homo sapiens chromosome 21 open reading frame 18 (C210RF18), mRNA	3.0E-94 AF152309.1 NT	3.0E-94 AB014579.1 NT	5 3.0E-94 AF087942.1 NT Homo sapiens glycogenin-1L mRNA, complete cds		3.0E-94 U26711.1 NT	1.0E-94 BE295714.1 EST_HUMAN	1.0E-94 BE253433.1 EST_HUMAN	1.0E-94 BE253433.1 EST_HUMAN	1.0E-94 9506692 NT	1.0E-94 11428710 NT Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAXS), mRNA	1.0E-94 BE780478.1 EST_HUMAN	1.0E-94 U65590.1 NT	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1.0E-84 PAZZZZ44.1 EST HUMAN ASZS43 NEUKAL CELL ADHESION PROTEIN BIG-2 PRECURSOR.;	O DE OF A PENSON 1 NIT	9.0E-95 7662027 NT	9.0E-95 7662027 NT	7 9.0E-95 AF274753.1 NT Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds	8.0E-95 AI700998.1 EST HUMAN	8.0E-95 A1700998.1 EST HUMAN	8.0E-95 11426529 NT	8.0E-95 11426529 NT	8.0E-95 AF032897.1 NT	8.0E-95 11420944 NT	8.0E-95 11420944 NT	
		3.0E-94	3.0E-94 AA4	3.0E-94	3.0E-94	3.0E-94 AF1	3.0E-94 AB0	3.0E-94 AF0	3.0E-94	3.0E-94 U26	1.0E-94 BE2	1.0E-94 BE2		1.0E-94	1.0E-94	1.0E-94 BE7	1.0E-94 U65	10 4	1.0E-94 AIZ/	0.05.05.05	9.0E-95	9.0E-95	9.0E-95 AF2	8.0E-95 AI70	8.0E-95 A170	8.0E-95	8.0E-95	8.0E-95 AF0	8.0E-95	8.0E-95	8.0E-95
	Expression Signal	3.45	0.82	3.58	4.16	1.16	3.79	4.36	1.75	2.27	2.24	1.91	1.91	1.13	1.93	1.41	2.49	Č	4.19	1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1	1.13	1.13	1.87	1.59	1.59	1.83	1.83	2.05	1.73	1.73	2.82
	ORF SEQ ID NO:	21504	5 23772	25466	25909			27596	28580		19937	22769	22770	23938	27439	27707	28546		75001				26869	24119			26315	26837	27515		27744
	Exon SEQ ID NO:	11636	13995	15403	15787	16650	16869	17384		18736	10117	12977	12977	L	17235	17487	18292		10300				16680	14331	14331	16158	16158	16649	17309		17517
	Probe SEQ ID NO:	1735	4095	5484	5881	6771	6992	7533	8448	8928	143	3050	3050	4261	7331	7636	8418	2000	0750	27.00	3118	3118	6801	4436	4436	6294	6294	6770	7391	7391	7667

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Single Exon Probes Expressed in Heart

Top Hit Acession					Most Similar			
17531 2.83 8.0.E-95 AB037816.1 NT 17597 28236 2.41 8.0E-95 AF112152.1 NT 19242 8.68 8.0E-95 AAC28056.1 EST_HUMAN 10240 20058 9.46 7.0E-95 DB7675.1 NT 10240 20059 9.46 7.0E-95 DB7675.1 NT 14169 23047 5.94 7.0E-95 DB7675.1 NT 14213 7.0E-95 DB7675.1 NT NT 14213 7.0E-95 DB7675.1 NT NT 14857 24623 1.06 7.0E-95 MS708.1 NT 14857 25087 1.76 3.0E-95 MS629.1 NT 11529 21387 1.6 2.0E-95 AF50437 NT 11529 21387 1.6 2.0E-95 AF60437 NT 11529 21672 7.79 2.0E-95 AF60437 NT 11529 21672 7.79 2.0E-95 AF60437 NT 12246 22147 1.3 2.0E-95 AF60437 NT	Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Viost Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
17987 28236 2.41 8.0E-95 AF712152.1 NT 19242 8.68 8.0E-95 AA629056.1 EST HUMAN 10240 20059 9.46 7.0E-95 D87675.1 NT 10240 20059 9.46 7.0E-95 D87675.1 NT 14169 23947 5.94 7.0E-95 D87675.1 NT 14213 23947 5.94 7.0E-95 D87675.1 NT 14213 27623 1.03 7.0E-95 AF763246.2 NT 14857 24623 1.76 3.0E-95 BF25041.1 EST HUMAN 11529 21387 1.6 2.0E-95 A504374 NT 11529 21387 1.6 2.0E-95 A504374 NT 11729 2147 1.3 2.0E-95 A504374 NT 11729 2148 1.3 2.0E-95 A53665 NT 12256 22147 1.3 2.0E-95 A53665 NT <t< td=""><td>7681</td><td></td><td></td><td>2.83</td><td></td><td></td><td>NT</td><td>Homo sapiens mRNA for KIAA1395 protein, partial cds</td></t<>	7681			2.83			NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
19242 8 68 8 0E-95 AAGZ9D56.1 EST_HUMAN 10240 20058 9.46 7.0E-95 D87675.1 NT 10240 20059 9.46 7.0E-95 D87675.1 NT 14051 23047 5.94 7.0E-95 D87675.1 NT 14213 7.0E-96 M95708.1 NT NT 14213 7.0E-96 M95708.1 NT NT 16261 25087 1.76 3.0E-95 BFE2604.1 EST_HUMAN 11529 21387 1.6 2.0E-95 A504374 NT 11529 21387 1.6 2.0E-95 A504374 NT 11529 2147 1.3 2.0E-95 A553665 NT 11786 22147 1.3 2.0E-95 A553665 NT 11786 22147 1.3 2.0E-95 A553665 NT 12256 22147 1.3 2.0E-95 A553665 NT 1224 2.0E-95	8096		28236			1	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
19242 8 68 8,0E-95 AA622056.1 EST HUMAN 10240 20058 9,46 7.0E-95 D87675.1 NT 10240 20059 9,46 7.0E-95 D87675.1 NT 10240 20059 9,46 7.0E-95 D87675.1 NT 14163 23947 5.94 7.0E-95 M9508.1 NT 14857 24623 1.03 7.0E-95 M9508.1 NT 14857 24623 1.03 7.0E-95 M95029.1 NT 14857 25084 0.86 2.0E-95 M95029.1 NT 11529 21387 1.6 2.0E-95 M95029.1 NT 11529 21387 1.6 2.0E-95 M95029.1 NT 11529 21387 1.6 2.0E-95 M95029.1 NT 11793 21676 3.3 2.0E-95 M95029.1 NT 12240 22147 1.3 2.0E-95 M95029.1 NT 12256 22147 1.3 2.0E-95 M95029.1 NT 12342 22235 2.46 2.0								ZUB4b01.s1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:744649 3' similar to contains I.1.t1 L1
10240 20058 9.46 7.0E-95 D87675.1 NT 10240 20059 9.46 7.0E-95 M87675.1 NT 10240 20059 9.46 7.0E-95 M87675.1 NT 14163 23947 1.38 7.0E-95 M87675.1 NT 14251 2.4623 1.03 7.0E-95 M85029.1 NT 14857 2.6623 1.03 7.0E-95 M95029.1 NT 11529 2.1387 1.16 2.0E-95 M95029.1 NT 11529 2.1387 1.6 2.0E-95 M95020.1 NT 11529 2.1388 1.6 2.0E-95 M95020.1 NT 11529 2.1388 1.6 2.0E-95 M95020.1 NT 11796 2.1676 3.3 2.0E-95 M95020.1 NT 12256 2.2147 1.3 2.0E-95 M95050.1 NT 12256 2.2147 1.3 2.0E-95 M95050.1 NT 12342 2.2235 2.46 2.0E-95 M95050.1 NT 13045 2.2842 <t< td=""><td>9689</td><td></td><td></td><td></td><td>8.0E-95</td><td>_</td><td>-"</td><td>repetitive element;</td></t<>	9689				8.0E-95	_	-"	repetitive element;
10240 20059 9.46 7.0E-95 D87675.1 NT 14169 23947 5.94 7.0E-95 M95708.1 NT 14169 23947 5.94 7.0E-95 M95708.1 NT 14213 7.0E-95 M95229.1 NT NT 14857 24623 1.76 3.0E-95 BF526041 NT 16261 25087 1.76 2.0E-95 A50374 NT 11529 21387 1.6 2.0E-95 A562027 NT 11750 21672 7.79 2.0E-95 A56365 NT 11750 22147 1.3 2.0E-95 A55365 NT 12256 22148 1.3 2.0E-95 A55365 NT 12240 22247 1.3 2.0E-95 A54365 NT 12256 22148 1.3 2.0E-95 A54365 NT 12256 22147 1.3 2.0E-95 A54365 NT 12256 22148 1.3 2.0E-95 A54365 NT 13045 22242 2.46 2.0E-95 A546365 <	274		20058		7.0E-95		LN	Homo sapiens DNA for amyloid precursor protein, complete cds
14169 23947 5.94 7.0E-96 M95708.1 NT 14213 1.38 7.0E-95 AL163246.2 NT 14857 24623 1.03 7.0E-95 M26329.1 NT 14857 24623 1.03 7.0E-95 M95929.1 NT 16261 25087 1.76 3.0E-95 M56204.1 EST HUMAN 16261 25087 1.76 3.0E-95 M562027 NT 11529 21387 1.6 2.0E-95 M62027 NT 11756 21676 3.3 2.0E-95 M56207 NT 11759 21878 1.6 2.0E-95 M57512 NT 11756 22147 1.3 2.0E-95 M57512 NT 12256 22148 1.3 2.0E-95 M7 A778408 12256 22148 1.3 2.0E-95 M7 A778408 12256 22148 1.3 2.0E-95 M7 A778408 12256 22148 1.3 2.0E-95 M7 A786408 13445 22282 2.46 2.0E-95 M7	274		20059		7.0E-95		ΝT	Homo sapiens DNA for amyloid precursor protein, complete cds
14213 1.38 7.0E-96 AL-163246.2 NT 14857 24623 1.03 7.0E-96 M95929.1 NT 15261 25087 1.76 3.0E-96 BF526041.1 EST_HUMAN 10847 20694 0.86 2.0E-95 T662027 NT 11529 21387 1.6 2.0E-95 T662027 NT 11793 21672 7.79 2.0E-95 T662027 NT 11794 21672 7.79 2.0E-95 T662027 NT 11795 21676 3.3 2.0E-95 T662027 NT 11796 21676 3.3 2.0E-95 T662027 NT 11796 21676 3.3 2.0E-95 T662027 NT 12294 21676 3.3 2.0E-95 T662027 NT 12294 21676 3.3 2.0E-95 T662027 NT 12246 226-95 T662027 NT NT 12246 226-95 T664374 NT NT 13045 22235 246 2.0E-95 T64038 NT	4270		23947	5.94	7.0E-95		TN	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds
14857 24623 1.03 7.0E-95 M95929.1 NT 15261 25087 1.76 3.0E-95 BF526041.1 EST HUMAN 10847 20694 0.86 2.0E-95 4504374 NT 11529 21387 1.6 2.0E-95 7662027 NT 11792 21388 1.6 2.0E-95 7662027 NT 11796 21676 3.3 2.0E-95 7662027 NT 12256 22147 1.3 2.0E-95 5453665 NT 12256 22148 1.3 2.0E-95 5453665 NT 1224 1.3 2.0E-95 5453665 NT 1224 2.2 2.0E-95 5453665 NT 12256 2.2148 1.3 2.0E-95 5453665 NT 1224 2.2 2.0E-95 5453665 NT NT 13045 2.235 2.46 2.0E-95 4504374 NT 13433 2.3232 </td <td>4316</td> <td></td> <td></td> <td>1.38</td> <td>7.0E-95</td> <td>2</td> <td>N⊤</td> <td>Homo saplens chromosome 21 segment HS21C046</td>	4316			1.38	7.0E-95	2	N⊤	Homo saplens chromosome 21 segment HS21C046
15261 25087 1.76 3.0E-95 BF526041.1 EST HUMAN 10847 20694 0.86 2.0E-95 4504374 NT 11529 21387 1.6 2.0E-95 7662027 NT 11792 21388 1.6 2.0E-95 7662027 NT 11796 21676 3.3 2.0E-95 7562027 NT 12256 22147 1.3 2.0E-95 5453665 NT 12256 22148 1.3 2.0E-95 5453665 NT 12294 22148 1.3 2.0E-95 5453665 NT 1224 1.3 2.0E-95 5453665 NT 1224 2.2 2.46 2.0E-95 5453665 NT 1224 2.2 2.46 2.0E-95 5453665 NT 13045 2.2842 3.51 2.0E-95 4504374 NT 13433 2.3232 2.78 2.0E-95 4504374 NT 13433 </td <td>4982</td> <td></td> <td>24623</td> <td>1.03</td> <td>7.0E-95</td> <td></td> <td>LN L</td> <td>Human homeobox protein (PHOX1) mRNA, 3' end</td>	4982		24623	1.03	7.0E-95		LN L	Human homeobox protein (PHOX1) mRNA, 3' end
10847 20694 0.86 2.0E-95 4504374 NT 11529 21387 1.6 2.0E-95 7662027 NT 11529 21388 1.6 2.0E-95 7662027 NT 11793 21672 7.79 2.0E-95 4507512 NT 11796 21676 3.3 2.0E-95 8E393873.1 EST HUMAN 12256 22147 1.3 2.0E-95 8453665 NT 12256 22148 1.3 2.0E-95 8453665 NT 1226 22148 1.3 2.0E-95 8453665 NT 12242 2.46 2.0E-95 8453665 NT 13045 22235 2.46 2.0E-95 4504374 NT 13045 22235 2.78 2.0E-95 4504374 NT 13433 23232 2.78 2.0E-95 AF015462.1 NT 13479 23268 0.96 2.0E-95 AB037807.1 NT 14163 23390 1.02 2.0E-95 AB037807.1 EST HUMAN <td< td=""><td>5340</td><td></td><td>25087</td><td>1.76</td><td>3.0E-95</td><td>BF526041.1</td><td>EST_HUMAN</td><td>602071146F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214147 5'</td></td<>	5340		25087	1.76	3.0E-95	BF526041.1	EST_HUMAN	602071146F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214147 5'
11629 21387 1.6 2.0E-95 7662027 NT 11529 21388 1.6 2.0E-95 7662027 NT 11796 21676 3.3 2.0E-95 4507512 NT 12256 22147 1.3 2.0E-95 8E393873.1 EST HUMAN 12256 22148 1.3 2.0E-95 5453665 NT 12256 22148 1.3 2.0E-95 5453665 NT 12256 22148 1.3 2.0E-95 456423 NT 12342 22235 2.46 2.0E-95 4564374 NT 13045 22235 2.78 2.0E-95 4504374 NT 13045 22233 2.78 2.0E-95 4504374 NT 13479 23268 0.96 2.0E-95 AB037807.1 NT 14403 23269 1.02 2.0E-95 AB037807.1 NT 14846 24615 2.57 2.0E-95 AA447931.1 EST HUMAN<	922	L	20694	98.0	2.0E-95		N	Homo sapiens H factor 1 (complement) (HF1) mRNA
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11793 2.0E-95 4507512 NT 11796 2.0F-95 BE393873.1 EST HUMAN 12256 22147 1.3 2.0E-95 BE393873.1 EST HUMAN 12256 22147 1.3 2.0E-95 5453665 NT 12256 22148 1.3 2.0E-95 5453665 NT 12342 22236 2.46 2.0E-95 476423 NT 10846 20693 0.86 2.0E-95 4564374 NT 13045 22842 3.51 2.0E-95 4504374 NT 13433 23232 2.78 2.0E-95 AF015452.1 NT 13479 23268 0.96 2.0E-95 AF015452.1 NT 14163 23240 1.02 2.0E-95 AR037807.1 NT 14846 24615 2.57 2.0E-95 AA447931.1 EST HUMAN 14895 24663 0.98 2.0E-95 AA447931.1 EST HUMAN 15287 2512	1625		21388		2.0E-95	7	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
11793 21672 7.79 2.0E-95 BE393873.1 EST_HUMAN 11796 21676 3.3 2.0E-95 BE393873.1 EST_HUMAN 12256 22147 1.3 2.0E-95 5453665 NT 12256 22148 1.3 2.0E-95 5453665 NT 12242 22191 16.55 2.0E-95 4758423 NT 10846 20693 0.86 2.0E-95 4564374 NT 13045 22842 3.51 2.0E-95 4564374 NT 13433 23232 2.78 2.0E-95 4504374 NT 13479 23268 0.96 2.0E-95 4504374 NT 13479 23268 0.96 2.0E-95 AR037807.1 NT 14846 23390 1.02 2.0E-95 AR447931.1 EST_HUMAN 14846 24663 0.98 2.0E-95 AA447931.1 EST_HUMAN 14895 24664 0.98 2.0E-95 AA447	İ							Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3)
11796 21676 3.3 2.0E-95 BE393873.1 EST HUMAN 12256 22147 1.3 2.0E-95 5453665 NT 12256 22148 1.3 2.0E-95 5453665 NT 12294 22191 16.55 2.0E-95 4758423 NT 12342 22235 2.46 2.0E-95 4758423 NT 13045 22842 3.51 2.0E-95 4504374 NT 13045 22842 3.51 2.0E-95 4504374 NT 13433 23233 2.78 2.0E-95 4504374 NT 13479 23268 0.96 2.0E-95 7705900 NT 14163 23268 0.96 2.0E-95 AR037807.1 NT 14846 24615 2.3 2.0E-95 AR447931.1 EST HUMAN 14895 24663 0.98 2.0E-95 AA447931.1 EST HUMAN 15287 25121 3.69 2.0E-95 AA447931.1	1897				2.0E-95	4507512	NT	mRNA
12256 22147 1.3 2.0E-95 5453665 NT 12256 22148 1.3 2.0E-95 5453665 NT 12294 22191 16.55 2.0E-95 4758423 NT 12342 22235 2.46 2.0E-95 4758423 NT 13045 22842 3.51 2.0E-95 4504374 NT 13045 22842 3.51 2.0E-95 4504374 NT 13433 23233 2.78 2.0E-95 7705900 NT 13479 23268 0.96 2.0E-95 770590 NT 144163 23268 0.96 2.0E-95 AR037807.1 NT 14846 24615 2.57 2.0E-95 AR447931.1 EST HUMAN 14895 24663 0.98 2.0E-95 AA447931.1 EST HUMAN 15287 2569 2.0E-95 AA447931.1 EST HUMAN 15287 2569 2.0E-95 AA447931.1 EST HUMAN <tr< td=""><td>1900</td><td></td><td>21676</td><td></td><td>2.0E-95</td><td>BE393873.1</td><td>_</td><td>601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5</td></tr<>	1900		21676		2.0E-95	BE393873.1	_	601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5
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12294 22191 16.55 2.0E-95 AF240786.1 NT 12342 22235 2.46 2.0E-95 4758423 NT 10846 20693 0.86 2.0E-95 4504374 NT 13045 22842 3.51 2.0E-95 4504374 NT 13433 22332 2.78 2.0E-95 7705900 NT 13479 23268 0.96 2.0E-95 770590 NT 14163 23360 1.02 2.0E-95 AR30284.1 EST_HUMAN 14896 24615 2.57 2.0E-95 AA447931.1 EST_HUMAN 14895 24664 0.98 2.0E-95 AA447931.1 EST_HUMAN 15287 25121 3.69 2.0E-95 AA447931.1 EST_HUMAN 15287 25122 3.69 2.0E-95 AA447931.1 EST_HUMAN	2376		22148		2.0E-95		NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
12342 22355 2.46 2.0E-95 4758423 NT 10846 20693 0.86 2.0E-95 4504374 NT 13045 22842 3.51 2.0E-95 4504374 NT 13433 23232 2.78 2.0E-95 7705900 NT 13479 23268 0.96 2.0E-95 770590 NT 13604 23390 1.02 2.0E-95 AR037807.1 NT 14163 23340 2.3 2.0E-95 AR290264.1 EST HUMAN 14896 24615 2.57 2.0E-95 AA447931.1 EST HUMAN 14895 24664 0.98 2.0E-95 AA447931.1 EST HUMAN 15287 25121 3.69 2.0E-95 AA447931.1 EST HUMAN 15287 25121 3.69 2.0E-95 AA447931.1 EST HUMAN	2417		22191	16.55	2.0E-95		L L	Homo saplens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GST11) genes, complete cds
10846 20693 0.86 2.0E-95 4504374 NT 13045 22842 3.51 2.0E-95 AF015452.1 NT 13433 23232 2.78 2.0E-95 7705900 NT 13479 23268 0.96 2.0E-95 AR37807.1 NT 13604 23390 1.02 2.0E-95 AR30284.1 EST_HUMAN 14163 23940 2.3 2.0E-95 A61290284.1 EST_HUMAN 14896 24615 2.57 2.0E-95 AA447931.1 EST_HUMAN 14895 24664 0.98 2.0E-95 AA447931.1 EST_HUMAN 15287 25121 3.69 2.0E-95 AA447931.1 EST_HUMAN 15287 25122 3.69 2.0E-95 A705764 NT	2466		22235		2.0E-95		N	Homo sapiens glycine cleavage system protein H (aminomothyl carrier) (GCSH) mRNA
13045 22842 3.51 2.0E-95 AF015452.1 NT 13433 23232 2.78 2.0E-95 7705900 NT 13479 23268 0.96 2.0E-95 AB037807.1 NT 13604 23360 1.02 2.0E-95 AB037807.1 NT 14163 23360 1.02 2.0E-95 AB037807.1 NT 14846 24615 2.57 2.0E-95 AA447931.1 EST_HUMAN 14895 24663 0.96 2.0E-95 AA447931.1 EST_HUMAN 14896 24664 0.98 2.0E-95 AA447931.1 EST_HUMAN 15287 25121 3.69 2.0E-95 AA447931.1 EST_HUMAN 15287 25122 3.69 2.0E-95 AA447931.1 EST_HUMAN	2787		20693	;	2.0E-95		NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
13433 23232 2.78 2.0E-95 7705900 NT 13473 23233 2.78 2.0E-95 AB037807.1 NT 13479 23268 0.96 2.0E-95 AB037807.1 NT 14163 23390 1.02 2.0E-95 AR290284.1 EST HUMAN 14846 24615 2.57 2.0E-95 7661979 NT 14895 24663 0.98 2.0E-95 AA447931.1 EST HUMAN 14895 24664 0.98 2.0E-95 AA447931.1 EST HUMAN 15287 25121 3.69 2.0E-95 AA447931.1 EST HUMAN 15287 25122 3.69 2.0E-95 AA447931.1 EST HUMAN	3120		22842	3.51	2.0E-95	1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
13433 23233 2.78 2.0E-95 7705900 NT 13479 23268 0.96 2.0E-95 AB037807.1 NT 13604 23390 1.02 2.0E-95 AR290284.1 EST_HUMAN 14846 24615 2.57 2.0E-95 7661979 NT 14895 24663 0.98 2.0E-95 AA447931.1 EST_HUMAN 14896 2564 0.98 2.0E-95 AA447931.1 EST_HUMAN 15287 25121 3.69 2.0E-95 AA447931.1 EST_HUMAN 15287 25122 3.69 2.0E-95 AA447931.1 EST_HUMAN	3517	_	23232	2.78	2.0E-95		NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
13604 23268 0.96 2.0E-95 AB037807.1 NT 13604 23390 1.02 2.0E-95 AI290264.1 EST HUMAN 14163 23940 2.3 2.0E-95 A7290264.1 EST HUMAN 14846 24615 2.57 2.0E-95 A747931.1 T661979 NT 14895 24663 0.98 2.0E-95 AA447931.1 EST HUMAN 15287 25121 3.69 2.0E-95 AA447931.1 EST HUMAN 15287 25122 3.69 2.0E-95 A7705764 NT	3517		23233			7	L	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
13604 23390 1.02 2.0E-95 AI290284.1 EST HUMAN 14163 23940 2.3 2.0E-95 7657185 NT 14846 24615 2.57 2.0E-95 7661979 NT 14895 24663 0.98 2.0E-95 AA447931.1 EST HUMAN 14895 24664 0.98 2.0E-95 AA447931.1 EST HUMAN 15287 25121 3.69 2.0E-95 AA447931.1 EST HUMAN 15287 25122 3.69 2.0E-95 AA447931.1 EST HUMAN	3565		23268		2.0E-95	11	LΝ	Homo sapiens mRNA for KIAA1386 protein, partial cds
14163 23940 2.3 2.0E-95 7657185 NT Homo sapiens hypothetical protein (HS322B1A), mRNA 14846 24615 2.57 2.0E-95 7661979 NT Homo sapiens KIAA0187 gene product (KIAA0187), mRNA 14895 24663 0.98 2.0E-95 AA447931.1 EST HUMAN zx14d07.11 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 14895 24664 0.98 2.0E-95 AA447931.1 EST HUMAN zx11d07.11 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 15287 25121 3.69 2.0E-95 AA447931.1 Homo sapiens CGI-48 protein (LOC51096), mRNA 15287 25122 3.69 2.0E-95 7705764 NT Homo sapiens CGI-48 protein (LOC51096), mRNA	3690		23390		2.0E-95	ν-	EST HUMAN	qm01c02.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7 4 CE03705;
14896 24615 2.57 2.0E-95 7661979 NT Homo sapiens KIAA0187 gene product (KIAA0187), mRNA 14895 24663 0.98 2.0E-95 AA447931.1 EST HUMAN zx11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 14895 24664 0.98 2.0E-95 AA447931.1 EST HUMAN zx11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 15287 25121 3.69 2.0E-95 AA447931.1 Homo sapiens CGI-48 protein (LOC51096), mRNA 15287 25122 3.69 2.0E-95 7705764 NT Homo sapiens CGI-48 protein (LOC51096), mRNA	4264	1	23940		2.0E-95	7657185	N	Homo sapiens hypothetical protein (HS322B1A), mRNA
14895 24663 0.98 2.0E-95 AA447931.1 EST_HUMAN zx11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 14895 24664 0.98 2.0E-95 AA447931.1 EST_HUMAN zx11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 15287 25121 3.69 2.0E-95 AA447931.1 Homo sapiens CGI-48 protein (LOC51096), mRNA 15287 25122 3.69 2.0E-95 7705764 NT Homo sapiens CGI-48 protein (LOC51096), mRNA	4971		24615		2.0E-95	1	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
14895 24664 0.98 2.0E-95 A4447931.1 EST_HUMAN x11407.r1 Soares_total_fetus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:786157 15287 25121 3.69 2.0E-95 7705764 NT Homo saplens CGI-48 protein (LOC51096), mRNA 15287 25122 3.69 2.0E-95 7705764 NT Homo saplens CGI-48 protein (LOC51096), mRNA	5022	L	24663	0.98	2.0E-95	AA447931.1		
15287 25121 3.69 2.0E-95 7705764 NT 15287 25122 3.69 2.0E-95 7705764 NT	5022		24664			<u>-</u> -		zx11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5
15287 25122 3.69 2.0E-95 7705764 NT	5367		25121	3.69		7	TN	Homo sapiens CGI-48 protein (LOC51096), mRNA
	5367	`	25122	3.69	2.0E-95	7	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA

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Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in realt	Most Similar Top Hit Acession (Top) Hit Acession Signal BLASTE No. Signal Value	25748 4.54 2.0E-95 M59724.1 NT Human muscle-type phosphofructokinase (PFK-M) gene, exon 7	25984 2.0E-95 AF257737.1 NT Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	26179 1.62 2.0E-95 11435773 NT Homo sapiens huntingtin (Huntington disease) (HD), mRNA	28245 2.36	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	25211 4.34 2.0E-95 11418164 NT	25427 7.73	25428 7.73 1.0E-95 AA284651.1	26460 4.85 1.0E-95 BF370000.1	26461 4.85 1.0E-95 BF370000.1	26835 1.67 9.0E-96 BE897259.1 EST_HUMAN	20201 0.82 8.0E-96 BE907607.1 EST HUMAN	20202 0.82 8.0E-96 BE907607.1 EST_HUMAN	2.66 8.0E-96 AW836047.1	23538 0.95 7.0E-96 AF231920.1 NT	22003 0.85 6.0E-96 BE171984.1 EST_HUMAN	22997 0.96 6.0E-96 AL163201.2 NT	F 23159 26.15 6.0E-96 M26873.1 NT Human glyceraldehydre-3-phosphate dehydrogenase pseudogene 3'end	1.98 6.0E-96 7662289 NT Homo sapiens KIAA0763 gene product (KIAA0763), mRNA	28928 1.98 6.0E-96 7662289 NT	28972 2.09 6.0E-96 8923939 NT	20096 2.7 5.0E-96 AB032998.1	20599 3.06 5.0E-96 AB032998.1 NT	20600 3.06 5.0E-96 AB032998.1 NT	2.31 5.0E-96 11416767 NT Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA	22713 0.98 5.0E-96 6912735 NT	1.22	26193 4.23 5.0E-96 11424399 NT	26194 4.23 5.0E-96 11424399 NT	26788 1.81 5.0E-96 M68347.1 NT	26789
	ORF SEQ ID NO:																							20599	20600							
	Exon D SEQ ID NO:	15642	15862	55 16038		19084		}			L	37 16646	435 12666	435 12666	15302	13746		76 13197		18644	18644	70 18682	10279	824 10751	824 10751	76 12447	12919	14694	35 16048	35 16048		16599
	Probe SEQ ID NO:	5734	5957	6055	8106	9452	9840	5450	5450	6437	6437	29/9	4	4	5383	3834	2213	3276	3437	8831	8831	8870	317	80	ω,	2576	2991	4810	6065	6065	6719	6719

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Table 4
Single Exon Probes Expressed in Heart

		1	7	Т	\neg	7	Т	7	\neg	Т	Т	Т	\neg		_	1	-		-			-		T		- +		-+	-				
Single Exon Probes Expressed in Heart	Top Hit Descriptor	W87h12r1 Sogres fefal liver spleen 1NFI S Homo capions only along 1990 Cases Fr	Homo sepiens chondroitin sulfate protections a 4 (melanome accorded) (10000)	Homo sapiens chromosome 21 segment HS21C048	RC3-HT0230-040500-110-a02 HT0230 Homo saniens cDNA	AV689461 GKC Homo sapiens cDNA clone GKCFMDn7 5'	2819351.5prime NIH MGC 7 Homo saniens cDNA clane IMAGE: 2819345 51	Human endogenous retrovirus type K (HERV-K), deg nol and env genes	EST367124 MAGE reseguences. MAGC Homo sanians CDNA	EST367124 MAGE resequences. MAGC Homo sanians CONA	Homo sapiens flavin containing monoxymenase 2 /FMO3) mPNA	Homo sapiens flavin containing monoxymenase 2 (FMAO2) mRNA	Human hebatocyte growth factor gene evon 1	Human hepatocyte growth factor gene expn 1	Felis catus superfast myosin heavy chain (sMvHC) mRNA complete cdc	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterese 3 (H. sapiens) (LOC63214), mRNA		Homo sapiens secretory pathway component Sec31B-1 mRNA alternatively enlined	Homo sapiens mRNA for KIAA1290 protein, partial cds	Homo sapiens mRNA for KIAA1250 protein partial cds	601863712F1 NIH MGC 57 Homo sapiens cDNA clone IMAGF 4081202 5	L5-HT0117-011099-004-D07 HT0117 Homo sapiens cDNA	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5	zv97e12.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' sImilar to TR:G1304125 G1304125 PMS4 MRNA	RC0-BT0812-250900-032-a09 BT0812 Home seniers cONA	MR0-HT0241-150500-010-b02 HT0241 Homo sanisans cONA	MR0-HT0241-150500-010-h07 HT0241 Home sapiens CDNA	CM0-BN0106-170300-293-e06 BN0106 Homo seniens CDNA	Homo sapiens brefeldin A-inhibited quantipe nucleotide exchange motoring 2 (2) 200	Homo sapiens mRNA for GalNac alpha-2 Residultransferase I Inne form	Homo sapiens mRNA for GalNAc aloha-2. A statytransferase I hand form	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncorrene homolog (SBC) (SBC)	Homo sapiens mRNA for KIAA0594 protein, partial cds
gle Exon Pro	Top Hit Database Source	EST HUMAN	Ί.	IN	EST HUMAN	EST HUMAN	EST HUMAN	NT	EST HUMAN	EST HUMAN	N	N	LN	N	F			LX.	NT	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	Т	T HUMAN					
Sin	Top Hit Acession No.	H68656.1	4503098 NT		BE148074.1	AV689461.1	2.0E-96 AW249440.1		1.0E-96 AW955054.1	1.0E-96 AW955054.1	3756	4503756 NT	1	-	2	11419429 NT		1.0E-96 AF274863.1	6.1			9.1	4.2	5.0E-97 AA418026.1					5453572	Y11339.2	Y11339.2	11421793	4.0E-97 AB011166.1 NT
	Most Similar (Top) Hit BLAST E Value	3.0E-96 H68656	2.0E-96	2.0E-96 AL16324	2.0E-96 BE1480	2.0E-96 AV68946	2.0E-96	1.0E-96 Y18890.	1.0E-96	1.0E-96 /	1.0E-96	1.0E-96	1.0E-96 M75967	1.0E-96 M75967	1.0E-96 U51472.	1.0E-96		1.0E-96	1.0E-96 AB03311	1.0E-96 AB03311	6.0E-97	6.0E-97	5.0E-97 AL04331	5.0E-97	5.0E-97 BF15491	5.0E-97	5.0E-97	4.0E-97 B	4.0E-97	4.0E-97 Y	4.0E-97 Y	4.0E-97	4.0E-97
	Expression Signal	6.22	3.49	1.56	1.58	5.08	2.05	1.69	2.03	2.03	0.89	0.89	1.33	1.33	1.88	20.65		1.98	1.64	1.64	0.95	2.75	1.76	10.79	2.76	1.87	1.87	1.26	1.08	6.1	6.1	1.41	1.17
	ORF SEQ ID NO:			20494	24326			20408	21510	21511	21580	21581	21969	21970	22009	27125		27208	27938	27939	23006		26747	26804	27643	28929	28930	20697	21638	26167	26168	26939	27433
	Exon SEQ ID NO:	13997	10355	10662	14537	17068	18902	10590	11643	11643	11703	11703	12068	12068	12650	16935		17015	17693	17693	13206	16319	16552	16614	17429	18645	18645	10849	11764	16027	16027	16746	17232
	Probe SEQ ID NO:	4097	409	730	4651	7191	9151	655	1742	1742	1806	1806	2181	2181	2219	7058		7138	7843	7843	3285	6429	6672	6735	7578	8832	8832	924	1868	6082	6082	2989	7328

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Single Exon Probes Expressed in Heart

Oligie Lyon Flores Lypressed III leaf	Top Hit Acession Top Hit Descriptor Top Hit Descriptor Source	4.0E-97 AB011166.1 NT Homo sapiens mRNA for KIAA0594 protein, partial cds	E-97 11863122 NT Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA	11863122 NT	4.0E-97 AB042557.1 NT Homo sapiens mRNA, similar to rat myomegalin, complete cds	4.0E-97 AB033116.1 NT Homo sapiens mRNA for KIAA1290 protein, partial cds	, L	4.0E-97 11418318 NT Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA	3.0E-97 AB032998.1 NT Homo sapiens mRNA for KIAA1172 protein, partial cds	E-97 4502166 NT Homo sapiens amyloid beta (A4) precursor protein (protease nexin-li, Alzheimer disease) (APP), mRNA	4502166 NT	4758813 NT	U36255.1 NT	5174478 NT	E-97 4503470 NT Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	1.0E-97 BE566486.1 EST_HUMAN 601339520F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3881821 5:	11427757 NT	E-97 11427757 NT Homo sapiens KIAA0649 gene product (KIAA0649), mRNA	AA5537	11426272 NT	11426272 NT	BE090973.1 EST_HUMAN		4758119 NT	E-98 4758119 NT Homo sapiens death-associated protein (DAP), mRNA	X06989.1 NT	11321580 NT	TN	NT	LN	EST_HUMAN	AB033768.1 NT	5031810 NT
Single CANI			11863122 NT	11863122 NT	7.1			11418318 NT		4502166 NT	4502166 NT	4758813 NT		5174478 NT	4503470 NT	=566486.1 EST_HUMA	11427757 NT	11427757 NT	.1 EST	11426272 NT	6272		8393092 NT	4758119 NT	4758119 NT		11321580 NT						5031810 NT
	Most Similar (Top) Hit BLAST E Value	4.0E-97 AF	4.0E-97	4.0E-97						3.0E-97		3.0E-97		3.0E-97	1.0E-97		1.0E-97	1.0E-97		1.0E-97	1.0E-97	9.0E-98 BE	9.0E-98	9.0E-98	9.0E-98	9.0E-98 X0	9.0E-98	9.0E-98 AE	9.0E-98 AE	9.0E-98 AE	9.0E-98 BE	8.0E-98 AE	8.0E-98
	Expression	1.17	1.76	1.76	15.68		2.31	3.83	1.17	10.96	10.96	1.77	1.92	1.14	12.55	219					13.5		1.29	4.74				1.39					1.04
	ORF SEQ ID NO:	27434	28641	28642	28124	28128	28129		20026	20633	20634	21195	22161	22948		25897																	21303
	Exon SEQ ID NO:	17232	18376	18376	17882	17885	17885	19012	10210	10783	10783	12694	12652	13147	14556	15778				17912	17912	10809	11162	16503	16503					_		11256	11444
	Probe SEQ ID NO:	7328	8503	8503	8733	8736	8736	9331	243	856	856	1423	2389	3223	4670	5872	8088	8088	8629	8763	8763	883	1255	6623	6623	7271	7319	7355	8369	8369	9345	1350	1540

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Single Exon Probes Expressed in Heart

		Т	Т	Т		Т	Т	_	1	-	Т	Т	_		-	\neg		_		_	÷			_		_		_	_						
Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens IL2-inducible T-cell kinase (ITK) mRNA	Homo sapiens PMS2L16 mRNA partial cds	Homo saplens PMS2L16 mRNA, partial cds	Human mitochondrial creatine kinase (CKMT) gene, complete cds	Homo saplens chromosome 21 segment HS21C001	H68f02.x NC CGAP Lu24 Homo saniens cDNA clone IMAGE:3151803.3	AJ403124 3.4 (downregulated in larvinx carcinoma) Homo sapiens CDNA close is	Homo sapiens mRNA for KIAA0707 protein narfial cds	7818H01 Chromosome 7 Fetal Brain cDNA Library Homo saniens cDNA class 2848H01	Homo sapiens activator of S phase kinase (ASK) mRNA	Homo sapiens activator of S ohase kinase (ASK) mRNA	vo17d09.r1 Soares adult brain N2h5HR55V Home sanians cDNA close MACE area of ri	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sanians CONA clans in	AJ403124 3.4 (downrequiated in larux carcinoma) Home canions child state to	Old High Colored Carlotter (All Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carlotter Carl	Human fumarase precursor (FH) mRNA, nuclear gene encoding mitrochondrial protein	Homo sapiens Ran GTPase activating protein 1 (RANGAP1) mRNA	601172658F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE 3528137 E	Homo saplens chromosome 21 segment HS21 Cnn2	Homo sapiens polassium channel subunit (HFRC-3) mRNA complete ode	Homo sapiens fath-acid-Coenzyme A ligase, long-chain 4 (FACI 4) mRNA	Homo saplens attractin precursor (ATRN) gene, exon 16	Homo sapiens attractin precursor (ATRN) gene, exon 16	Homo sapiens low density lipoprotein receptor related protein-deleted in tringr (I RDDIT)	Homo sapiens low density lipoprotein receptor related protein-deleted in turnor (I RPDIT) mRNA	Homo sapiens protein tyrosine kinase 2 beta (PTK2B) mRNA	Homo sapiens PDZ domain-containing quanine nucleotide exchange factor 1710054735)	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA	H.sapiens arginase gene exon 3 (EC 3.5.3.1)	Homo sapiens AIM-1 protein (LOC51151) mRNA	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3) mRNA	W36b04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN 23A	
gie Exon Pro	Top Hit Database Source	N	F	LN	NT	NT	EST HUMAN	EST HUMAN	F	EST_HUMAN	1	LN	EST HUMAN	EST HUMAN	EST HUMAN		NT	NT	EST HUMAN	LN LN	N.	F	N	IN	F	N F	卜	TN	L	NT	IN	L	FZ	EST HUMAN	
uio	Top Hit Acession No.	5031810 NT	8.0E-98 AB017007.1	8.0E-98 AB017007.1	J04469.1	8.0E-98 AL163201.2	4.0E-98 BE348727.1	3.0E-98 AJ403124.1	3.0E-98 AB014607.1	3.0E-98 AA077498.1	11419210 NT	. 11419210 NT	_	3.0E-98 AJ403124.1			1	11418177 NT	2.0E-98 BE294281.1			8331	2.1	2.1	9055269 NT	9055269 NT	4758975 NT	7706512 NT	11428813 NT	1428813		7705868 NT	11435947 NT	5	
	Most Similar (Top) Hit BLAST E Value	8.0E-98	8.0E-98	8.0E-98	8.0E-98 J04469.	8.0E-98	4.0E-98	3.0E-98	3.0E-98	3.0E-98	3.0E-98	3.0E-98	3.0E-98 H46698.	3.0E-98	3.0E-98		3.0E-98 U59309.	3.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98 AF21890	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98 X12664.1	2.0E-98	2.0E-98	1.0E-98 AI862007	
	Expression Signal	1.04	96.0	96.0	5.03	0.88	1.29	1.21	1.85	2.09	1.7	1.7	3.31	1.6	1.6		5.15	2.47	29.05	1.45	96.0	4.94	1.51	1.51	6.39	6:38	1.09	4.66	3.87	3.87	1.5	1.18	1.43	18.93	
	ORF SEQ ID NO:	21304	21468	21469	23424		25220	21917	22329		26159	26160	27153	27759	27760		28448		21816	21983	23880	23916	24390	24391	24711	24712	24795	25028	27073	27074	27572		25301	20172	
	Exon SEQ ID NO:	11444	11597	11597		14921	19258	12019	12436	12582	16020	16020	16960	17535	17535		18199	19373	11924	12078	14099	14143	14606	14606	14939	14939	15029	15224	16881	16881	17367	17801	19026	10345	
	Probe SEQ ID NO:	1540	1695	1695	3726	5049	9717	2131	2565	2720	6147	6147	7083	7685	7685		8322	9895	2033	2191	4199	4244	4720	4720	2069	2069	5163	5303	7004	7004	7497	7951	9350	399	

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Table 4
Single Exon Probes Expressed in Heart

	Top Hit Descriptor	PM0-BN0065-100300-001-c06 EN0065 Homo sapiens cDNA	y23f05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243585 5' slmllar to PIR:S54204 S54204 ribosomal protein L29 - human ;	zp98c09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G806562	Homo captane, bata tributin mDNA complete ede	Homo sapients bate tribulin mRMA complete cus	EST380711 MAGE reseguences. MAGJ Homo sapiens cDNA	tm69h07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BID_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONIST.	tm89h07x1 NCI_CGAP_Brn25 Homo saptens cDNA clone IMAGE:2163421 3' similar to SW.BID_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONIST;	zn90d02.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565443 5' similar to TR:0662994 G662994 GPI-ANCHORED PROTEIN P137.;	Human endogenous retrovirus, complete genome	Homo sapiens oscillin (hLn) gene, exon 5	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA	Homo saplens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA	EST388473 MAGE resequences, MAGN Homo sapiens cDNA	Homo sapiens CD34 antigen (CD34) mRNA	Homo saplens polycystic kidney disease (PKD1) gene, exons 27-30	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30	H.sapiens mRNA for estrogen receptor	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds	Homo sapiens lodestar protein mRNA, complete cds	Homo sapiens lodestar protein mRNA, complete cds	Homo sapiens BH3 interacting domain death agonist (BID), mRNA	Human protein C inhibitor (PCI-B) mRNA, complete cds	Human protein C inhibitor (PCI-B) mRNA, complete cds	H.sapiens IMPA gene, exon 8	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA	601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'
	Top Hit Database Source	EST_HUMAN P	EST_HUMAN P	1444			T HUMAN	HUMAN					H			EST_HUMAN E		NT H	H H			H IN	NT H		H IN	NT H	H IN			EST_HUMAN 6
2	Top Hit Acession No.	1.0E-98 AW998611.1	1.0E-98 N49818.1		1.0E-90 AA 193034.1				+	-	5487	7.0E-99 AF035808.1	7.0E-99 AF001886.1	11430555 NT	11430555 NT	6.0E-99 AW976364.1	4502660 NT					6.0E-99 AF080255.1	6.0E-99 AF080255.1	11526299 NT				5.0E-99 AF009660.1	1758697	5.0E-99 BE890177.1
	Most Similar (Top) Hit BLAST E Value	1.0E-98	1.0E-98	0 7	00-00	1.0E-90	9.E-99	9.0E-99	9.0E-99	9.0E-99	8.0E-99	7.0E-99	7.0E-99	6.0E-99	6.0E-99	6.0E-99	6.0E-99	6.0E-99 L43610.1	6.0E-99 L43610.1	6.0E-99 X99101.1	6.0E-99	6.0E-99	6.0E-99	6.0E-99	5.0E-99	5.0E-99	5.0E-99	5.0E-99	5.0E-99	5.0E-99
	Expression Signal	2.38	16.96	9	0.30	1.30	82.4	2.6	2.6	1.84	1.19	9.2	2,31	0.93	0.93	1.87	1.16	2.36	2.36	1.21	2.18	3.57	3.57	3.72	0.86	0.86	2.36	1.35	2.46	2.1
-	ORF SEQ ID NO:	20212	21526	24062	24933	27267	25692	28602	28603	28817	27134	25550	28988	21863	21864	23517	24318	26047	26048	26787	27160	27213	27214	28241	20671	20672	21696	24148	24709	
	Exon SEQ ID NO:	10391	11655	764.70	0/101	47080	15590		İ	18533	16942	15477	18695	11970	11970	13726	14530	15917		16598	16966	17020	17020	17992	10827	10827	11817			19032
	Probe SEQ ID NO:	447	1756	9303	0070	7203	5681	8465	8465	8716	7065	5561	8884	2080	2080	3814	4642	6013	6013	6718	7089	7143	7143	8102	305	905	1922	4463	5066	9360

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Table 4
Single Exon Probes Expressed in Heart

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6844	16723		5.37	3.0E-99	3.0E-99 M95586.1	NT	Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds
1219	11128		3.46		2.0E-99 AW274792.1	EST_HUMAN	xp09e06.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE.2739874 3' similar to gb.M31212 MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
3220	13144	22947	1.08	2.0E-99		NT L	Human Ku (p70/p80) subunit mRNA, complete cds
3	7 4007	74407	6 7		3 OE 00 A E006 703 4	TN	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein complete etc.
2	100		2				zb46d06.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306635 5' similar to
7053	16930	27121	9.75	2.0E-99		EST HUMAN	gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
8451	18324	28583			2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
312	10274	20093	1.53	1.0E-99	AF114487.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
375	10329	20152	1.04	1.0E-99	11526150 NT	LΝ	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1401	11306	21166	2.11	1.0E-99	1.0E-99 M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1537	11441	21298	1.47	1.0E-99	1.0E-99 AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1537	11441	21299	1.47	1.0E-99	1.0E-99 AF192523.1	L	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1885	11781	21656	1.1	1.0E-99	4503730 NT	TN	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
1885	11781	21657	1.1	1.0E-99	4503730 NT	TN	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
3046	12973	22766	0.89		1.0E-99 J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4283	14182	23960	2.74			NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4283	14182	23961	2.74		1.0E-99 AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
5200	15063		1.18		1.0E-99 AL163281.2	L	Homo sapiens chromosome 21 segment HS21C081
7305	17181		1.15	1.0E-99	11419721 NT	Į.	Homo saplens ALEX1 protein (LOC51309), mRNA
7483	17353	27557	1,68		1.0E-99.AW340174.1	EST HUMAN	hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711
8683	18571				7.	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
9125	18884		3.76		1.0E-99 AF240786.1	NT	genes, complete cds
+	6866	19780	1.13		1.0E-100 AL163247.2	IN	Homo sapiens chromosome 21 segment HS21C047
2	6866	19780	1.93			NT	Homo sapiens chromosome 21 segment HS210047
62	10048	19859	1.48	1.0E-100	11418230 NT	LN.	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
62	10048	19860	1.48		11418230 NT	卜	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
81	10065	19883	1.52		7.1	EST_HUMAN	xv78b11.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE.2824605 3'
162	10135	19950	1.16		2	LN	Homo sapiens chromosome 21 segment HS21C005
314	10276		1.01	1.0E-100	1.0E-100 AL163249.2	N	Homo sapiens chromosome 21 segment HS21C049
340	10299	20114	2.43		1.0E-100 T05087.1	EST_HUMAN	EST02975 Fetal brain, Stratagene (cat#938206) Homo sapiens cDNA clone HFBCR32

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Single Exon Probes Expressed in Heart

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
-	<u> </u>		i.	70.4	,	Ŀ	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
430	103/5		7.04	1.0E-100	1.0E-100 AF003526.1		Goorilla DNA for ZNF80 gene homolog
101		20255		1 OF-100	2.1	FST HUMAN	RC3-HT0625-040500-022-b09 HT0625 Homo sapiens cDNA
1002				1 0F-100	561685	.	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122); mRNA
1002	1	20764		1.0E-100		N	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1528	l			1.0E-100	1.0E-100 AW 207555.1	EST_HUMAN	UI-H-BI1-afk-c-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1533	11437	21294	1.46		1.0E-100 AI200857.1	EST_HUMAN	qf62f09.X1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA P81061 CYSTATIN;
2195	12082		1.45		1.0E-100 D83349.1	N	Rat mRNA for short type PB-cadherin, complete cds
2388	12267		1.08		1.0E-100 X62468.1	NT	H.sapiens mRNA for IFN-gamma (pKC-0)
2674	12539	22429	1.87	1.0E-100	11418976 NT	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
2985	12913		2.45		1.0E-100 D11078.1	LN	Homo sapiens RGH2 gene, retrovirus-like element
4116	14016	23796	1.49		1.0E-100 AF057354.1	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
4143	14043	23816	1.87	1.0E-100		IN	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5024	14897	24665	3.07	1.0E-100		LN	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5024	14897		3.07	1.0E-100	5032104 NT	INT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5232	15156		1.8			EST_HUMAN	601863164F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080999 5
5496	15415	25478	1.4		1.0E-100 AU118182.1	EST HUMAN	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
5514	15432	25496	1.55			IN	Homo sapiens NF-E2-related factor 3 gene, complete cds
5915	15821	25946	5.1	1.0E-100	1.0E-100 AU140214.1	EST_HUMAN	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6015	15919	26049	1.41	1.0E-100	1.0E-100 R10887.1	EST_HUMAN	yf38c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
6116	16010	26146	1.4		1.0E-100 BF376478.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
6116	16010	26147	1.4		1.0E-100 BF376478.1	EST HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
6119	16013	26151	66.9		1.0E-100 X04571.1	TN	Human mRNA for kidney epidermal growth factor (EGF) precursor
6963	16841	27033	6.19		1.0E-100 BF103853.1	EST_HUMAN	601647357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 5
6983	16860		5.44		1.0E-100 AL163203.2	LΝ	Homo sapiens chromosome 21 segment HS21C003
7322	17198	27398	3.2		1.0E-100 AB040918.1	IN	Homo sapiens mRNA for KIAA1485 protein, partial cds
							wr37g09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2489920 3' similar to contains element
7369	17347		1.53		1.0E-100 AI972388.1	EST_HUMAN	MER22 repetitive element;
7426	16439		1.67	1.0E-100		EST_HUMAN	PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA
7527	17378				1	LN	Homo sapiens mRNA for KIAA1626 protein, partial cds
7527					1	Į.	Homo sapiens mRNA for KIAA1626 protein, partial cds
7664	17514	27740	1.69		1.0E-100 AW630487.1	EST_HUMAN	hh83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'

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	Τ					Γ	Γ		<u> </u>			T								Γ	T	T	T				T		Τ		Γ	T	
Top Hit Descriptor	hh83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'	Human endogenous retrovirus HERV-K, pol gene	MR0-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA	H.sapiens CD97 gene exon 4	H. sapiens CD97 gene exon 4	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens chromosome 21 segment HS21C047	Homo sapiens golgin-ilke protein (GLP) gene, complete cds	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	Homo conjunctive dancin binding evaluin 4 (CU20DA) DMA	Home serians transcapholomis II: morecastic moming (TOMN) DNA	Truing septemble agreement in macrocytic and in CNZ), minny	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA	Homo sapiens mRNA for KIAA0446 protein, partial cds	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo saplens phosphoribosylgtycinamide formyltransferase, phosphoribosylgtycinamide synthetase,	Hopping of carliar alpha-mixein heavy chain done	602156474F1 NIH MGC 83 Homo sapiens cDNA clone IMAGE:4297291 5	qg99e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo saplens carboxypeptidase A1 (pancreatic) (CPA1) mRNA	RC3-ST0281-160600-016-h09 ST0281 Homo sapiens cDNA	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA	H. sapiens EWS gene, exon 5	Homo sapiens RIBIIR gene (partial), exon 12	Homo sapiens RIBIIR gene (partial), exon 12	Homo sapiens genomic downstream Rhesus box	Homo sapiens gamma-glutamytransferase 1 (GGT1) mRNA
Top Hit Database Source	ST HUMAN	トラ	ST HUMAN	トフ	レ	レフ	レフ	トフ	77						トラ	イブ	L,	T	7	Ŀ	- 1-	EST HUMAN	ST_HUMAN	5	77	5	EST_HUMAN	77	77	Ļ	トフ	17	トラ
op Hit Acession No.	7.1		2.1			3	3	2			67575	1104011	1411814	7110714	0714		7110734	7110734	7657454		† I	8.1	1	7662183	7662183	4502996	E843070.1	5729892		.1	1	1	4885270 NT
	1.0E-100 A	1.0E-100 Y	1.0E-100 B	1.0E-100 X	1.0E-100 X	1.0E-100 A	1.0E-100(A	1.0E-100 A	1.0E-100 A	1 00 400	1.01-100	1.00-100	1.05-100	1.0E-101	1.0E-101	1.0E-101 A	1.0E-101	1.0E-101	1.0E-101	707	1 OF 101 7	1.0E-101B	1.0E-101 A	1.0E-101	1.0E-101	1.0E-101	1.0E-101 B	1.0E-101	1.0E-101 X	1.0E-101 A	1.0E-101 A	1.0E-101 A	1.0E-101
Expression Signal	1.69	1.29	5.23	2.14	2.14	4.58	4.56	1.96	1.86	7 50	2000	2 28	0.30	122	1.22	1.16	4.45	4.45	1.32	90,	3.44	12.74	1.63	0.87	0.87	1.62	1.6	1.66	4.4	2.56	2.56	12.14	2.51
ORF SEQ ID NO:	27741			28745	28746	28831	28832	19780		20114	25000	25102	1		19872	20422	20447	20448	20521	. 2000	20012	20741	20796	21483	21484	21677	21792	22080	22335	22468	22469		22897
Exon SEQ ID NO:	17514	17866	18029	18473	18473	18549	18549	9989	18738	18827	10002	10400	18408	10055	10055	10605	10621	10621	10684	40760	10832	10892	10954	11613	11613	11797	11902	12718	12443	12576	12576	12852	13092
Probe SEQ ID NO:	7664	8016	8141	9098	9098	8660	8660	8688	8930	00.48	3040	0000	3340	2	22	671	688	888	754	700	300	696	1036	1712	1712	1901	2010	2301	2572	2714	2714	2925	3167
	Exon SEQ ID NO:ORF SEQ ID NO:Expression SignalTop Hit Acession (Top) Hit BLAST ETop Hit Acession No.Top Hit Acession Source	Exon SEQ ID ID NO: ORF SEQ Signal NO: Expression Signal Value Most Similar (Top) Hit BLAST E Value Top Hit Acession No. Top Hit Acession No. Database Source 17514 27741 1.69 1.0E-100 AW630487.1 EST_HUMAN	Exon SEQ ID ID NO: ORF SEQ Signal NO: Expression Signal Value Most Similar ID NO: Top Hit Acession No: Database Source Source 17514 27741 1.69 1.0E-100 AW630487.1 EST_HUMAN 17866 1.0E-100 AV6391.1 NT	Exon SEQ ID ID NO: ORF SEQ ID NO: Expression Signal Value (Top) Hit No: Top Hit Acession No: Top Hit Database No: Top Hit No: Top Hit Source 17514 27741 1.69 1.0E-100 AW630487.1 EST_HUMAN 18029 28275 5.23 1.0E-100 BF327292.1 EST_HUMAN	Exon SEQ ID ID NO: CAPE SEQ Signal ID NO: Expression Signal ID NO: Most Similar BLASTE Velue ID NO: Top Hit Acession No: r>SEQ ID ID NO: CAPE SEQ Signal ID NO: Expression Signal ID NO: Most Similar BLASTE Value ID NO: Top Hit Acession NO: r>SEQ ID ID NO: CAPE SEQ Signal ID NO: Expression Signal ID NO: (Top) Hit BLASTE Value ID NO: Top Hit Acession NO: Top Hit Acession NO: Top Hit Database Source NO: 17514 27741 1.69 1.0E-100 AW630487.1 EST HUMAN 17866 28275 5.23 1.0E-100 AY10391.1 NT 18473 28746 2.14 1.0E-100 X94633.1 NT 18473 28874 2.14 1.0E-100 X94633.1 NT 18549 28831 4.56 1.0E-100 AF111170.3 NT	Exon SEQ ID ID NO: CAPE SEQ Signal ID NO: Expression Signal ID NO: Most Similar BLASTE Value ID NO: Top Hit Acession NO: EQ ID NO: CXF SEQ Signal ID NO: Most Similar Signal ID NO: Most Similar Accession Signal ID NO: Most Signal ID NO: Most Signal ID NO: Top Hit Accession Accession ID Database ID Accession ID NO: Top Hit Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID Accession ID 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Single Exon Probes Expressed in Heart

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Human mRNA for pancreatic camma-chittamilianity	Homo sapiens gamma-di Itamyltransferses 4 / PCT-1 1	601472808T1 NIH MGC 68 Home saniers CINA class INACE 20175010 2	601472808T1 NIH MGC 68 Homo sapiens CDNA close INA/OE:2925623 3	Homo saplens Janus Kinase 2 (a protein tyrosine kinase) (JAK 2) mRNA	branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit (human, Genomic, 195 nt,	Homo saniene mBNA for KIA A0840	OVI-DIONER 20000 085 -04 Diones II.	2) coco-2-1-2-2-2-2-3-3-1 D L U008 From Sapiens cDNA	601108202E1 MILL MCC 42.1	Home carious dates a conference of Home sapiens con MAGE:3344326 5'	Himps address user the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contrac	Home satisfies all the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA	Suprementation of the lighting of the contracted glucose transporter), member 9 (SLC2A9), mRNA
le Exon Probe	Top Hit Database Source	EST HUMAN 6	T						EST HUMAN E					T HUMAN	Т	Т	EST HIMAN GO	_		Ĭ	1		T HUMAN	Π	NT Ho	Dr.		HIMAN	Т	HIMAN	NO TO				
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	Most Similar (Top) Hit BLAST E Value	1.0E-101 BF03532	1.0E-101	1.0E-101	1.0E-101 AJ237744	1.0E-101	1.0E-101	1.0E-101			1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101 BF029174		1.0E-101 AA036800	1.0E-101 X60069.1	1.0E-101 X60069.1	1.0E-101	1.0E-101 BE619667		1.0E-101	1.0E-101	1.0E-101	1.0E-101 AW939051	1.0E-102 AL 163303	1.0E-102 B	1.0E-102	1.0E-102 M10976 1	1.0E-102	1.0E-102	-
	Expression Signal	2.16	1.67	1.75	1.75	4.83	1.67	1.67	1.4	3.73	3.73	4.16	4.16	5.63	1.56	5.3	2.65		1.15	16.52	16.52	18.4	5.64	5.64	1.76	2.88	1.78	11.62	3.24	0.89	1.46	1.95	1.39	1.39	
	ORF SEQ ID NO:		23059	22468	22469	23499	24609	24610	24954	25658	25659	26356	26357	26441		26581	26764		27274	26650	26651	27468	27694	27695	28040	28381	28586		20111	20350	20526	20859	21002	21003	
	Exch SEQ ID NO:	13127	13254	12576	12576	13712	14840	14840	15179	15563	15563	16196	16196	16278	16330	16402	16573		17085	16458	16458	17263	17474	17474	17800	18132	18327	19189	10297	10540	10688	11017	11154	11154	
	Probe SEQ ID NO:	3203	3334	3354	3354	3800	4965	4965	5257	5651	5651	6333	6333	6416	6471	6544	6693		7208	7446	7446	7454	7623	7623	7950	8252	8454	9610	338	604	758	1101	1247	1247	

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Single Exon Probes Expressed in Heart

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Single Exori Probes Expressed in Heart	Top Hit Descriptor	601299982F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3629901 5	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95 HUMAN Q08379 GOLGIN-95.	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95 HUMAN 008379 GOI GINLOS.	Homo saplens KIAA0187 gene product (KIAA0187) mRNA	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5	Homo sapiens chromosome 21 segment HS21C007	601107843F1 NIH_MGC 16 Homo sapiens cDNA clone IMAGE 3343882 5	y32c04.r1 Sogres placenta Nb2HP Homo sapiens cDNA clone IMAGE 140934.51	Homo saplens protein phosphatase-1 regulatory subminit 7 (PPPAR7) remains avon 7	Homo sapiens HSC54 mRNA for heat shock cognate protein 54 complete cde	Homo sapiens histone deacetylase 7 (HDAC7) mRNA	Homo sapiens histone deacetylase 7 (HDAC7), mRNA	ar82f09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137 Q13137 NDP52.	Homo sapiens mRNA for Centaurin-alpha2 protein	AV710738 Cu Homo saniens cDNA clane CudAKD03 si	QV3-NT0025-210600-236-h08 NT0025 H0mo saniens CDNA	601501107F1 NIH MGC 70 Homo saniens cDNA clone IMAGE 3003145 FI	AV694817 GKC Homo sapiens cDNA clone GKCEE115	AV694817 GKC Homo sapiens cDNA clone GKCEEF115'	Homo sapiens mRNA for KIAA0454 protein, partial cds	yd13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGF-67021 5	yd13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE 67021 5	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA	RC-BT074-260499-014 BT074 Homo sapiens cDNA	RC-BT074-260499-014 BT074 Hamo sapiens cDNA	on57h04.s1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to SW:CAV2_HUMAN P51636 CAVEOLIN-2_111	601439392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924166 5
JIE LAUII FIU	Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	4	EST HUMAN	EST HUMAN	LN	EST HUMAN	EST HUMAN	N	NT	LN	LN LN	EST HUMAN	NT	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	Ν	, L	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN
	Top Hit Acession No.	BE408447.1	1.0E-102 AI124669.1	1.0E-102 AI124669.1	7661979	1.0E-102 AU141005.1	1.0E-102 AU141005.1		1.0E-102 BE251310.1		3.1	1.1	7705398 NT	7705398 NT	τ-	-						3.1			1.0E-102 AU124629.1	11425430 NT	11425430 NT	-	-	1.0E-102 AA970786.1	1.0E-102 BE897468.1
	Most Similar (Top) Hit BLAST E Value	1.0E-102 BE40844	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102 AL163207	1.0E-102	1.0E-102 R66488.1	1.0E-102 AF06713	1.0E-102	1.0E-102	1.0E-102	1.0E-102 AJ459825	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102 T70393.1	1.0E-102 T70393.1	1.0E-102	1.0E-102	1.0E-102	1.0E-102 AI905037	1.0E-102 AI905037	1.0E-102	1.0E-102
	Expression Signal	90.24	1.34	1.34	1.51	5.61	5.61	1.46	2.11	1.09	1.88	7.27	3.46	3.46	2.54	6.56	2.53	42	2.53	1.36	1.36	4.06	1.52	1.52	3.58	2.03	2.03	2.9	2.9	2.3	2.38
	ORF SEQ ID NO:	21162	22044	22045	22747	22815	22816	23814	23994	24705	25025		25522	25523	25818	26376	26524	26857	26904	27014	27015	27069	27448	27449	27490	28052	28053	28070	28071	28096	28549
	Exan SEQ ID NO:	11303	12145	12145	12954	13021	13021	14039	14211	14933	15221	15433	15453	15453	15706	16214	16354	16666	16711	16823	16823	16878	17243	17243	17282	17811	17811	17831	17831	17855	18295
	Probe SEQ ID NO:	1398	2261	2261	3026	3094	3094	4139	4314	5063	5300	5515	5536	5536	2800	6351	6495	6787	6832	6945	6945	7001	7374	7374	7415	7961	7961	7981	7981	8002	8421

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sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA</td> <td>Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA</td> <td>RC6-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA</td> <td>Human chromosome 16 creatine transporter (SLO6A8) and (CDM) parajonnus genes, complete cels</td> <td>Homo saplens chromosome 21 segment HS21C080</td> <td>xk07c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE.2666038 3</td> <td>601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'</td> <td>601500405F1 NIH_MGC_70 Homo saplens cDNA clone IMAGE:3902305 5'</td> <td>Homo sapiens mRNA for KIAA0235 protein, partial cds</td> <td>Homo sapiens nucleolar protein (KKE/D repeat) (NOP56) mRNA</td> <td>Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)</td> <td>601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5</td> <td>Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds</td> <td>Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA</td> <td>Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA</td> <td>Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA</td> <td>AU134991 PLACE1 Homo sepiens cDNA clone PLACE1000965 5'</td> <td>Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds</td> <td>MACCIAIR EN Contract of Committee of Committee of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of 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<td>Homo sapiens septin 2 (SEP2) mRNA, partial cds</td> <td>Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4</td> <td>tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13789 ANONYMOUS</td> <td></td>	es Expressed in Heart	Top Hit Descriptor	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA	RC6-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA	Human chromosome 16 creatine transporter (SLO6A8) and (CDM) parajonnus genes, complete cels	Homo saplens chromosome 21 segment HS21C080	xk07c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE.2666038 3	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'	601500405F1 NIH_MGC_70 Homo saplens cDNA clone IMAGE:3902305 5'	Homo sapiens mRNA for KIAA0235 protein, partial cds	Homo sapiens nucleolar protein (KKE/D repeat) (NOP56) mRNA	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA	AU134991 PLACE1 Homo sepiens cDNA clone PLACE1000965 5'	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds	MACCIAIR EN Contract of Committee of Committee of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of Contract of 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Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-7 3'	Homo sapiens septin 2 (SEP2) mRNA, partial cds	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13789 ANONYMOUS	
Exon No.: Rost Similar Signal Top) Hit Aces No. SEQ ID NO.: Signal Top) Hit Top Hit Aces No. 18298 28553 1.99 1.0E-102 450 18298 28554 1.99 1.0E-102 450 18525 28807 2.78 1.0E-102 450 18525 28807 2.78 1.0E-102 450 18525 28807 2.78 1.0E-102 450 18525 28807 2.78 1.0E-102 450 18525 28807 2.78 1.0E-102 450 18625 28807 2.77 1.0E-102 AL163280.2 19827 4.04 1.0E-102 BE368158.1 10049 19861 0.82 1.0E-103 BE908158.1 10078 19894 8.1 1.0E-103 BE908158.1 10078 2032 1.0E-103 BE908158.1 11827 21049 1.27 1.0E-103 AF01828245.1 11827 21049 1.27<	gle Exon Pro	Top Hit Database Source	Ν	NT	EST_HUMAN	F	LN	EST_HUMAN	EST HUMAN	EST_HUMAN	N	Z	LZ LZ	EST_HUMAN	LN	TN	N	NT	EST_HUMAN	L	TOTAL LANGE	EST HUMAN	EST HUMAN	NT	FZ		⊢'l	NT	EST_HUMAN	NT	NT	EST HUMAN	
Exon NO: ORF SEQ ID ID NO: Expression Signal SEQ ID NO: Moderance Signal Signal Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal ID NO: Moderance Signal	SID.	Top Hit Acession No.	4507822	4507822	BF359243.1	U41302.1		AW300862.1	BE908158.1	BE908158.1	D87078.2	5453793	AJ278348.1	3E877541.1	4F012872.1	7657592	4502428	4502428	AU134991.1	4F060568.1	132770 4	3E744722.1	4W 298245.1	AB040892.1	AF023861.1		1	← I		4F179995.1	AF053490.1	1590071.1	
Exon ORF SEQ Express NO: Signe NO: NO: NO: Signe NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:		Most Similar (Top) Hit BLAST E Value	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103 /	1 OF-103	1.0E-103	1.0E-103	1.0E-103 /	1.0E-103 /		1.0E-103 /	1.0E-103	1.0E-103	1.0E-103 /	1.0E-103 /	1.0E-103 AI590071.1	
Exon ORF SEQ ID ID ID ID ID ID ID ID ID ID ID ID ID		Expression Signal	1.99	1.99	2.78	4.04	2.82	4.77	0.82	0.82	8.1	0.83	1.01	7.29	2:32	1.04	1.27	1.27	1.57	2.22	980	2.43	3.44	1.06	2.41		1.16	1.39	3.02	1.72	5.37	1.68	
		ORF SEQ ID NO:		28554				25247	19861	19862	19894	19989	20734	20985	21342	21643	21708	21709	22040	22175	22340		23058	23108			23423	23454	23611	25619	26027	26069	
		Exon SEQ ID NO:	18298	18298	18525	18755	18837	19183	10049	10049	10078	10173	10888	11131	11482	11768	11827	11827	12141	12278	12449	12958	13253	13310	13609		13637	13670	13831	15534	15903	15936	
			8424	8424	8708	8947	9054	9601	63	63	93	201	965	1223	1578	1872	1932	1932	2257	2401	2578	3030	3333	3393	3695		3/25	3757	3922	5619	5998	6033	

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						210	
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6033	15936	26070	1.68		1.0E-103 Al590071.1	EST_HUMAN	tm68b05x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
6092	15102	24878	1.68	1.05-103	5032282 NT	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS154, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript varient Dp427π, mRNA
6092	15102	24879	1.68	1.0E-103	5032282 NT	N	Homo saplens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DX\$142, DX\$164, DX\$206, DX\$230, DX\$239, DX\$268, DX\$269, DX\$270, DX\$272 (DMD), transcript variant Dp427m, mRNA
6289	16153	26310	1.64		1.0E-103 AW965776.1	EST_HUMAN	EST377849 MAGE resequences, MAGI Homo sapiens cDNA
6338	16201	26361	3.21	1.0E-103	1.0E-103 BE748158.1	EST_HUMAN	601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838545 5'
6568	16426	26607	3.28		1.0E-103 AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR.Q13769 Q13769 ANONYMOUS.;
6568	16426	26608			1.0E-103 AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to 1R:Q13769 Q13769 ANONYMOUS.;
6823	16702	26896	2.95		1.0E-103 T31080.1	EST_HUMAN	EST27193 Human Brain Homo sapiens cDNA 5' end similar to None
7010	16887	27079	1.17	1.0E-103	1.0E-103 AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
7010	16887	27080	1.17	1.0E-103	1.0E-103 AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
7050	16927	27118	1.43		BF10924	EST_HUMAN	7/60e03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525964 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1;
7267	17144	27337			6005921 NT	IN	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7267	17144	27338	3.08		6005921 NT	LN	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7787	17637	27870	2.02		1.0E-103 Z37976.1	LN	H.saplens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7815	17665		2.09		1.0E-103 AW963676.1	EST_HUMAN	EST375749 MAGE resequences, MAGH Homo sapiens cDNA
7878	17728	27972	9.93		1.0E-103 AI878956.1	EST_HUMAN	au51g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518326 5' similar to TR:O15046 015046 KIAA0338;
8115	18004	28250	3.08		1.0E-103 AI792759.1	EST_HUMAN	ol02d06.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522283.5' similar to TR:052084 Q62084 PHOSPHOLIPASE C NEIGHBORING;
8218	18101	28353	2.74		1.0E-103 AF149773.1	NT	Homo sepiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
8218	18101	28354	2.74		1.0E-103 AF149773.1	TN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
8681	18569		2.56		1.0E-103 AU136283.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
8743	17892	28136	6.49		1.0E-103 L43610.1	TN	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8973	18778	29070	3.42		1.0E-103 BE644611.1	EST_HUMAN	7e68a10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:3287610 3' similar to contains MER29.t3 MER29 repetitive element;

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	Top Hit Descriptor	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	rotein FLJ20454 (FLJ20454), mRNA	complete cds	nonyrı: hfbr2) Homo sapiens cDNA clone DKFZp564H1072 5'	nonym: hfbr2) Homo sapiens cDNA clone DKFZp564H1072 5'	renetic protein 8 (osteogenic protein 2) (BMP8) mRNA	(#937204) Homo saplens cDNA clone IMAGE:587626 3' similar to coprome to coprome the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t	Homo sapiens cDNA clone IMAGE:3926438 5	2 CT0249 Homo sapiens cDNA	2 CT0249 Homo sapiens cDNA	elated protein 2, yeast) homolog (ACTR2), mRNA	3D59/MEM43 mRNA, complete cds	anylpyruvate tautomerase II	tor Homo sapiens cDNA 5' end	A1276 protein, partial cds	A1276 protein, partial cds	A1172 protein, partial cds	(FN precursor)	21 unknown mRNA	21 unknown mRNA	on of chromosome 21 DNA	on of chromosome 21 DNA	wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN, contains element LTR7 repetitive element :	wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145	ins element Link repetitive element.	Homo sapiens cDNA clone IMAGE:3503220 5'	Homo sapiens cDNA clone IMAGE:3503220 5'	1 protein complex 2, beta 1 subunit (AP2B1), mRNA	24 Homo sapiens cDNA clone IMAGE:3365948 3'	IRNA, complete cds	IRNA, complete cds
Olligie Exul Flobes Expressed III riedit	Top Hit Descriptor	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquiti (UBE2D3) genes, complete cds	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA	Homo sapiens gene for AF-6, complete cds	DKFZp564H1072_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564H1072	DKFZp564H1072_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564H1072 5	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP3) mRNA	zo22c06.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587626 3' similar to gb:Z14116 mat CD59 GLYCOPROTEIN PRECURSOR (HUMAN);	601577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA	Human lymphocytic antigen CD59/MEM43 mRNA, complete cds	H.sapiens gene encoding phenylpyruvate tautomerase II	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end	Homo sapiens mRNA for KIAA1276 protein, partial cds	Homo sapiens mRNA for KIAA1276 protein, partial cds	Homo sapiens mRNA for KIAA1172 protein, partial cds	Human mRNA for fibronectin (FN precursor)	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Human Down Syndrome region of chromosome 21 DNA	Human Down Syndrome region of chromosome 21 DNA	wjo3b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 KIAA0132 PROTEIN .contains element LTR7 repetitive element :	wj03b12.x1 NCI_CGAP_Kid12 Hamo sapiens cDNA clone IMAGE:2401727	AND 132 FINO I EINT, JOHNS REMEMBER LIN / JEPENNYE EIGHEN ,	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA	nad16g11x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3	Homo sapiens Trio isoform mRNA, complete cds	Homo sapiens Trio isoform mRNA, complete cds
IE EXUIT FIODES	Top Hit Database Source	H U)		NT	EST_HUMAN DA	EST_HUMAN DM		EST HUMAN gb		EST_HUMAN RO	EST_HUMAN RO		NT H	H	EST_HUMAN ES	NT TN			H.	H H	NT Ho	NT	보 H	EST HUMAN KI	1	Т		EST HUMAN 60		T_HUMAN		NT
Silis	Top Hit Acession No.	1.0E-103 AF224669.1	11526291 NT			1.0E-104 AL037549.3	4502428 NT	1.0E-104 AA132975.1		-	1.0E-104 BF334221.1	5031570 NT			1.0E-104 AA319436.1	1.0E-104 AB033102.1	1	8.1		1.0E-104 AF231920.1	1.0E-104 AF231920.1								11425572 NT	1	1	.0E-104 AF091395.1
	Most Similar (Top) Hit BLAST E Value	1.0E-103	1.0E-103	1.0E-103	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104 BF334221	1.0E-104	1.0E-104	1.0E-104 M34671.1	1.0E-104 Y11151.1	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104 X02761.1	1.0E-104	1.0E-104	1.0E-104 U43379.1	1.0E-104 U43379.1	1.0E-104 AI768797.	707	+01-30.1	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104
	Expression Signal	1.72	2.65	2.21	2.6	2.6	1.81	7.16	1.91	1.15	1.15	1.55	7.64	2.82	1.54	0.99	66'0	0.91	4.28	6.0	6.0	1.33	1.33	8.46	0	0.40	1.52	1.52	2.38	2.24	4.66	4.66
	ORF SEQ ID NO:			25323	20016	20017	21617	21932	21944	22097	22098	22159	22559			23260	23261	23564	23957	24182	24183	25615	25616	25919	000	07807	26204	26205	26309	27363	27442	27443
	Exon SEQ ID NO:	18833	18855	18979	10202	10202	11741	12035	12044	12199	12199	12266	12770	12813	13265	13465	13465	13772	14179	14397	14397	15532	15532	15797	10137	18/01	16056	16056	16152	17164	17239	17239
	Probe SEQ ID NO:	9049	9079	9275	233	233	1845	2147	2157	2318	2318	2387	2842	2886	3345	3550	3550	3861	4280	4204	4204	2617	5617	5891		800	6073	6073	6288	7288	7370	7370

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Table 4
Single Exon Probes Expressed in Heart

Oligie Lydi Frones Lypresseu III realt	Most Similar (Top) Hit Acession (Top) Hit Acession Signal BLASTE No. Source Source	3.84 1.0E-104 BF352841.1 EST_HUMAN IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA	3.84 1.0E-104 BF352841.1 EST_HUMAN IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA	3.14 1.0E-104 BE791713.1 EST_HUMAN 601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'	3.14 1.0E-104 BE791713.1 EST_HUMAN 601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'	1.42 1.0E-104 AV728070.1 EST_HUMAN AV728070 HTC Homo sapiens cDNA clone HTCBYA07 5	4.51 1.0E-104 AU130765.1 EST_HUMAN AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5	NT	1.0E-104 BE720191.1 EST_HUMAN		4.49 1.0E-104 BF684298.1 EST_HUMAN 602141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5		2.86 1.0E-105 4502166 NT Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA	16.85 1.0E-105 4505150 NT Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA	3.22 1.0E-105 AF032897.1 INT Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	3.22 1.0E-105 AF032897.1 NT Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	1.16 1.0E-105 AL163280.2 NT Homo sapiens chromosome 21 segment HS21C080	1.0E-105 D50918.1 NT	1 EST_HUMAN	1.0E-105 AA584808.1 EST_HUMAN	1.0E-105 AJ229041.1 NT			1.26 1.0E-105 11425532 NT Homo sapiens dermatopontin (DPT), mRNA		1.0E-105 BE868881.1 EST_HUMAN	1.0E-105 BE868881.1		1.0E-105 AB018339.1 NT	2.23 1.0E-105 AB020673.1 NT Homo sapiens mRNA for KIAA0866 protein, complete cds	1.3 1.0E-105 AB018339.1 NT Homo saplens mRNA for KIAA0796 protein, partial cds	3.06 1.0E-105 11419196 NT Homo sapiens GTPase activating protein-like (GAPL), mRNA	1.0E-105 11419196 NT	6.43 1.0E-105 T05087.1 EST_HUMAN EST02975 Fetal brain, Stratagene (cat#936206) Homo saplens cDNA clone HFBCR32
		1.0E-104					1.0E-104			1.0E-104		1.0E-104 E				1.0E-105			1.0E-105	1.0E-105			1.0E-105			1.0E-105				1.0E-105	1.0E-105	1.0E-105		1.0E-105
	Expression Signal	3.84	3.84	3.14	3.14	1.42	4.51	4.24	1.84	1.84	4.49	1.37	2.86	16.85	3.22	3.22	1.16	1.75	1.64	78.0	2.57	0.93	0.93	1.26	2.15	0.84	0.84	3.74	0.95	2.23	1.3	3.06	3.06	6.43
	ORF SEQ ID NO:	26630	26631		27899	28037	28057		28755		28783		20062	19777			21553		21928				23033		23689		24314				24690	24840		26754
	Exon SEQ ID NO:	16443	16443	17659	17659	17797	17816	17864	18484	18484	18505	19340	12637	9866	10517	10517	11676	11780	12030						13914					14965	14916	15124		16559
	Probe SEQ ID NO:	7430	7430	7809	7809	7947	7966	8014	8617	8617	8641	9842	277	419	579	579	1777	1884	2142	2689	2975	3307	3307	3592	4008	4638	4638	4855	5044	5095	5161	6167	6167	6299

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Single Exon Probes Expressed in Heart

1		Τ	T	T	Т	T	Т	-1		7	Τ-	1	_	$\overline{}$	-			Ť	1	1		1	1	Τ-	1	1	1	7,7	.,	···· ·	1
	Top Hit Descriptor	ws50c10.x1 NCL_CGAP_Brin25 Homo sapiens cDNA clone IMAGE:2500626 3' similar to SW:ACSA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE	UI-H-Biop-abi-b-12-0-UI.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced	Homo sapiens COL4A6 gene for a6(IV) collagen, exon 31	Homo saplens Ran binding protein 11 (LOC51194), mRNA	wv74f07.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892	HILHE-BNO akt a 07-0-11 of Niju McC By Harms seemen about a seemen with or seemen.	tq79c01.x1 NCI_CGAP_Ut1 Homo sapiens cDNA_clone IMAGE-22156848 3	EST377629 MAGE resequences, WAGI Homo sapiens cDNA	Human dihydrofolate reductase pseudogene (psi-hd1)	Human dihydrofolate reductase pseudogene (psi-hd1)	Homo sapiens soluble neuropilin-1 mRNA, complete cds	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds	ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element	ENTRY CONTROLL OF CONTROLL - MIN -1 MIN CT CONTROLL - "	ing troops in vol. Cook in the sapiens convenient was E.937352.3 similar to contains element. LTR3 repetitive element;	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA	Homo saplens X-linked antildrolitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5	q/76h10 x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA	Homo saplens mRNA for KIAA1326 protein, partial cds	Homo sapiens mRNA for KIAA1326 protein, partial cds	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA	Homo sapiens gene for activin receptor type IIB, complete cds	Homo sapiens mRNA for KIAA1278 protein, partial cds
מו וווער מו	Top Hit Database Source	EST_HUMAN	EST_HUMAN	LN	N	NT	HOT HIMAN	EST HIMAN	EST HUMAN	EST HUMAN	N	N	TN	N	ECT HIMAN	NUMBER OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PART	EST_HUMAN	EST_HUMAN	NT	N	N-	EST_HUMAN	EST_HUMAN	LN LN	N	LN_	L	LN	LΝ	LN⊤	TN
	Top Hit Acession No.	1.0E-105 AW007194.1	1.0E-105 AW016879.1	AF254822.1	J63548.1	7705936 NT	1 0E-105 AW027554 1	- -		\ <u>-</u>			1		14527446 4		_	_	4504184 NT	-		.1		4504184 NT	4504184 NT			1N 2962298	8922965 NT		
	Most Similar (Top) Hit BLAST E Value	1.0E-105	1.0E-105	1.0E-105 AF254822	1.0E-105 D63548.1	1.0E-105	1 0E_105	1 0F-108	1.0E-106 AI565065.1	1.0E-106	1.0E-106 J00146.1	1.0E-106 J00146.1	1.0E-106 AF145712.	1.0E-106 U48724.1	1 0F-106 AA527446		1.0E-106 AA527446.	1.0E-106 BE144286.	1.0E-106	1.0E-106 AF003528	1.0E-106 U64675.2	1.0E-106 BE260201	1.0E-106 AIZ76526.1	1.0E-106	1.0E-106	1.0E-106 AB037747.1	1.0E-106 AB037747.1	1.0E-106	1.0E-106	1.0E-106 AB008681.1	1.0E-106 AB033104.
	Expresslon Signal	1.8	2.99	5.44	1.8	2.06	2.01	0.98	1.54	1.77	0.79	1.21	2.66	4.51	5.12		5.12	1.08	8.39	1.63	1.25	1.94	4.23	2.97	2.97	5.01	5.01	2.36	2.36	0.8	0.98
	ORF SEQ ID NO:	26967	27304	28428	28699	28740	28968		19987	20286	20334	20334	21272	21444	21533		21534	21858	22052	22229	22322	22324	22487	21183	21184	22635	22636	22867	22868	23053	23109
	Exon SEQ ID NO:	16773	17111	18181	18430	18469	18679	10110	10170	10473	10527	10527	11413	11576	11661		11661	11965	12153	12333	12429	12431	12591	11319	11319	12837	12837	13068	13068	13248	13311
	Probe SEQ ID NO:	6894	7234	8303	8560	8602	8867	145	198	531	583	590	1508	1674	1762		1762	2075	2269	2456	2557	2559	2729	2795	2795	2911	2911	3143	3143	3328	3394

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens mRNA for KIAA1278 protein, partial cds	EST386875 MAGE resequences, MAGN Homo sapiens cDNA	EST386875 MAGE resequences, MAGN Homo sapiens cDNA	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA	Homo sapiens dystrophin gene, exon 41	aj24b09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN PHPs1.2 (HI IMAN).	602154012F1 NIH MGC 83 Homo sapiens cDNA clone IMAGE 4295067 로	Homo sapiens xylosytransferase II (XT2), mRNA	Homo sapiens xylosyltransferase II (XT2), mRNA	ae72e07.s1 Stretagene schizo brain S11 Homo sapiens cDNA clone IMAGE.969732 3' similar to gb.X65873	KINESIN HEAVY CHAIN (HUMAN); Homo sanjans XPMC2 motain (LOC52400) mBNA	ROAD OF STREET HILL MOCK AE LINEARY	Homo sapiens sorting period 13 FOMY41 mBMA	Home confine a court is (CIVILI), ININA Home confine a court of (CIVILIA)	FOLESOLATIFT NIH MCC 0 Dame continue Chita de contraction contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de contraction de 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COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE TOTAL COLOR OF THE 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COLOR	ou 1994331F1 NIH MIGC 9 Home sapiens cDNA clone IMAGE 3948463 5	ar68a07.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X06233 CALGRANULIN B (HUMAN);	ty62a05.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW∷CA6_HUMAN Q05084 69 KD ISLET CELL AUTOANTIGEN :	oc67e08.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE-1354700 31	oc67e08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'	on03a04.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTRC con 3a04 random	tm41f02.x1 NCI_CCAP_Kid11 Homo sepiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.t3 TAR1 PTR5 repetitive element:	tm41f02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE.2160699 3' similar to contains MSR1 t3	IAKT P I K5 repetitive element;	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5	np57b10.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'	np57b10.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
gle Exon Pro	Top Hit Database Source	TN	EST HUMAN	EST HUMAN	EST_HUMAN	NT	ERT HIMAN	EST HUMAN	1	LN		ESI HOMAN	EST LI IMANI		LIN	EST HIMAN	TOT LOUIS	ES HOMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	1	ESI_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN
Sing	Top Hit Acession No.	1.0E-106 AB033104.1	1.0E-106 AW974650.1	_	1.0E-106 BE144286.1	_41644.1	1 0F-106 AA781155 1	1.0E-106 BF679574.1	11545913 NT	11545913 NT	A ACC 2004 A	1.0E-106 AA003/79.1 ES	RE202722 4	11425503 NT	14.425502 NI	1		JE / 41408.1	41523066.1	N654123.1	1	AA825307.1	11750447.1	1479569.1	7 0000		_	1	-	-
	Most Similar (Top) Hit BLAST E Value	1.0E-106	1.0E-106	1.0E-106	1.0E-106	1.0E-106 L41644.1	1 0E-108	1,0E-106	1.0E-106	1.0E-106	700	1.0E-106		1.0E-106	1 OF 106	1.0E-100	400	1.05-100 (1.0E-106 AI523066.	1.0E-106 AI654123.	1.0E-106 AA825307	1.0E-106 AA825307	1.0E-106 AI750447.1	1.0E-106 AI479569	100	1.0E-106 AI4/9569.1	1.0E-106 BF027310.	1.0E-106 BF027310.	1.0E-106 AA604417.	1.0E-106 AA604417
	Expression Signal	0.98	7.22	7.22	1.21	1.21	2 08	6.78	16.4	16.4	C U	5.03 4.83	135	7.6	7.6	533	200 1	00.0	. 1.48	3.16	1.86	1.86	2.79	1.86	0	00.1	1.32	1.32	5.83	5.83
- - -	ORF SEQ ID NO:	23110		23635	24176		25022	25722	25891	25892	38386	26412	26453	26517	26518	26733	26734	40107	26821	27120	27353	27354	27419	27501	27502	2/302	27890	27891	27975	27976
	Exon SEQ ID NO:			13860		15047	15219	15619	15772	15772	16004	16252	16292	16348	16348	16537	16537	10001	16633	16929	17158	17158	17219	17291	17201	167/1	17653	17653	17730	17730
	Probe SEQ ID NO:	3394	3952	3952	4497	5183	5298	5711	5866	5866	6364	6390	6431	6490	6490	6657	6657		6754	7052	7281	7281	7351	7424	7424	1741	/803	7803	7880	7880

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	Top Hit Descriptor	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA	Horno sapiens chromosome 21 segment HS21C002	601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'	601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'	Human ryanodine receptor mRNA, complete cds	Human ryanodine receptor mRNA, complete cds	fh05h11.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961644 5'	601433087F1 NIH_MGC_72 Horno sapiens cDNA clone IMAGE:3918524 5'	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5	RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA	Homo sapiens Xq pseudoautosomal region; segment 1/2	Human IFNAR gene for interferon alpha/beta receptor	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA	Homo sapiens NY-REN-25 antigen mRNA, partial cds	Human IFNAR gene for Interferon alpha/beta receptor	Human IFNAR gene for interferon alpha/beta receptor	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA	Homo saplens cathepsin Z precursor (CTSZ) gene, exon 3	Homo sapiens mRNA for KIAA0453 protein, partial cds	Homo sapiens mRNA for KIAA0453 protein, partial cds	Human dipeptidyl peptidase IV (CD26) gene, exon 20	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'	PM1-CN0031-190100-001-d03 CN0031 Homo saplens cDNA	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA	Homo sapiens myokubularin (MTM1) gene, exon 9	601442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846494 5'	UI-HF-BN0-alf-c-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'	UI-HF-BN0-alf-c-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'	wh56h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384791 3'
שוב באטוו ו וט	Top Hit Database Source	EST HUMAN	LN	EST_HUMAN	EST_HUMAN	IN	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	NT	LN	IN	IN	NT	NT.	NT	EST HUMAN	NT	TN	TN	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
	Most Similar (Top Hit Acession BLAST E No.	1.0E-106 AW363299.1	1.0E-106 AL163202.2	1.0E-106 BF032755.1	1.0E-106 BF032755.1	1.0E-106 J05200.1	1.0E-106 J05200.1	1.0E-106 AW410405.1	1.0E-106 BE894488.1	1.0E-106 BE894488.1	1.0E-106 BE695905.1	1.0E-107 AJ271735.1	1.0E-107 X60459.1	1.0E-107 4826863 NT	1.0E-107 AF155103.1	1.0E-107 X60459.1	1.0E-107 X60459.1	1.0E-107 AF154121.1	1.0E-107 AB032253.1	1.0E-107 BF087405.1	1.0E-107 AF136275.1	1.0E-107 AB007922.2	1.0E-107 AB007922.2	1.0E-107 U13729.1	1.0E-107 BE732460.1	1.0E-107 BE732460.1	1.0E-107 AW842451.1	1.0E-107 AW842451.1	1.0E-107 5902097	1.0E-107 AF020671.1	1.0E-107 BE867469.1	1.0E-107 AW 503913.1	1.0E-107 AW 503913.1	1.0E-107 AI765078.1
	Most Expression (To Signal BLA	1.86 1.	3.66	5.21 1.	5.21 1.	2.28 1.		2.87	2.31	2.31	5.35 1.	3.48 1.		1.07	1.7 1.	0.86	1.16 1.	10.67	0.78 1.	2.13 1.	1.47		0.95	1.26 1.			1.94 1.		2.62	3.92 1.				1.63
	ORF SEQ ED ID NO:	27990	28113	28389	28390	28544	28545		25298	25299					20361	20565	20644	20724	21015	21314	21488	21571	21572	21949	22257	22258	22701	22702	22779	23450	25567	26380	26381	26471
	Exon SEQ ID NO:	17751	17869	18149	18149	18289	18289	19540	19022	19022	19152	10203	10229	10542	10550	10725	10794	10877	11164	11456	11619	11695	11695	12048	12362	12362	12903	12903	12988	13667	15490	16219	16219	16306
	Probe SEQ ID NO:	7901	8019	8269	8269	8415	8415	9122	9342	9342	9554	234	264	909	614	796	898	953	1257	1551	1718	1797	1797	2161	2487	2487	2976	2976	3061	3754	5275	6356	6356	6445

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Single Exon Probes Expressed In Heart

Single Exon Probes Expressed in Heart	Top Hit Descriptor	tg10d06.X1 NGLCGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICDI P05095 ALPHA-ACTININ 3, NON MUSCULAR;	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4	602123963F1 NIH_MGC_56 Homo sepiens cDNA clone IMAGE:4281039 5	601066681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5	Homo sapiens HSPC049 protein (HSPC049), mRNA	Homo sapiens HSPC049 protein (HSPC049), mRNA	ze45e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1 THR repetitive element	601177018F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:3532348 5	Homo sapiens NF2 gene	tt91e10.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);	tt91e10.x1 NCL_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);	Shork of NILL MOD 44 Dome continue advisor allows the MA OF consoners of a continue to viscos on	RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	Homo sapiens pericentriolar material 1 (PCM1) mRNA	hit2a11.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE P55194 SH3-BINDING PROTEIN 3BP-1.;	Human hepatocyte nuclear factor 4-alpha gene, exon 2	Human hepatocyte nuclear factor 4-alpha gene, exon 2	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA	Homo sapiens PSN1 gene, alternative transcript	RC0-HT0372-241199-031-d03 HT0372 Homo sapiens cDNA	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848930 5'	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848930 5'	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds	Homo sapiens FYVE domain containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
lie Exon Prop	Top Hit Database Source	EST_HUMAN		EST_HUMAN	T HUMAN			FST HIMAN			EST HUMAN	EST HUMAN		EST HUMAN		LZ		EST HUMAN	IN	LN		NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	Z	NT
OUIS	Top Hit Acession No.	1392850.1		3F666511.1	3E540550.1	11419701 NT	11419701 NT	1 0E-107 AA001415 1			A1686040.1	A1686040.1		1.0E-108 BE206694.1	1	-	5453855 NT	1.0E-108 AW664438.1			7661979 NT		1.0E-108 AW384094.1	1.0E-108 BE869016.1	1.0E-108 BE869016.1	1.0E-108 AF264717.1	1.0E-108 AF264717.1
	Most Similar (Top) Hit BLAST E Value	1.0E-107 Al392850.7	1.0E-107 L49141.1	1.0E-107 BF666511.	1.0E-107 BE540550	1.0E-107	1.0E-107	1 0E-107	1.0E-108	1.0E-108 Y18000.1	1.0E-108 AI686040.	1.0E-108 AI686040.		1.0E-108	1.0E-108 AF032897.	1.0E-108	1.0E-108	1.0E-108	1.0E-108 U72961.1	1.0E-108 U72961.1	1.0E-108	1.0E-108 AJ008005.	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108
	Expression Signal	2.73	1.82	1.98	9.12	4.21	4.21	3.94	1.46	1.55	7.41	7.41		7.2	0.94	0.94	0.92	1.33	1.99	1.39	2.85	2.19	1.53	2.77	2.77	5.06	5.06
	ORF SEQ ID NO:	28228	28443	28453	28779	28122	28123		20711	20999	22063	22064		22150	23028	23029	23437	23744	24106	24107	24376	24528	25120	25166		25745	25746
	Exon SEQ ID NO:	17978	18193	18204	18503	17881	17881	19673	10864	11151	12166	12166		12258	13226	13226	13654	13967	14320	14320	14585	14748	15286	15312	15312	15640	15640
	Probe SEQ ID NO:	8087	8316	8327	8638	8697	8697	9187	626	1244	2282	2282		2378	3305	3305	3742	4065	4425	4425	4699	4868	5366	5393	5393	5732	5732

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Simllar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5789	15695	25804	1.37	1.0E-108	1.0E-108 AJ133269.1	TN	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6247	16113	26265	5:35	1.0E-108	11431857	LN	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), mRNA
6388	16260	26421	3.34	1.0E-108	4758333 NT	NT	Homo sapiens delta-6 fatty acid desaturase (FADSD6) mRNA
8699			1.93	1.0E-108	1.0E-108 AF083500.1	LN	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8202	15099	24891	2.77	1.0E-108 Y12490.1	Y12490.1	IN	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
8593	18461	28731	4.26	1.0E-108	1.0E-108 AW966185.1	EST_HUMAN	EST378258 MAGE resequences, MAGI Homo sapiens cDNA
8677	18565		2.03	1.0E-108	11441465 NT	INT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
8706	12166	22063	4.14	1.0E-108	1.0E-108 AI686040.1	EST HUMAN	tt91e10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
8706	12166	22064	4 14	1 0F-108	1 0F-108 AIG86040 1	EST HIMAN	#BOTECO: YCAN II PRECI IRSOR (HI IMAN):
9357	1.	25303	2.79	1.0E-108	1.0E-108 AK024447.1	LN	Homo sapiens mRNA for FLJ00037 protein, partiel cds
9736	19270		5.59	1.0E-108	1.0E-108 BF346356.1	EST HUMAN	602018571F1 NCI CGAP Brn67 Homo sapiens cDNA clone IMAGF-4154297 5
58	10044	19856	6.0	1.0E-109 D86974.1	D86974.1		Human mRNA for KIAA0220 gene, partial cds
212	10183	19997	0.92	1.0E-109	11422486 NT	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
222	10192	20003	1.51	1.0E-109	11438391 NT	IN	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
459		20219	3.64	1.0E-109	4507712 NT	NT	Homo sapiens tetratricopeptide repeat domain 2 (TTC2) mRNA
583		20328	14.64	1.0E-109	1.0E-109 AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
283	_	20329	14.64	1.0E-109	1.0E-109 AB023216.1	LN	Homo sapiens mRNA for KIAA0999 protein, partial cds
1184		20941	9.63	1.0E-109 M28699.1	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1185	_	20941	4.89	1.0E-109 M28699.1	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1831		21602	1.48	1.0E-109 D13643.2	D13643.2	LN⊤	Homo sapiens mRNA for KIAA0018 protein, partial cds
2194		21985	2.03	1.0E-109	1.0E-109 AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2204	12091	21993	1.97	1.0E-109 Y17123.1	Y17123.1	N⊤	Homo sapiens SNF5/INI1 gene, exon 6
2581	12452	22344	3.88	1.0E-109	1.0E-109 AI022328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536.3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.
2581	12452	22345	3.88	1.0E-109	1.0E-109 AI022328.1	EST HUMAN	ow95a01x1 Soares fetal liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN
2582		22346	2.75	1.0E-109	04206	LN	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
3020	42048	07700	1 00	4 OF 400 NISE400 4	7 00 7	MALE TOO	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC
2242		03066	1.00	1.0E-109	7	NIMINION TO HOM	TINGEN FOR STATE
3240	-	22000	1.45	1.05-109	_[,	TOT TOWAR	CM3-INDOCUS-19040U-10U-11U NNU009 Homo sapiens cDNA
2450	1	50000	1.43	1.0E-109	1.0E-109/AW893192.1	ES! HOMAN	CM3-NNVCUU9-190400-150-110 NN00009 Homo sapiens cDNA

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Single Exon Plobes Expressed in Heart	Top Hit Descriptor	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds	MR0-HT0209-110400-108-e04 HT0209 Homo sapiens cDNA	Homo sapiens mRNA for KIAA0609 protein, partial cds	Homo sapiens mRNA for KIAA0609 protein, partial cds	ts98e06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP:F53A2.8 CE16100 ;	nu93c12.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN P30712 GLUTHATHIONE S-TRANSFERASE THETA 2;	nu93c12.s1 NCI_CGAP_PI22 Homo sapiens cDNA clone IMAGE:12182623' similar to SW:GTT2_HUMAN P30712 GLUTHATHIONE S-TRANSFERASE THETA 2:	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA	ya48e06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53057 5'	601186922F2 NIH_MGC_15 Hamo sapiens cDNA clone IMAGE:2859636 5	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA	RC1-HT0615-200400-022-d04 HT0615 Homo sapiens cDNA	Homo saplens AT-binding transcription factor 1 (ATBF1), mRNA	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'	Novel human gene mapping to chomosome 13	PM0-BT0340-091299-002-e05 BT0340 Homo sapiens cDNA	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01	601479417F1 NIH_MGC_68 Homo sepiens cDNA done IMAGE:3882124 6'	601479417F1 NIH_MGC_68 Horro sapiens cDNA clone IMAGE:3882124 5'	ys90g08.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP:A53491 A53491 RUMETANIDE-SENSITIVE NA.KC1 COTPANSDOPTED CONV.	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-1e-12	601063030F1 NIH MGC 10 Homo sapiens cDNA clone IMAGE:3449599 5'	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA	Homo sapiens KIAA0744 gene product, histone deacetylase 7 (KIAA0744), mRNA	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002690 51
JIE EXOII PIOD	Top Hit Database Source	N	EST_HUMAN	F	뉟	EST_HUMAN		T HUMAN			T_HUMAN	HUMAN	EST_HUMAN		EST_HUMAN		EST_HUMAN	EST_HUMAN					EST HUMAN	EST HIMAN	Т	EST HUMAN	EST_HUMAN	EST_HUMAN			EST_HUMAN /
3,10	Top Hit Acession No.	AF240698.1	3E146144.1	2	2	1.0E-109 AI655417.1	AA662274.1	AA662274.1	4504206 NT	7662083 NT		_	1	5174622 NT	1.0E-109 BE179356.1	11432574 NT	1	.1		1.0E-109 AW749130.1	+	1	1			-	۲-	_	7662279 NT	562279	
	Most Similar (Top) Hit BLAST E Value	1.0E-109 AF240698.	1.0E-109 BE146144	1.0E-109 AB011181	1.0E-109 AB011181	1.0E-109	1.0E-109 AA662274	1.0E-109 AA662274.	1.0E-109	1.0E-109	1.0E-109 R15400.1	1.0E-109 BE293673	1.0E-109 BE293673.	1.0E-109	1.0E-109	1.0E-109	1.0E-109 BF182707	1.0E-109 BF182707	1.0E-109 AL049784.	1.0E-109	1.0E-109 AA077498.	1.0E-109 BE787540.	1.0E-109 BE787540.	1.0E-109 H84860.1	1.0E-109 F06604.1	1.0E-109 BE540909	1.0E-109 BE540909	1.0E-109 BF694831.	1.0E-109	1.0E-109	1.0E-109 AU121370.
	Expression Signal	1.2	1.53	1.54	1.54	3.67	1.02	1.02	2.25	1.19	1.04	0.86	0.86	2.31	1.48	3.66	5.01	5.01	1.36	1.23	1.72	5.71	5.71	N	1.41	2.93	2.93	14.2	2.12	2.12	1.88
	ORF SEQ ID NO:	23195		23601	23602	23732	23749	23750	23986	24175	24503	24626	24627	24950		26491	26492	26493	26820	26892		27139	27140	27402	27528	28294	28295	28318	28464	28465	28606
	Exon SEQ ID NO:	13390	13680	13821	13821	13956	13972	13972	14202	14390	14720	14859	14859	15176	15364	16325	16326	16326	16632	16699	16907	16948	16948	17202	17322	18043	18043	18069	18212	18212	18341
	Probe SEQ ID NO:	3474	3767	3911	3911	4054	4070	4070	4304	4498	4839	4984	4984	5254	5648	6465	6466	6466	6753	6820	7030	7071	7071	7326	7462	8155	8155	8183	8335	8335	8468

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		_	,	_	_	_		7	_	_	_		_	-		_	_			1777					-	*****	-			دو: خود	وتحيثها
Single Exon Mobes Expressed in Heart	Top Hit Descriptor	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA	zb08b12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to PIR:S43969 S43969 p54-beta stress-activated protein kinases - rat;	Homo sapiens SNF5/INI1 gene, exon 6	Homo saplens gene for AF-6, complete cds	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA	Homo sapiens leucine-zipper-ilka transcriptional regulator, 1 (LZTR1), mRNA	Homo saplens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA	C04498 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC3467	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA	Human mRNA for Inward rectifier potassium channel, complete cds	Human dystrobrevin (DTN) gene, exon 20	Homo sapiens calcitonin receptor-like (CALCRL) mRNA	Homo saplens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5'	Ul-H-BI4-aos-b-05-0-Ul.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomai protein (L44L) and FTP3 (FTP3) genes, complete cds	Homo sapiens pregnancy-zone protein (PZP), mRNA	Homo sapiens pregnancy-zone protein (PZP), mRNA	bb82a05.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048848 5' similar to TR:O60312 O60312 KIAA0566 PROTEIN;	ou32b10x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to SW:N121_RAT P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121:	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'	Homo saplens KIAA1002 protein (KIAA1002), mRNA	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA	Homo saplens hypothetical protein FLJ10300 (FLJ10300), mRNA	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'	Homo sapiens mRNA for KIAA0868 protein, partial cds
Jie Exori Pior	Top Hit Database Source	IN	EST_HUMAN	NT	NT	NT	TN	NT	EST_HUMAN	NT	NT	L	NT	NT	EST_HUMAN	EST HUMAN	NT	LN.	LN	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	TN	EST HUMAN	NT	NT	٦	EST_HUMAN	EST_HUMAN	님
in l	Top Hit Acession No.	4502838 NT	1.0E-109 W16510.1	Y17123.1	1.0E-109 AB011399.1	7549804 NT	5803073 NT	5803073 NT		7549804 NT	087291.1	U84550.1	5031620 NT	1.0E-110 AB032253.1	BE379477.1	1.0E-110 BF508896.1	4503098 NT	J78027.1	11436041 NT	11436041 NT	1.0E-110 BE018556.1	AI017213.1	1.0E-110 AU117812.1	7662441	1.0E-110 BE299406.1 ES	11419323 NT	11419323 NT	M55112.1	1.0E-110 AV714276.1		1.0E-110 AB020675.1
	Most Similar (Top) Hit BLAST E Value	1.0E-109	1.0E-109	1.0E-109 Y17123.1	1.0E-109	1.0E-110	1.0E-110	1.0E-110	1.0E-110 C04498.1	1.0E-110	1.0E-110 D87291.1	1.0E-110 U84550.1	1.0E-110	1.0E-110	1.0E-110 BE379477	1.0E-110	1.0E-110	1.0E-110 U78027.1	1.0E-110	1.0E-110	1.0E-110	1.0E-110 AI017213.	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110 M55112.1	1.0E-110	1.0E-110	1.0E-110
	Expression Signal	2.19	4.83	1.65	2.8	1.48	3.88	3.88	30.63	1.67	0.91	1.16	1.09	1.01	1.5	1.86	1.02	1.07	1.87	1.87	0.92	2.06	2.08	234	1.9	7.34	7.34	4.36	10.04	10.04	2.7
	ORF SEQ ID NO:	28848	28810	21993	25275	19781	19817	19818	19876	19781		20269	20921	21016	21650				22885	22886	23650	24207	24232		24929	25492	25493	26068			26432
	Exan SEQ ID NO:	18564	18527	12091	19176	9990	10021	10021	10059	0666	10255	10458	11076	11165	11775	11904	12739	12975	13083	13083	13873	14426	14447	14778	15161	15429	15429	19458	16253	16253	16270
	Probe SEQ ID NO:	8676	8710	9259	9594	3	34	34	75	104	291	516	1163	1258	1879	2012	2810	3048	3158	3158	3966	4533	4555	4898	5237	5511	5511	6032	6391	6391	6409

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Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	QV2-LT0053-020400-119-e04 LT0053 Homo sapiens cDNA	Homo sapiens galactokinase 2 (GALK2), mRNA	H. sapiens mRNA for myotonic dystrophy protein kinase like protein	601565504F1 NIH_MGC_21 Homo sepiens cDNA clone IMAGE:3840433 5'	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5	zw67g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781298 5' similar to TR:G1145816 G1145816 FKBP54:	601439784F1 NIH MGC 72 Homo sapiens cDNA clone IMAGE 3924548 5	LO-BT0163-040899-094-g10 BT0163 Homo sapiens cDNA	Homo sapiens gene for AF-6, complete cds	PM3-NN1082-140900-006-f12 NN1082 Homo sapiens cDNA	Human ribosomal protein L23a mRNA, complete cds	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'	Homo saplens cat eye syndrome critical region gene 1 (CECR1), mRNA	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA	Human enkephalin B (enkB) gene, exon 4 and 3' flank and complete cds	247b07.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN):	247b07.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN)	qp09g12.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M29893 RAS-RELATED PROTEIN RAL-A (HUMAN):	L2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA	zn62c12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE 562774 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MISCLE (HIIMAN).	Human beta4-integrin (ITGB4) gene, exon 13	601847132F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE 4078303 5'	Human mRNA for integrin alpha-2 subunit	Human mRNA for integrin alpha-2 subunit	Homo sapiens Trio isoform mRNA, complete cds
gle Exon Prob	Top Hit Database Source	EST_HUMAN	F	IN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	N F	EST_HUMAN	TN	NT	EST_HUMAN	NT	NT	TN	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST HUMAN		EST HUMAN		T_HUMAN		L	닏
Sin	Top Hit Acession No.	1.0E-110 AW838394.1 EST_	11432732	(12337.1	3E734357.1	3E734357.1	1.0E-110 AA446529.1	1.0E-110 BE897218.1		1.0E-110 AB011399.1			4758807 NT	BF035327.1	8393092 NT	125142.1	6912641 NT	6912641	7661569 NT	(02268.1	VA151017.1	VA151017.1	N344679.1	3F366228.1	A133914.1		-			
	Most Similar (Top) Hit BLAST E	1.0E-110	1.0E-110	1.0E-110 Y12337.1	1.0E-110 BE734357	1.0E-110 BE734357	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110 BF364546.	1.0E-111 U43701.1	1.0E-111	1.0E-111	1.0E-111	1.0E-111 M25142.1	1.0E-111	1.0E-111	1.0E-111	1.0E-111 K02268.1	1.0E-111 AA151017	1.0E-111 AA151017	1.0E-111 Al344679.	1.0E-111 BF366228.	1.0E-111 AA133914	1.0E-111 U66533.1	1.0E-111 BF214902	1.0E-111 X17033.1	1.0E-111 X17033.1	1.0E-111 AF091395.
	Expression Signal	2.91	4.27	3.7	3.49	3.49	2.43	4.15	5.78	1.63	5.07	16.85	1.02	1.87	3.58	73.62	1.17	1.17	1.08	4.45	2.82	2.82	1.71	3.03	2.29	3.13	10.8	13.75	13.75	3.26
-	ORF SEQ ID NO:	27583	28004	28266	28462	28463	28133						19978		20489	20684	23342	23343	23760	23909	25117	25118	25685	26423	26622	26866		27221	27222	27321
	Exon SEQ ID NO:	17374		18018	18211	18211	17889	18857	18935	19080		10140	10161				13556	13556	13982	14133	15284	15284	15584	16263	16437	16674	16990	17026	17026	17128
	Probe SEQ ID NO:	7523	7915	8130	8334	8334	8740	9081	9204	9444	9278	168	189	718	726	911	3642	3642	4080	4235	5364	5364	5675	6402	6229	6795	7113	7149	7149	7251

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Single Exon Probes Expressed in Heart

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Single Exon Plobes Expressed in real	Top Hit Descriptor	ae58g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:L09235 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);	zl31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE.503545 5'	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA	72C9 Human retina cDNA Tsp509I-cleaved sublibrary Homo saplens cDNA not directional	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA	Human steroidogenic acute regulatory protein (StAR) gene, exon 5	Human steroidogenic acute regulatory protein (StAR) gene, exon 5	UI-H-BI4-act-g-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'	UI-H-BI4-aof-g-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds	ZINC FINGER PROTEIN 135	Homo sapiens KIAA0440 protein (KIAA0440), mRNA	Homo sapiens KIAA0440 protein (KIAA0440), mRNA	601442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5'	MR2-BT0590-090300-113-f09 BT0590 Homo sapiens cDNA	Homo sapiens mRNA for KIAA1411 protein, partial cds	Homo sapiens mRNA for KIAA1411 protein, partial cds	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDIT), mRNA	yy35d07.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273229 5'	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'	780g07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to TR:Q9VW35 Q9VW35 G8743 PROTEIN.;	MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
Jie Exon Proc	Top Hit Database Source	EST_HUMAN	EST_HUMAN	NT		EST_HUMAN	Z	N	NT	NT	LN	EST_HUMAN	EST_HUMAN	NT	SWISSPROT	NT	NT	EST_HUMAN	EST_HUMAN	NT	NT	LN	EST_HUMAN	L L	K	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	LN
) II	Top Hit Acession No.	AA504160.1	\A131248.1	J68159.1	11417901 NT	N 22562.1	11430460 NT	11430460 NT	4501854 NT	J29103.1	J29103.1	3F509039.1	3F509039.1	4F157623.1	52742	7662125 NT	7662125 NT	1.0E-112 BE866859.1	3E076073.1	1.0E-112 AB037832.1	1.0E-112 AB037832.1	9055269 NT	N46046.1	11416777 NT	11416777 NT	1.0E-112 AU118051.1	1.0E-112 BE867635.1	1.0E-112 BE867635.1	1.0E-112 BF111413.1	1.0E-112 AW863327.1	1.0E-112 AJ249900.1
	Most Similar (Top) Hit BLAST E Value	1.0E-111 AA504160	1.0E-111 AA131248	1.0E-111 U68159.1	1.0E-111	1.0E-111 W22562.1	1.0E-111	1.0E-111	1.0E-112	1.0E-112 U29103.1	1.0E-112 U29103.1	1.0E-112 BF509039	1.0E-112 BF509039.	1.0E-112 AF157623	1.0E-112 P52742	1.0E-112	1.0E-112	1.0E-112	1.0E-112 BE076073	1.0E-112	1.0E-112	1.0E-112	1.0E-112 N46046.1	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112
	Expression Signal	1.51	6.35	4.52	3.04	1.69	1.39	1.39	2.66	4.49	4.49	1.48	1.48	2.78	1.72	5.88	5.88	2.45	0.83	5.12	5.12	0.94	33.34	1.81	1.81	1.65	2.25	2.25	2.09	4.25	2.86
	ORF SEQ ID NO:	27935	27986	28529	29110	25130	25171	25172	20335	20337	20338	20363	20364	20753	20805	21424	21425	22231	23510	24321	24322	24804	25463	26364	26365	26834			27767		
	Exon SEQ ID NO:	17690	17743	18277	18825	19489	19422	19422	10528	10530	10530	10552	10552	10908	10964	11560	11560	12337	13721	14533	14533	15036	15397	16203	16203	16645	17058	17058	17543	18047	18195
	Probe SEQ ID NO:	7840	7893	8401	9038	9896	9959	6966	265	594	594	616	616	982	1046	1658	1658	2460	3809	4646	4646	5170	5477	6340	6340	9929	7181	7181	7693	8159	8318

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Single Exon Probes Expressed in Heart

			362	362	T		T						T				T	Τ	T		T		T			T		T	T	T	T
Single Exon Probes Expressed in Heart	Top Hit Descriptor	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5'	qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMACE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES;	qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES;	PM0-CT0237-141099-001-h02 CT0237 Homo sapiens cDNA	a095f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625.3	ao95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'	Human X-linked phosphoglycerate kinase gene, exon 8	ao95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE 1953625 3'	ULH-BW1-anI-f-03-0-UI.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE: 3082876 3	Homo sapiens PLP gene	Homo sapiens mRNA for putative RNA helicase, 3' end	Homo sapiens v-ets avian enythroblastosis virus E26 oncodene related (FRG) mRNA	Homo sapiens v-ets avian erythroblastosis virus E26 oncodene related (FRG) mRNA	601469465F1 NIH_MGC_67 Homo saplens cDNA clone IMAGE:3872536 5	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'	Homo sapiens UDP-N-acetyt-alpha-D-galactosamine:polypeptide N-acetylgalactosaminytransferase 8 (GalNAc-TR) (GalNTR) mDNA	601297709F1 NIH MGC 19 Homo seniens cDNA clare IMAGE 3627554 F	601297709F1 NIH MGC 19 Homo sapiens cDNA clone IMAGE 3627554 5	Homo sapiens transmembrane protein 2 (TMEM2), mRNA	UI-HF-BN0-akj-b-12-0-UI.r1 NIH MGC 50 Homo sapiens cDNA clone IMAGE 30772326 5'	Homo sapiens glutamate receptor, ionotropic, N-methy D-aspartate 2A (GRIN2A) mRNA	Homo sapiens glutamate receptor, ionotropic, N-methy D-aspartate 24 (GRIN2A) mRNA	601105529F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE.2988365 5	yd15c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE 10898 3' similar to	gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN) contains All repetitive element:	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA	Homo sapiens rhabdoid fumor deletion region protein 1 (RTDR1) mRNA	Homo sapiens nucleoporin-like protein 1 (NLP 1), mRNA	Homo sapiens mRNA for KIAA1276 protein, partial cds
gle Exon Pro	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	EST HUMAN	EST_HUMAN	TN	N	Z	NT L	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN.	EST HUMAN	EST HUMAN	1	EST_HUMAN	N FA	F	EST HUMAN		EST_HUMAN	LN	N	NT	NT
CIS	Top Hit Acession No.	BE280479.1	AI792603.1	1.0E-112 AI792603.1	AW377670.1	Al365586.1	Al365586.1	M11965.1	1.0E-113 Al365586.1	1.0E-113 BF515218.1	1.0E-113 AJ006976.1	1.0E-113 AJ223948.1	7657065 NT	7657065 NT	1.0E-113 BE780858.1	4.1	1.1	11525737 NT	1.0E-113 BE382842.1	1.0E-113 BE382842.1	11429367 NT	9.1	F006002 NT	6006002 NT	1.0E-113 BE292968.1		T70551.1	8923087 NT	7657529 NT	6679073 NT	1.0E-114 AB033102.1
	Most Similar (Top) Hit BLAST E Value	1.0E-112	1.0E-112 AI792603	1.0E-112	1.0E-112 AW3776	1.0E-113 Al365586.	1.0E-113 AI365586.	1.0E-113 M11965.1	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113 AU12721	1.0E-113 AU14029	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113 AW 50051	1.0E-113	1.0E-113	1.0E-113 E		1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114 /
	Expression Signal	1.72	1.75	1.75	5	3.71	3.71	6.32	2.94	1.18	0.96	2.34	0.95	0.95	16.27	6.33	3.92	2.05	2.95	2.95	1.29	1.73	2.07	2.07	3.44		7.66	1.31	3.47	5.53	0.82
	ORF SEQ ID NO:	28578	28637	28638	28657	20487	20488	20700	21286	.21833	22179	22813	24677	24678		25144	25605	25710	27326	27327	27731	28604	25832	25833	28721		20379	20815	21053	21413	19823
	Exon SEQ ID NO:	18319	18373	18373	18393	10657	10657	10852	11428	11939	12282	13018	14907	14907	19524	15297	15523	15608	17134	17134	17506	18339	15719	15719	18452		10566	10972	11198	11552	10025
	Probe SEQ ID NO:	8445	8500	8500	8521	725	725	927	1523	2048	2405	3091	5035	5035	5211	5377	5608	5699	7257	7257	7656	8466	8550	8550	8584		629	1055	1291	1648	2773

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Single Exoll Flores Explessed III Healt	Top Hit Top Hit Descriptor Top Hit Descriptor	.1 NT Homo sapiens mRNA for KIAA1276 protein, partial cds	NT Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13	EST_HUMAN	LN	1 EST HUMAN	N	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain 506880 NT (TM) and short cytoplasmic domain, (semaphorin) 54 (SEMA5A) mRNA		NT Homo sapiens NF2 gene	NT Homo sapiens NF2 gene	57600 NT	EST_HUMAN	EST_HUMAN	TN	NT Homo sapiens mRNA for KIAA0561 protein, partial cds	1 NT	5.1 EST_HUMAN dq03f05.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE.2846744 5'	.1 NT Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds	2 NT Homo sapiens chromosome 21 segment HS21C027	ba73g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17206 40S RIBOSOMAI PROTEIN SA (ILIMAN): A-MARASOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARSOMA CLONE I BARS	Complete (MOUSE);	EST HUMAN	1 EST HUMAN	1 EST_HUMAN	EST_HUMAN			034850 NT Homo sapiens hypothetical protein (DJ1042K10.2), mRNA		505938 NT Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
algino.	Top Hit Acession No.	1.0E-114 AB033102.1 NT	1.0E-114 X04086.1	1.0E-114 BF206374.1 ES	1.0E-114 AF149773.1 NT	1.0E-114 AA194468.1 ES	_	4506880 NT	4506880 NT		1.0E-114 Y18000.1	4557600 NT	1.0E-114 Al363139.1 ES	1.0E-114 Al363139.1 ES		1.0E-114 AB011133.1 NT	1.0E-114 AB011133.1 NT	1.0E-114 AW327455.1 ES		1.0E-114 AL163227.2 NT		1.0E-114 BE302666.1 ES	1.0E-114 AV733454.1 ES	1.0E-114 AV733454.1 ES	1.0E-114 AV733454.1 ES	AV733454.1	11418041 NT	11034850 NT	11034850 NT	4758111 NT	4505938 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-114	1.0E-114	1.0E-114		1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114 Y18000.1	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114		1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-115	1.0E-115
	Expression Signal	0.82	2.29	1.2	1.95	1.2	2.31	1.37	1.37	7.08	7.08	1.86	1.73	1.73	3.39	6.35	6.35	3.79	3.13	1.31		7.14	4.58	4.58	2.86	2.86	3.21	3.06	3.06	3.36	0.95
	ORF SEQ ID NO:	19824	22814		23621	24762	24763	25040	25041	26338	26339	26673	26814	26815	27116	27161	27162		26652	27940			28666	28667	28932	28933		25222	25223	19801	19920
	Exon SEQ ID NO:	10025	13019	13060	13843	14988	14989	15237	15237	16179	16179	16486	16627	16627		16967	16967		16459	17694		18055	18399	18399	18647	18647					10099
	Probe SEQ ID NO:	2773	3092	3135	3934	5120	5121	5316	5316	6316	6316	9099	6748	6748	7048	7090	7090	7418	7447	7844		8167	8527	8527	8834	8834	9479	9729	9729	21	125

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Slight Excit Forces Expressed III real	Top Hit Descriptor	Homo sapiens keratin 18 (KRT18) mRNA	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA	qt06f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:000536 000536 TTF-I INTERACTING PEPTIDE 5;	q06f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR.O00536 O00536 TTF-I INTERACTING PEPTIDE 5 :	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds	Homo saplens partial TTN gene for titin	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)	Homo sapiens partial TTN gene for titin	Homo sapiens mRNA for KIAA0350 protein, partial cds	Novel human gene mapping to chomosome X	Homo sapiens sir2-like 3 (SIRT3), mRNA	Homo sapiens EphA4 (EPHA4) mRNA	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes	Homo sapiens chromosome 21 segment HS21C068	Homo saplens chromosome 21 segment HS21C068	EST382416 MAGE resequences, MAGK Homo sapiens cDNA	602119346F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276738 5	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63436), mRNA	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
פריים ווחתם	Top Hit Database Source		EST HUMAN Q	EST HUMAN T						NT	NT	H)	EST_HUMAN 60	EST_HUMAN 60	EST HUMAN Q		NT			N			N LN	NT		NT TN		EST HUMAN 6				
ignio.	Top Hit Acession No.	57887	1.0E-115 AW804759.1			74702	5174702 NT	4503794 NT	1.0E-115 AF229180.1	1.0E-115 AF229180.1	1.0E-115 AJ277892.1		-	-	1.0E-115 AW804759.1	1	1.0E-115 AJ245922.1	1.0E-115 AJ277892.1	2	1.0E-115 AL137163.1	6912659 NT	4758279 NT	1.0E-115 AL096857.1	1.0E-115 AL096857.1		2	1.0E-115 AW970335.1	1.0E-115 BF665387.1	11425128 NT	11425128 NT	1142603B NT	7661883 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-115	1.0E-115	1.0E-115 Al339206.1	1.0E-115 Al339206.1	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115 U78027.1	1.0E-115 BE745469	1.0E-115 BE745469.	1.0E-115	1.0E-115 AJ245922.	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115
	Expression Signal	1.99	2.17	1.08	1.08	1.83	1.83	49.82	0.92	0.92	3.14	1.42	0.87	78.0	1.78	2.1	2.1	4.03	4.04	1.09	3.41	3.83	2.58	2.58	2.96	2.96	1.75	7.22	2.05	2.05	12.92	1.93
	ORF SEQ ID NO:		20073	20278	20279	20537	20538	20540	21301	21302	21561	21573		21818		22795	22796	23149	23640	23844		24014	24254					25055	25369			25960
	Exon SEQ ID NO:	10103	10253	10467	10467	10699	10699	10701	11443	11443	11683	11696	1_	11925	12749	13004	13004	13344	L	14069	14199	14232	14468	14468		1_	15201	15250	15321	15321		15838
	Probe SEQ ID NO:	129	289	525	525	7697	769	777	1539	1539	1785	1798	2034	2034	2820	3077	3077	3427	3956	4169	4301	4335	4578	4578	4813	4813	5279	5330	5402	5402	5852	5933

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Table 4
Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA	oz31a06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'	oz31a06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'	Homo sapiens mRNA for KIAA0995 protein, partial cds	RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA	RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA	Human mRNA for KIAA0338 gene, partial cds	Human mRNA for KIAA0338 gene, partial cds	x32f08.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW:CAYP_CANFA P10463 CALCYPHOSINE;	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988875 5'	Homo sapiens synaptojanin 1 (SYNJ1), mRNA	Homo sapiens synaptojanin 1 (SYNJ1), mRNA	Homo sapiens pericentrin (PCNT) mRNA	Homo sapiens pericentrin (PCNT) mRNA	AU133080 NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5'	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18	Homo saplens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and	olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds	Homo sapiens mRNA for KIAA0790 protein, partial cds	601513337F1 NIH_MGC_71 Homo sapiens cDNA done IMAGE:3914600 5'	Homo sapiens DiGeorge syndrome critical region, centromeric end	Homo sapiens DiGeorge syndrome critical region, centromeric end	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA	PM-BT135-070499-016 BT135 Homo sapiens cDNA	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5	zc24d07.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW:MDHM_MOUSE P08249 MALATE DEHYDROGENASF_MITOCHONDRIAL PRECLIRSOR	Homo capiane mBNA for KTA A1636 profesion and John College and A1636 profesion and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John College and John Col	ווייטין וייטיטן אלאויון איזיין וויסיטן אלאוין וויסיטן אלאוין וויסיטן אלאוין וויסיטן אלאוין וויסיטן אלאוין וויסיסן
es Expr		Homo sal	oz31a06.	oz31a06.	Homo say	RC6-ET0	RC6-ET0	Homo sa	Human n	Human n	xx32f08.x P10463 C	Homo sa	6011213	Homo sa	Homo sa	Homo sa	Homo sal	AU13308	Human a	Human a	Homo sa	Human o	olfactory	Homo sa	6015133	Homo say	Homo sa	Homo sa	PM-BT13	Homo sa	zc24d07.	Homo	5 5 5
le Exon Prob	Top Hit Database Source	トフ	EST_HUMAN	EST_HUMAN	77	EST_HUMAN	EST_HUMAN	ΛΤ	N⊤	N⊺	EST_HUMAN	トラ	EST_HUMAN		FZ	NT	ラ	EST_HUMAN	, L	LN⊤	NT		NT NT		EST_HUMAN	NT	TN	T-Z	EST_HUMAN	לד	ST HUMAN	NT - I	
Sing	Top Hit Acession No.	7661883 NT	-	1	.1	.1	1.	11434772 NT		1.0E-115 AB002336.1	4.1	4502528 NT	1.0E-116 BE275502.1	4507334 NT	4507334 NT	5174478 NT	4478	1.0E-116 AU133080.1			5453941 NT				5.1			5031954 NT	1	.1		-	
	Most Similar (Top) Hit BLAST E Value	1.0E-115	1.0E-115 AI076598	1.0E-115 AI076598	1.0E-115	1.0E-115 BE830187	1.0E-115 BE830187	1.0E-115	1.0E-115	1.0E-115	1.0E-115 AW57154	1.0E-115	1.0E-116	1.0E-116	1.0E-116	1.0E-116	1.0E-116	1.0E-116	1.0E-116 M19824.1	1.0E-116 M19824.1	1.0E-116		1.0E-116 U78308.1	1.0E-116	1.0E-116	1.0E-116 L77570.1	1.0E-116 L77570.1	1.0E-116	1.0E-116 AI907096	1.0E-116 AJ243213	1.0E-116 W42822.1	1 OE 116 /	1011-10.
	Expression Signal	1.93	1.55	1.55	7.41	12.78	12.78	2.2	1.92	1.92	3.5	2.26	1.42	1.25	68.9	2.38	2.38	1.21	1.01	1.01	1.88		1.49	4.48	2.19	4.73	4.73	2.01	2.17	1.2	5.88	4 65	20.
	ORF SEQ ID NO:	25961	26333	26334	26401	26811	26812	27184	27816	27817	28239	28801	20306	20552		21733	21734	21765	21834	21835	22042			22181	22458	22860	22861	23958	24418	24764	25641	25781	40701
	Exon SEQ ID NO:	15838	16176	16176	16241	16623	16623	16993	17595	17595	17990	18519	10500	10713	10768	11847	11847	11873	12711	12711	12143		12175	12284	12656	13062	13062	14180	14632	14990	15550	15675	1202
	Probe SEQ ID NO:	5933	6313	6313	6379	6744	6744	7116	7745	7745	8100	8701	560	282	841	1952	1952	1980	2050	2050	2259		2293	2407	2704	3137	3137	4281	4747	5122	2637	5768	20.70

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Table 4
Single Exon Probes Expressed in Heart

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Single Extri Flobes Explessed in reali	Top Hit Descriptor	Homo sapiens mRNA for KIAA1636 protein, partial cds	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5	MR2-HT0379-210200-102-b04 HT0379 Homo sapiens cDNA	C02944 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC0567	AV716314 DCB Homo sapiens cDNA clane DCBBCG06 5'	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keralin 2	601338268F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680680 5'	qh09c05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844168 3' similar to gb:X53741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA	CM2-CT0482-300800-349-e05 CT0482 Homo sapiens cDNA	qq41e04.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1935102.3' similar to WP:B0495.7	CE01765;	601108350F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344580 5	DKFZp762L1110_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762L1110 5	Homo saplens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds	Human apolipoprotein B-100 (apoB) gene, exon 10	EST369769 MAGE resequences, MAGE Homo sapiens cDNA	op32c11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'	EST188414 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein 1.29	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA	DKFZp434C1120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1120 5'	H.sapiens mRNA for TPCR16 protein	H. sapiens mRNA for TPCR16 protein	Homo sapiens Scar2 (SCAR2) gene, partial cds	Homo sapiens Scar2 (SCAR2) gene, partial cds	Homo sapiens mRNA for KIAA0866 protein, complete cds	601562657F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
JIE EXOII PIOL	Top Hit Database Source	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	EST HUMAN		EST HUMAN	EST HUMAN	EST HUMAN	NT	LN	NT	NT	EST_HUMAN	EST_HUMAN	EST HIMAN	LN	EST HUMAN	NT	LZ.	LN	ΝΤ	NT	EST HUMAN	LN	L
) IIIC	Top Hit Acession No.	1.0E-116 AB046856.1	1.0E-116 BF677910.1	1.0E-116 BE158133.1	C02944.1	1.0E-116 AV716314.1	1.0E-116 AA354256.1		1.0E-116 BE565507.1	AI216352.1	11418646 NT	1.0E-116 BF335849.1				1.0E-116 AL134889.1	4826636 NT	1.0E-117 AF124393.1	1.0E-117 AF123320.1		1.0E-117 AW957699.1	1.0E-117 AA978114.1	1 0E-117 AA316723 1	8659564 NT	1.0E-117 AL042120.1	X89670.1	X89670.1	1.0E-117 AF134304.2	1.0E-117 AF134304.2	1.0E-117 AB020673.1	1.0E-117 BE730508.1	L76571.1	L76571.1
	Most Similar (Top) Hit BLAST E Value	1.0E-116	1.0E-116	1.0E-116	1.0E-116 C02944.1	1.0E-116	1.0E-116	1.0E-116	1.0E-116	1.0E-116 AI216352.	1.0E-116	1.0E-116		1.0E-116 Al367140	1.0E-116	1.0E-116	1.0E-117	1.0E-117	1.0E-117	1.0E-117 M19816.1	1.0E-117	1.0E-117	4 OE-447	1 0F-117	1.0E-117	1.0E-117 X89670.1	1.0E-117 X89670.1	1.0E-117	1.0E-117	1.0E-117	1.0E-117	1.0E-117 L76571.1	1.0E-117 L76571.1
	Expression Signal	1.65	72.79	1.8	3.59	79.7	1.99	1.99	1.43	1.98	1.77	3.68		3.23	2.08	2.68	1.18	1.59	6.25	2.3	2.99	1.75	69 6	1 86	1.88	1.35	1.35	9.22	9.22	3.36	2.5	4.99	4.99
	ORF SEQ ID NO:	25782	25877		26156	26295	26949	26950	27239	27330	27642			28615			20296	20821	21489	21564	21952	22953	23500					24382	24383	24516	24978		26427
	Exon SEQ ID NO:	15675	15759	15829	16018	16139	16753	16753	17050	17137	17428	17965		18350	19741	19614	10487	12684	11620	11688	12051		2,00,4		1		L.	14591	14591	14736	15202		16265
	Probe SEQ ID NO:	2768	5853	5924	6145	6275	6874	6874	7173	7260	7577	8074		8477	9591	9776	546	1061	1719	1790	2164	3230	000	7777	4475	4622	4622	4705	4705	4856	5280	6404	6404

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Table 4
Single Exon Probes Expressed in Heart

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| Top Hit Descriptor | AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5' | AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5' | wp86b07.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2468629 3' similar to TR:O75065
O75065 KIAA6477 PROTEIN | Homo sapiens neural cell adhesion molecule 1 (NCAM1) mRNA | Homo sapiens neural cell adhesion molecule 1 (NCAM1). mRNA | Human gene for very low density lipoprotein receptor, exon 11 | 601569317F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3843748 5' | zd83b11.1 Soares fetal heart NbHH19W Homo sepiens cDNA clone IMAGE:347229 5' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
 | Homo sapiens mRNA for MEGF8, partial cds | Homo sapiens mRNA for MEGF8, partial cds | 601186203F1 NIH_MGC_8 Homo saplens cDNA clone IMAGE:3544296 5 | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA | Homo sapiens HSPC151 mRNA, complete cds | DKFZp434l056_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434l056 5 | Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA | Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
 | 601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5' | 601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5' | 601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5' | EST363799 MAGE resequences, MAGB Homo sapiens cDNA

 | Human breakpoint cluster region (BCR) gene, complete cds | Human breakpoint cluster region (BCR) gene, complete cds
 | Homo sapiens PRKY exon 7 | qp01f05x1 NCI_CGAP_Kld5 Homo sapiens cDNA clone IMAGE:1916769 3' | qp01f05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
 | Human mRNA for ribosomal protein, complete cds | Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3 | Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3 | Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
 | Homo saplens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA | Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA |
| Top Hit
Database
Source | EST_HUMAN | EST_HUMAN | EST HIMAN | N LN | TN | ĽZ. | EST_HUMAN | EST_HUMAN
 | N | ΝŢ | EST_HUMAN | LN LN | NT | NT | EST_HUMAN | LN | N
 | EST HUMAN | EST_HUMAN | EST_HUMAN | EST_HUMAN

 | NT | NT
 | LN | EST_HUMAN | EST_HUMAN
 | N | NT | NT | LN
 | LZ | NT |
| Top Hit Acession
No. | 4V717788.1 | 4V717788.1 | A1950145 1 | 10834989 | 10834989 | J16524.1 | 3E733922.1 | N 80605.1
 | AB011541.1 | AB011541.1 | 3E269856.1 | 4501848 | 4501848 | 4F161500.1 | AL045854.1 | 7657016 | 5174680
 | - | _ | _ | 4W951729.1

 | J07000.1 | J07000.1
 | /13932.1 | |
 | | 1 | 1 | 11420764
 | 4557732 | 4557732 NT |
| Most Similar
(Top) Hit
BLAST E
Value | 1.0E-117 | 1.0E-117 | | | 1.0E-117 | 1.0E-117 | 1.0E-117 | 1.0E-117
 | 1.0E-117 | 1.0E-117 | 1.0E-117 | 1.0E-117 | 1.0E-117 | 1.0E-118 | 1.0E-118 | 1.0E-118 | 1.0E-118
 | 1.0E-118 | 1.0E-118 | 1.0E-118 | 1.0E-118

 | 1.0E-118 | 1.0E-118
 | 1.0E-118 | 1.0E-118 | 1.0E-118
 | 1.0E-118 | 1.0E-118 | 1.0E-118 | 1.0E-118
 | 1.0E-118 | 1.0E-118 |
| Expression
Signal | 3.77 | 3.77 | 5.93 | 1.7 | 1.7 | 2.28 | 1.51 | 10.31
 | 3.98 | 3.96 | 15.63 | 222 | 2.22 | 9.54 | 2.59 | 5.09 | 86.0
 | 2.39 | 2.39 | 2.39 | 3.77

 | 2.38 | 2.38
 | 3.73 | 4.51 | 4.51
 | 7.67 | 2.02 | 2.02 | 1.88
 | 1.87 | 1.87 |
| ORF SEQ
ID NO: | 26482 | 26483 | 26725 | 26908 | 26909 | | 27706 | 28512
 | 28732 | 28733 | | 28974 | 28975 | 19863 | 19890 | 20261 | 20667
 | 21975 | 21976 | 21977 |

 | 22465 | 22466
 | | 22887 | 22888
 | 23679 | 25053 | 25054 | 25620
 | 28054 | 26055 |
| Exon
SEQ ID
NO: | 16316 | 16316 | 16531 | 16716 | 16716 | 17228 | 17486 | 18262
 | 18462 | 18462 | 18516 | 18684 | 18684 | 10050 | 10074 | 10448 | 12680
 | 12073 | 12073 | 12073 | 12165

 | 12574 | 12574
 | 12993 | 13084 | 13084
 | 13904 | 15249 | 15249 | 15535
 | 15924 | 15924 |
| Probe
SEQ ID
NO: | 6455 | 6455 | 6651 | 6837 | 6837 | 7361 | 7635 | 8385
 | 8595 | 8595 | 8698 | 8872 | 8872 | 64 | 80 | 506 | 968
 | 2186 | 2186 | 2186 | 2281

 | 2711 | 2711
 | 9908 | 3159 | 3159
 | 3998 | 5329 | 5329 | 5620
 | 6020 | 6020 |
| | Exon
SEQ ID NO:ORF SEQ
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Source | Exon ORF SEQ ID NO: Expression NO: (Top) Hit Acession NO: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit Acession No: Top Hit 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Table 4
Single Exon Probes Expressed in Heart

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Exon ORF SEQ Expression (Top) Hit Top Hit Acess No. SEQ ID ID NO: Signal (Top) Hit Top Hit Acess No. 16528 26722 2.23 1.0E-118 BEC62855.1 16728 26722 2.23 1.0E-118 BEC62855.1 16763 26960 7.81 1.0E-118 BEC62855.1 16767 26963 7.81 1.0E-118 BEC62855.1 16767 26964 7.81 1.0E-118 BEC62855.1 16767 26964 7.81 1.0E-118 BEC62855.1 16767 26964 1.34 1.0E-118 BEC62855.1 16767 26964 1.34 1.0E-118 BEC6285.1 16767 26964 1.34 1.0E-118 BA443024.1 16939 27129 1.28 1.0E-118 BA43024.1 1700 27286 5.71 1.0E-118 BA5507.1 18659 28947 1.75 1.0E-118 BF195407.1 18659 28947 1.75	שום ביותים פול	Top Hit Database Source	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N	NT	NT	NT	EST HUMAN	EST_HUMAN		EST_HUMAN	EST HUMAN	EST_HUMAN	TN	LN⊤	TN	NT	FCT HIMAN	L	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N⊤	EST_HUMAN	EST HUMAN
Exon ORF SEQ Expression Most Similar (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top) Hit (Top)	CIIC	Top Hit Acession No.	11431050	3E781223.1	3E062855.1	3E062855.1	AA443024.1	4A443024.1	AB002381.1	AB002381.1	4557732	4557732	3E263134.1	3F195407.1		AA315007.1	3F093687.1	3F093687.1	AF170492.1		AB023147.1	8922205	A A O 1 R 7 R D 1	4504116	AA077394.1	AU133399.1	M89914.1	BE936121.1	AV693731.1	AI150703.1	X06292.1	AW974193.1	BE796614.1
Exon ORF SEQ Expression SEQ ID NO: Signal NO: NO: Signal NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:			1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118 /	1.0E-118	1.0E-118 /	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118		1.0E-118	1.0E-118	1.0E-118	1.0E-119	1.0E-119	1.0E-119	1.0E-119	4 OF 140	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119 BE79661
Exon ORF SEQ 1D DR NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:			4.13	2.23	7.81	7.81	48.1	1.34	1.16	1.16	1.28	1.28	5.71	1.18		3.06	1.75	1.75	0.81	1.55	2.09	1.81	α .	1.15	0.95	2.45	14.93	3.32	2.24	7.19	2.79	4.26	1.42
		ORF SEQ ID NO:	26509					26964					27288																			25925	26403
Probe SEQ ID NO: NO: NO: NO: NO: NO: 10548 6884 6884 6888 6888 7035 7035 7035 7035 7035 7035 7035 7035		Exon SEQ ID NO:	16341	16528	16763	16763	16767	16767	16912	16912	16939	16939	17100	17786		18465	18659	18659	10672	12683	11786	12991	42126	13781	14979	15194	15204	15207	15256			15801	16243
		Probe SEQ ID NO:	6482	6648	6884	6884	6888	6888	7035	7035	7062	7062	7223	7936		8598	8847	8847	741	1021	1891	3064	2000	3870	5111	5272	5282	5285	5336	5726	5887	5835	6381

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Ongo Evol Topos Expressed III Topos	Top Hit Descriptor	aa32f05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5'	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17	602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'	RC3-CT0212-240999-011-f03 CT0212 Homo sapiens cDNA	Homo sapiens mRNA for KIAA0758 protein, partial cds	Homo saplens synaptojanin 1 (SYNJ1), mRNA	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds	yy40g12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273766 5'	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds	Homo sapiens gene for AF-6, complete cds	Homo sapiens gene for AF-6, complete cds	Homo sapiens aquaporin 4 (AQP4), splice variant b, mRNA	Homo sapiens synaptojanin 1 (SYNJ1), mRNA	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds	Homo sapiens stanniocalcin (STC) gene, partial cds	Homo sapiens stanniocalcin (STC) gene, partial cds	qd61f03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733981 3'	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5	Human TBXAS1 gene for thromboxane synthase, exon 7	Human gene for neurofilament subunit M (NF-M)	Human gene for neurofilament subunit M (NF-M)	602035352F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183333 5	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495	Homo sapiens mRNA for KIAA0465 protein, partial cds	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'	601888956F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4122876 5'	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'	Homo sapiens mRNA for KIAA1077 protein, partial cds	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone (WAGE:3532015 5'
201 1 1000	Top Hit Database Source	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	NT	LN	LN	LN	EST_HUMAN	NT	NT	LN	LN	NT	NT	NT	LN	LN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	LN	NT	EST_HUMAN	LN	TN	NT	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN
ב <u>ֿ</u>	Top Hit Acession No.	∿A465124.1	4J297701.1	3F569571.1	4W847519.1	AB018301.1	4507334 NT	1.0E-120 AF248540.1	1.0E-120 AF248540.1	V44873.1	1.0E-120 AF167706.1	1.0E-120 AB011399.1	1.0E-120 AB011399.1	4755124 NT	4507334 NT	1.0E-120 AF056490.1	AF056490.1	AF098463.1	AF098463.1	41190903.1	2.1	2.1		Y00067.1	Y00067.1	1.0E-120 BF337599.1	4B007964.1	AB007964.1	1.0E-120 AB007934.1	1.0E-120 BE392102.1	BE392102.1	BF306541.1	1.0E-120 AU133205.1	1.0E-120 AB029000.1	BE296387.1
	Most Similar (Top) Hit BLAST E Value	1.0E-119 AA46512	1.0E-119 AJ297701	1.0E-119 BF56957	1.0E-119 AW84751	1.0E-120 AB01830	1.0E-120	1.0E-120	1.0E-120	1.0E-120 N44873.1	1.0E-120	1.0⊑-120 /	1.0E-120	1.0E-120	1.0E-120	1.0E-120	1.0E-120 AF056490	1.0E-120 AF098463	1.0E-120 AF098463	1.0E-120 AI190903	1.0E-120 BF568222	1.0E-120 BF568222	1.0E-120 D34619.1	1.0E-120 Y00067.1	1.0E-120 Y00067.1	1.0E-120	1.0E-120 AB007964	1.0E-120 AB00796	1.0E-120	1.0E-120	1.0E-120 BE39210;	1.0E-120 BF30654*	1.0E-120	1.0E-120 /	1.0E-120 BE29638
	Expression Signal	1.48	1.42	9.72	1.37	1.4	1.34	1.67	1.67	4.53	3.87	6.0	6.0	0.84	1.13	1.17	1.17	2.79	2.79	0.89	13.84	13.84	1.49	1.67	1.67	2.44	2.43	2.43	1.33	4.54	4.54	4.72	7.31	2.53	6.4
	ORF SEQ ID NO:	27977	28089			20022	20082	20787	20788	21172	21348	21847	21848	22250	20082		23937	24242	24243	24801	25488	25489	26495	26674	26675		26971	2692	26993	27535	27536	27687	27698		28607
	Exon SEQ ID NO:	17733	17848	18407	19671	10205	10262	10943	10943	11311	11487	11950	11950	12358	10262	14159	14159	14455	14455	15034	15426	15426	16328	16488	16488	16729	16777	16777	16800	17330	17330	17468	17477		18342
	Probe SEQ ID NO:	7883	7998	8535	9348	237	298	1025	1025	1406	1583	2060	2060	2482	3267	4260	4260	4563	4563	5168	5508	5508	6469	8099	8099	6850	8689	8689	6922	7470	7470	7617	7626	7798	8469

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Table 4
Single Exon Probes Expressed in Heart

								nt a, mRNA	nt a, mRNA														MKNA	E458 allele,								V kappa II)
Single Exultriones Expressed in regard	Top Hit Descriptor	Human muscle glycogen phosphorylase (PYGM) gene, 5'UTR and exon 1	Homo sapiens calcineurin binding protein 1 (KIAA0330), ml⊀NA	Homo sapiens NF2 gene	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5	Homo sapiens TNF receptor-associated factor 1 (TKAF1) mKNA	Homo sapiens mRNA for KIAA0581 protein, partial cds	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds	602014759F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150286 5	602014759F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150286 5	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9	Homo sapiens mRNA for KIAA1337 protein, partial cds	Homo sapiens mRNA for KIAA1337 protein, partial cds	Homo saplens adaptor-related protein complex AP-4 epsilon subunit mKNA, complete cds	qx57b01x1 NCI_CGAP_Pan1 Homo sapiens culva cione IMAGE:2003417 3	H.sapiens ECE-1 gene (exon 17)	CM-BT043-090299-075 BT043 Homo sapiens cDINA	Homo sapiens DNA for prostacyclin synthase, exon 8	Homo sapiens DNA for prostacyclin synthase, exon 8	Homo saplens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), miXNA	Homo sapiens UDP-glucuronosytransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele,	Lower cariese chloride interellular channel 4 like (CHC41) mRNA	TOTIO Sapretto Callotte intraccitate, citatine Films conjunc of NA CE: 248448.3	yv/4c01.s1 Soares fetal liver spicen Tiving Shorifo Sapiens Coline living C. 246446 3	Homo sapiens T-cell lymphoma invasion and metastasis 1 (11AM1), mRNA	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA	Homo sepiens intersectin short isoform (ITSN) mRNA, complete cds	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
le Exoll rion	Top Hit Database Source			LΝ	T HUMAN		NT	FN.	LN	NT	EST HUMAN	EST_HUMAN	NT	N	닐	LN		EST_HUMAN	TN	EST_HUMAN	NT	NT	NT	Ė		Z	EST_HUMAN	NT	NT	NT	LN TN	۲.
Sing	Top Hit Acession No.	U94774.1	11417862 NT		1.0E-121 AU134963.1	5032192 NT	1.0E-121 AB011153.1	4755139 NT	4755139 NT	76631.1	BF344378.1	3F344378.1	719208.1	Y19208.1	1.0E-121 AB037758.1	1.0E-121 AB037758.1	1.0E-121 AF155156.2	1.0E-121 AI263294.1	X91937.1	AI904151.1	D84122.1		11427788 NT	7 0007	AF-054200.1	/330334 N		11526176 NT	1.0E-122 AF114488.1	11526176 NT	1.0E-122 AF114488.1	M20707.1
	Most Similar (Top) Hit BLAST E Value	1.0E-120 L	1.0E-120	1.0E-121 Y18000.1	1.0E-121 ₽	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121 L76631.1	1.0E-121	1.0E-121 BF34437	1.0E-121 Y19208.	1.0E-121 Y19208.1	1.0E-121	1.0E-121 /	1.0E-121	1.0E-121	1.0E-121 X91937.1	1.0E-121 AI904151	1.0E-121 D84122.	1.0E-121 D84122.	1.0E-121		_	1.0E-121	1.0E-121 N59624.	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122 M20707
	Expression Signal	2.07	1.36	1.04	0.98	1.23	0.99	0.89	0.89	1.17	1.05	1.05	3.09	3.09	1.09	1.09	6.61	1.21	2.55	1.03	2.58	2.58	4.44		2.28	4.91	3.48	3.99	2.22	1.54	2.85	3.41
	ORF SEQ ID NO:	29013	25288	19867	20151	20465	21319	21697	21698	21841	22295	22296	22763	22764	23213		23325	23910	24556		26701		28297				28489	20047			20641	20957
,	Exen SEQ ID NO:	18722	19111	10052	10328	12674	11461	11818	11818	11945	1			<u> </u>	13408	13408	13538	14134	14781	L	16512	16512	18045	<u> </u>			18240	10232		10312	10790	11111
	Probe SEQ ID NO:	8914	9495	29	374	707	1556	1923	1923	2055	2530	2530	3042	3042	3492	3492	3624	4236	4901	5050	6632	6632	8157		8163	8336	8363	267	333	355	864	1201

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Single Exoli Flobes Expressed in	Top Hit Database Source						EST_HUMAN 6			HOMAN			Т	٦	HOMAN						LZ LZ		Z			NT	LN	EST_HUMAN	EST_HUMAN	Ŋ	EST_HUMAN	L
Billo	Top Hit Acession No.	F167706.1	11418424 NT	11418424 NT			1.0E-122 BF316170.1	4502166 NT		1.0E-122 BE256039.1	11424216 NT	11418187 NT		1.0E-123 BF345274.1	1.0E-123 BF345274.1	1.0E-123 AL163249.2	5803114 NT	4505818 NT		4505818 NT	AJ388641.1	1.0E-123 M55419.1	M55419.1		7705962 NT	1.0E-123 L34219.1	1,0E-123 L34219.1	1.0E-123 BE799746.1	1.0E-123 AU118435.1	1.0E-123 U42224.1	1.0E-123 BE263001.1	1.0E-123 AB007923.1
	Most Similar (Top) Hit BLAST E Value	1.0E-122 AF167706.	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122 AW 50464	1.0E-122	1.0E-122	1.0E-122	1.0E-123 U31519.1	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1 0F-123		1.0E-123	1 0E-123 AJ38864	1.0E-123	1.0E-123 M55419.	1.0E-123 M55419.	1.0E-123	1.0E-123						
	Expression Signal	1.32	2.01	2.01	5.91	10.56	10.56	1.82	1.2	6.41	1.35	4.35	1.07	1.72	1.72	3.79	5.06	3.35	233	3.35	1 76	2.98	2.98	2.98	4.5	1.75	1.75	1.29	2.27	1.3	1.95	4.14
	ORF SEQ E	21435	21458	21459	21549	22215	22216	24409	-	25390	27286		19968	20517	20518	20760	20767		20310	20977	24244					25091						27517
	Exon SEQ ID NO:	11569	11586	11586	11671	12318	12318	1			1_	L		┶	L	L	1			11126	<u> </u>			1		\perp	L					2 17310
	Probe SEQ ID NO:	1667	1684	1684	1772	2441	2441	4738	4918	6051	7219	8606	181	751	751	966	1005		1218	1218	100	2052	2052	2052	7967	5244	2044	3 3	5893	6186	629	7392

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Table 4
Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	Top Hit Descriptor	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) niRNA, complete cds	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens chromosome 21 segment HS21C046	zt81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);	zi81504.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);	Human putative ribosomal protein S1 mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens hypothetical protein (HSPC068), mRNA	Homo sapiens ring finger protein (RNF), mRNA	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds	Homo sapiens mRNA for nucleolar RNA-helicase (noH61 gene)	601491715F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893854 5'	Homo sapiens gene for B120, exon 11	Homo saplens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon	H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and Joined CDS)	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA	Homo sapiens gene for B120, exon 11	Human fibronectin gene extra type III repeat (EDII), exon x+1	qf56h03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754069 3'	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA	602124644F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281635 5	M.musculus mRNA for hoxa3 gene	Homo sapiens ribosomal protein L5 (RPL5) mRNA
e Exon Probes	Top Hit Database Source	Ŋ		T_HUMAN			H H	N	EST_HUMAN G	EST_HUMAN G					NT			EST_HUMAN 60					NT H				TN TN	EST_HUMAN of		T_HUMAN		
Sing	Top Hit Acession No.		2.1	2.1	4507500 NT	4507500 NT		1.0E-124 AL163246.2	5	1.1	AF155654.1	4507500 NT	7705446 NT	11419092 NT	2.1	2.1	2.1	4.1	1.0E-124 AB024069.1	4504116				4507500 NT	4504116 NT	1.0E-124 AB024069.1	1	1.0E-124 AI204535.1	8922337 NT	5.1	Y11717.1	4506654 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-123 U09823.1	1.0E-123 BF677292	1.0E-123 BF677292	1.0E-124	1.0E~124	1.0E-124 D87675.1	1.0E-124	1.0E-124 AA39755	1.0E-124 AA39755	1.0E-124 AF155654	1.0E-124	1.0E-124	1.0E-124	1.0E-124 AF27489	1.0E-124 AF27489;	1.0E-124 AJ131713	1.0E-124 BE87952	1.0E-124	- 1.0E-124	1.0E-124 S78684.1	1.0E-124 S78684.1	1.0E-124 X13794.1	1.0E-124	1.0E-124	1.0E-124	1.0E-124 M18178.	1.0E-124	1.0E-124	1.0E-124	1.0E-124 Y11717.1	1.0E-124
	Expression Signal	12.23	5	5	1.1	1.1	1.98	2.11	2.03	2.03	3.67	1.06	1.81	2.59	5.54	5.54	2.35	2.23	0.85	0.85	96.0	96.0	2.95	1.09	1.19	1.58	1.12	2.72	8.97	6.43	3.31	5.66
	ORF SEQ ID NO:	27537	29057	29058	20048	20049		20238	20429		20509	20561		21056	21086	21087	21550	21797	22182		23169	23170	23300	23528	23666			24685	24934	25580		26874
	Exon SEQ ID NO:	17331	18765	18765	10233	10233	10239	10421	10609	1		10720		Ŀ	11231	11231	11672	11907	12285	13240	13363	13363	13512	13737	13890		14731	14911	15164	15505	il	16684
	Probe SEQ ID NO:	7471	8958	8928	268	268	273	477	676	676	742	791	988	1293	1324	1324	1773	2016	2408	3319	3446	3446	3598	3825	3983	4639	4850	5039	5240	5590	6185	6805

Page 351 of 413 Table 4 Single Exon Probes Expressed in Heart

		6.									J31662	J31662	3300482	3300482						Ĭ.		0			T		
Single Lyones Lypressed III near	Top Hit Descríptor	hg94a09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:095162 095162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE.	hg94a09.x1 NOL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:095162 095162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'	wi93f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE.2400391 3'	wi93f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'	UI-HF-BN0-akz-b-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078846 5'	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17	hj05c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE.2980906 3'	t/19e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN.;	ignocative of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of	zt81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT)	zl81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT)	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens mRNA for KIAA1172 protein, partial cds	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'	HA0086 Human fetal liver cDNA library Homo sapiens cDNA	HA0086 Human fetal liver cDNA library Homo sapiens cDNA	Homo sapiens ALR-like protein mRNA, partial cds	zk33c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE.486540 3' similar to gb:X65857_cds1_OLFACTORY_RECEPTOR-LIKE_PROTEIN_HGMP07E_(HUMAN).	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA	Homo sapiens Usurpin-alpha mRNA, complete cds	Homo sapiens Usurpin-alpha mRNA, complete cds
שוב באחוו רוטג	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT L	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	NT	N	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN	NT	NT	NT	NT	NT
	Top Hit Acession No.	1.0E-124 AW612106.1	1.0E-124 AW612106.1	4V645633.1	4V645633.1	N767133.1	AI767133.1	1.0E-124 AW503755:1	194776.1	1.0E-124 AW665663.1	1446455.1	71446455.1	VA397551.1	AA397551.1	11417862	11417862 NT	AB032998.1	3E743922.1	N110656.1	N1110656.1	AF264750.1	AA042813.1	AL163210.2	7662279 NT	661867	_	VF015450.1
	Most Similar (Top) Hit BLAST E Value	1.0E-124	1.0E-124	1.0E-124 AV645633	1.0E-124 AV645633	1.0E-124 AI767133.	1.0E-124 AI767133.	1.0E-124	1.0E-124 U94776.1	1.0E-124 /	1.0E-124 AI446455.	1.0E-124 AI446455.	1.0E-124 AA397551	1.0E-124 AA397551	1.0E-124	1.0E-124	1.0E-125 AB032998.	1.0E-125 BE743922	1.0E-125 AI110656.1	1.0E-125 AI110656.1	1.0E-125 AF264750	1.0E-125 AA042813.	1.0E-125 AL163210.	1.0E-125	1.0E-125	1.0E-125 AF015450	1.0E-125 AF015450.
	Expression Signal	1.35	1.35	2.44	2.44	7.8	7.8	1.25	2.25	2.25	1.87	1.87	3.98	3.98	1.99	1.99	5.41	3.92	1.63	1.63	1.24	2.13	1.53	1.63	1.08	3.81	3.81
	ORF SEQ ID NO:	27002	27003	27532	27533	27604	27605	27752	28532	28788	28162	28163	20429	20430	25005	25006		19778	20377	20378	20469	20619	20750	20890	21414	21545	21546
	Exon SEQ ID NO:	16808	16808	17326	17326	17393	17393	17526	18280	18509	17916	17916	10609	10609	19626	19626	10278	9987	10565	10565	10643	10769	10905	11050	12700	11668	11668
	Probe SEQ ID NO:	0669	6930	7466	7466	7542	7542	7676	8404	8645	1918	8767	9173	9173	9846	9846	316	420	628	628	711	842	885	1136	1649	1769	1769

Page 352 of 413 Table 4 Single Exon Probes Expressed in Heart

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Top Hit Descriptor	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X85857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);	Homo sapiens inhibin, alpha (INHA) mRNA	Homo sapiens inhibin, alpha (INHA) mRNA	oh64d02.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1471779 3'	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA	Homo saplens zinc finger protein ZNF287 (ZNF287), mRNA	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140796 5'	Homo sapiens KIAA0985 protein (KIAA0985), mRNA	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3889790 5	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5	Homo sapiens IGF-II gene, exon 5	Homo sapiens IGF-II gene, exon 5	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10	Human chromosome 10 dunificated adteander (kodvetronby / ALD) kana sogmant and and an and an and an and an and an an and an an and an an and an an an and an an an an an an an an an an an an an	NAME OF TAXABLE SEQUENCES OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF THE SEQUENCE OF T	QV 1-H 1 0638-0 / 050U-191-d12 H 10638 Homo sapiens cDNA	TAVITACOOUTIVE TO THE TOTAL BUILDING SAPIENS CLINA	Homo sapiens I-REL gene, exon 5	xf59f02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284 LAMBDA/IOTA PROTEIN KINASE C-INTERACTING PROTEIN. [1];	xf59f02.x1 NCI_CGAP_Gas4 Homo saplens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q:3284 LAMBDA/JOTA PROTEIN KINASE C-INTERACTING PROTEIN 111	Homo sapiens mRNA for KIAA0667 protein, partial cds	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA	Homo saplens poly(A) binding protein II (PABP2) gene, complete cds	RC3-ST0186-250200-018-c11 ST0186 Homo sapiens cDNA	QV3-BT0569-020200-075-g09 BT0569 Home sapiens cDNA	QV3-BT0569-020200-075-909 BT0569 Homo sapiens cDNA	Homo sapiens mRNA for KIAA0667 protein, partial cds	Homo sapiens CDC-like kinase (CLK) mRNA	Human lamhin B1 chain gene, exon 20
Top Hit Database Source	EST_HUMAN	NT	Z	EST_HUMAN	NT	님	EST HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	Z	Ł	COT LIBRARI	FST HOMAN	NIMINIOL I COL	L	EST_HUMAN	EST HUMAN	NT	PA PA	LN.	EST_HUMAN	EST_HUMAN	EST_HUMAN	Z	닐	NT
Top Hit Acession No.	AA042813.1	4504696 NT	4504696 NT	AI732966.1	11425114 NT	11425114 NT	1.0E-125 BE315412.1	11436448 NT	1.0E-125 BE892660.1	1.0E-125 BE562528.1	1.0E-125 BE562526.1	X03427.1	X03427.1	J90288.1	190788 1	4 05 405 054040 4	1.0E-125 BE181040.1	DE 101040.1	1.0E-125 AF043458.1	4W131202.1	4W131202.1	AB014567.1	7669505 NT	1.0E-125 AF026029.1	1.0E-125 AW812899.1	3E074267.1	3E074267.1	AB014567.1	4758007 NT	M61936.1
Most Similar (Top) Hit BLAST E Value	1.0E-125 AA042813	1.0E-125	1.0E-125	1.0E-125 AI732966.	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125 X03427.1	1.0E-125 X03427.1	1.0E-125 U90288.1	1 0F-125	4 0 1 4 2 5	1.05-125	1.051-120.1	1.0E-125	1.0E-125 AW13120	1.0E-125 AW13120	1.0E-125 AB014567	1.0E-125	1.0E-125	1.0E-125	1.0E-125 BE074267	1.0E-125 BE074267	1.0E-125 AB014567	1.0E-126	1.0E-126 M61936.1
Expression Signal	1.15	1.65	1.65	2.45	1.98	1.98	0.84	1.41	3.44	1.48	1.48	6.36	6.36	1.22	1.22	104	4.31	5.4	3.15	1.86	1.86	5.13	292	5.15	2.49	4.36	4.36	1.96	0.88	1.2
ORF SEQ ID NO:		22315	22316	22320	24136	24137	24195	25573	25610	25993	25994	26093	26094	27043	27044	27242	27343	11000	28211	28289	28290	28616	28748	28754	28804	28896	28897	29044	20525	20528
Exon SEQ ID NO:	12332	12424	12424	12427	14344	14344	14409	15496	15527	15870	15870	15961	15961	16851	16851	17440	174.49	St 1 / 1	17960	18040	18040	18351	18476	18482	18522	18607	18607	18749	10687	10690
Probe SEQ ID NO:	2455	2551	2551	2555	4450	4450	4516	5581	5612	5965	2962	6201	6201	6974	6974	7272	70707	7171	8069	8152	8152	8478	8609	8615	8704	8793	8793	8941	757	760

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Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	H.sapiens gene for alphaf-antichymotrypsin, exon 3	Homo saplens RAN binding protein 2 (RANBP2), mRNA	zo72c03.r1 Stratagene pancreas (#937208) Homo sapiens culva cione invacationada e	zo72c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE: 392420 3	H.saplens DNA for liver cytochrome by pseudogene	Homo sapiens death receptor 6 (UK6), mKNA	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon by	Homo saplens collagen type At alpha-1 (COLTIA) gene, explines	yx/8c06,r1 Soares melanocyte Zindhiwi Hollio Sapiells Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control	zx66e03.r1 Soares_total_tetus_NbZHF8_9w Homo sapiens cipina cipina ivinace.750444 5 siriina io TR:G1145880 G1145880 TITIN;	Homo sapiens mRNA for KIAA1525 protein, partial cds	Homo sapiens mRNA for KIAA1525 protein, partial cds	Human mRNA for ankyrin (variant 2.1)	602139138F1 NIH_MGC_46 Homo sapiens cDNA done IMAGE:4298240 5'	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	Homo sapiens lost on transformation LOT1 mKNA, complete cds	Homo sapiens ubiquitin specific protease 8 (USP8) mKNA	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with 1M domain), member 1 (LILEMAT),	mRNA	Homo sapiens leukocyte immunoglobulin-like receptor, subtamily A (with 1M domain), member (LiLros 1),	MKNA " 1 OF (DD) OF) TONA	Homo sapiens ribosomal protein L20 (RPL20) IIIRNYA	Homo sapiens adlican mKNA, complete cds	Human mRNA for cytokeratin 18	ZAZZUZ,TI SOBIES (Otal Jetus INDZINIO SAPIETIS CUMA CIOTE IMPOLIT COSCO C
le Exon Prob	Top Hit Database Source	IN		EST HUMAN	EST_HUMAN	NT	L	NT	ĮN.	EST HUMAN	EST HUMAN	LN	N.	NT	EST HUMAN	EST HUMAN	EST HUMAN	F	IN	TN	Z	뉟	F	L	NT	NT		NT		TN	LN L	NT	LN	EST_HUMAN
Sing	Top Hit Acession No.	X68735.1	6382078				7657038 NT	8.1	8.1		7.	18.1			5.1				B024597.1	1 0F-127 AB024597.1	1.0E-127 AB024597.1	87675.1	087675.1	1.0E-127 AF114488.1	172621.2	4827053 NT		5803065 NT		5803065 NT	4506620 NT	AF245505.1	(12881.1	4A450131.1
	Most Similar (Top) Hit BLAST E Value	1.0E-126 X		1.0E-126 AA160709.1	1.0E-126 AA160709.1	1.0E-126 X53941.1	1.0E-126	1.0E-126 AF101108.1	1.0E-126 AF10110	1.0E-126 N34078.	1 OE_126 AA46007	1 0F-126 AB040958.1	1 0E-126 AB040958.1	1 0F-126 X16609	1.0E-126 BF683175.1	1 0F-128 P	1 0F-126 P	1 0E-127 A	1 OF-127 AB024597 1	1 0F-127 A	1.0E-127	1.0E-127 D87675.	1.0E-127 D87675.	1.0E-127	1.0E-127 U72621	1.0E-127		1.0E-127		1.0E-127	1:0E-127	1.0E-127		1.0E-127 AA4501
	Expression Signal	2.03	2.24	6.07	6.07	1.21	2.04	96.0	96.0	1.57															1.28			1.59		1.59	7.45	4.01		0.96
	ORF SEQ ID NO:	20670			22758	23281				24400							24900											21800		21801	1 21939	5 22075		5 22341
	Exon SEQ ID NO:	10826	12425			13491	13519	14563	14563	14614	1				18414	L	15000		L	L	L	1_		L	L		_	11911	-	11911	12041		L	12450
	Probe SEQ ID NO:	500	2552	3035	3035	3577	3605	4677	4677	4728		27.75	1816	1870	0000	020	8800	9035	3 5	165	166	27.0	27.2	863	808	1665		2020		2020	2153	2294	2566	2579

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Table 4
Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	zx42a02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'	au80e06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' sintilar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;contains element MER22	repetitive element ;	Homo sapiens delayed rectifier potassium channel subunit IsK mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C047	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA	Homo sapiens cytochrome P450 retinoid metabolizing protein P450KAI-2 mKNA, complete cds	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products	Homo sapiens chromosome 21 segment HS21C068	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA	H. sapiens NOS2 gene, exon 6	H.sapiens TCF11 gene, exon 3-6	Homo sapiens integrin, beta 8 (ITGB8) mRNA	Homo sapiens Pendred syndrome (PDS), mRNA	Homo sapiens Pendred syndrome (PDS), mRNA	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA	601434784F1 NIH_MGC_72 Homo saplens cDNA clone IMAGE:3919917 5'	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo sapiens gene for AF-6, complete cds	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA	Human FAU1P pseudogene, trinucleotide repeat regions	Human FAU1P pseudogene, trinucleotide repeat regions
le Exon Prob	Top Hit Database Source	EST_HUMAN		EST HUMAN	NT	NT	NT	NT	Z	NT	NT	NT	NT	NT	NT	NT	LN	LN	LΝ	LN	LN	NT	EST_HUMAN	EST HUMAN	NT	NT	LN	EST_HUMAN	NT	N	LN.	LN
Sing	Top Hit Acession No.			τ.	_		7706239 NT	06239	AF252297.1	4506384 NT	1.0E-127 AL163268.2	6912639 NT		(84060.1	4504778 NT	11421914 NT	11421914 NT	4F274863.1	1.0E-127 AF274863.1	11427235 NT	11417339 NT	11417339 NT	3E895415.1	3E895415.1	AB024597.1	AB024597.1	1.0E-127 AB011399.1		4758081 NT	4758081 NT	U02523.1	U02523.1
	Most Similar (Top) Hit BLAST E Value	1.0E-127 AA450131.1		1.0E-127 AW161297.	1.0E-127 AF135188.	1.0E-127 AL163247.2	1.0E-127	1.0E-127	ì	1.0E-127	1.0E-127 A	1.0E-127	1.0E-127 X85764.1	1.0E-127 X84060.1	1.0E-127	1.0E-127	1.0E-127	1.0E-127 AF274863.	1.0E-127	1.0E-127	1.0E-127	1.0E-127	1.0E-127 BE895415.	1.0E-127 BE895415	1.0E-127 AB024597	1.0E-127 AB024597	1.0E-127	1.0E-128 BE385617	1.0E-128	1.0E-128		1.0E-128 U02523.1
	Expression Signal	0.96		0.88	1.09	0.86	21.46	21.46	0.92	4.16	1.93	0.98	3.72	2.67	6.76	1.38	1.38	4.97	4.97	1.17	6.74	6.74	2.46	2.46	1.66	1.66	2.1	4.46	1.48	1.48	12.19	12.19
	ORF SEQ ID NO:	22342		23435	23706	23802	23833	23834	24075	24178		24252	25533	25757	25835	26620		27624	27625				29001		19954		25276		20892	20893		21806
	Exon SEQ ID NO:	12450	1	13652	1.	1	14060	14060	14291			Ì	15462	<u> </u>		16436	<u> </u>		17409		1_	18371	18707		L	L	L	10396	11052	11052	11916	11916
	Probe SEQ ID NO:	2579		3740	4026	4128	4160	4160	4395	4499	4532	4575	5546	5742	5816	6578	6578	7558	7558	7923	8498	8498	8888	8888	9397	9397	9595	452	1138	1138	2025	2025

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens ribosomal protein S2 (RPS2) mRNA	Homo saplens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA	Homo sapiens mRNA for KIAA1247 protein, partial cds	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA	Homo saplens phosphodlesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA	7q86b10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'	Homo sapiens mRNA for KIAA0454 protein, partial cds	Homo sapiens mRNA for KIAA0454 protein, partial cds	ns04a11.11 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR:C951338 G951338 CHROMOSOME SEGREGATION GENE HOMOLOG CAS.;	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA	om68h08.s1 NCI_CGAP_GC4 Home sapiens cDNA clone IMAGE:1552383 3' similar to gb:X54941 CYCLIN-DEPENDENT KINASES RECLII ATORY SURI INIT 4 (HI IMAN).	601277826F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618750 5	EST367360 MAGE resequences, MAGC Homo sapiens cDNA	insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]	Novel human mRNA containing Zinc finger C2H2 type domains	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	Homo saplens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	genes, complete cds	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA	ZINC FINGER PROTEIN HZF10	ZINC FINGER PROTEIN HZF10	ZINC FINGER PROTEIN HZF10	Homo sapiens mRNA for KIAA1459 protein, partial cds	CMYA5 Human cardiac muscle expression library Homo saplens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5	CMVA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5	
le Exon Probes	Top Hit Database Source			NT			EST_HUMAN 74		Ĭ	r_HUMAN		ON THE TOTAL	Т	EST HUMAN ES	Г	NT TN	NT LN	N FN	Ĭ	NT				SWISSPROT ZI		SWISSPROT ZI	NT	CP EST HUMAN CA	EST HUMAN C	1
Sing	Top Hit Acession No.	4506718 NT	11437455 NT	1.0E-128 AB033073.1	11426673 NT	11420965 NT	1.0E-128 BF224345.1	1.0E-128 AB007923.1	1.0E-128 AB007923.1	1.0E-128 AA639198.1	11425254 NT	1 0F-128 AA926959 1		2			1.0E-129 AL096880.1	1.0E-129 AF240786.1		1.0E-129 AF240786.1	11418522 NT	4505682 NT	4505682 NT				1.0E-129 AB040892.1	1.0E-129 AW755254.1	1.0E-129 AW755254.1	
	Most Similar (Top) Hit BLAST E Value	1.0E-128	1.0E-128	1.0E-128	1.0E-128	1.0E-128	1.0E-128	1.0E-128	1.0E-128	1.0E-128	1.0E-128	1 0F-128	1.0E-128	1.0E-128	1.0E-129 S37722.1	1.0E-129 S37722.1	1.0E-129	1.0E-129		1.0E-129	1.0E-129	1.0E-129	1.0E-129	1.0E-129 Q14585	1.0E-129 Q14585	1.0E-129 Q14585	1.0E-129	1.0E-129	1.0E-129	
	Expression Signel	13.3	0.85	1.13	5.46	2.67	7.23	3.28	3.28	1.25	5.94	3 87	1.79	3.66	2.19	1.35	2.86	2.29		2.29	2.43	1.19	1.19	1.35	1.35	1.35	2.2	9.7	9.7	T
	ORF SEQ ID NO:	21950		23071	24245	25890	26123	27046	27047	27929	28232	28240	28364		20182	20182	21461	21465		21466			22504		j		23754	23856	23857	
	Exon SEQ ID NO:	12049	12273	13268	14457	15771	15988	16853	16853	17684	17983	17991		18968	10353	10353	11591	11595		11595	11699	12613	12613	13016	13016	13016	13975	14083	14083	
	Probe SEQ ID NO:	2162	2395	3348	4565	5865	6140	9269	6976	7834	8092	8404	8230	9263	116	407	1689	1693		1693	1802	2751	2751	3089	3089	3089	4073	4183	4183	

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Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA zr58c04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 zr58c04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 yq49c05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199112 5' similar to SP:B48150 B48150 HP-25=HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN UI-HF-BNO-aky-g-06-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5' DKFZp762K171_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K171 5 Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13 Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA af72f07.rd Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047589 601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE.3346366 5' 601343016F1 NIH_MGC_53 Homo sapiens cDNA done IMAGE:3685466 5' 601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5 601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5 601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5' 601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5' Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 2, 3 and 4 Homo sapiens RET finger protein-like 1 antisense transcript, partial AU143115 Y79AA1 Homo sapiens cDNA clone Y79AA1001410 5' AU143115 Y79AA1 Homo sapiens cDNA clone Y79AA1001410 5 Top Hit Descriptor EST368312 MAGE resequences, MAGD Homo sapiens cDNA CM4-CN0045-180200-511-f02 CN0045 Homo sapiens cDNA RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA Homo sapiens checkpoint suppressor 1 (CHES1), mRNA G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.; Homo sapiens mRNA for KIAA1335 protein, partial cds G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. Homo sapiens mRNA for KIAA0634 protein, partial cds Homo sapiens KVLQT1 gene Homo sapiens KVLQT1 gene EST_HUMAN EST HUMAN EST HUMAN EST_HUMAN **EST HUMAN** EST_HUMAN EST HUMAN **EST HUMAN EST HUMAN** EST_HUMAN EST HUMAN EST_HUMAN HUMAN EST HUMAN EST HUMAN EST HUMAN **EST HUMAN** EST_HUMAN Top Hit Database Source EST Z 눋 ż z 4885136 NT 11420850 11416777 11420850 Top Hit Acession 1.0E-130 AW956242.1 1.0E-129 AB014534.1 AU143115.1 1.0E-129 AU143115.1 BE564219.1 I.0E-130 AW 503580.1 AW363299.1 1.0E-130 BE564219.1 1.0E-130 AW843993.1 1.0E-130 AW 363299.1 0.0E+00 AA228128.1 1.0E-129 AA625526.1 1.0E-130 BE564219.1 BE564219.1 0.0E+00(AA228126.1 1.0E-129 AJ006345.1 AJ006345.1 1.0E-129 AL120739.1 BE275192.1 1.0E-130 BE275192.1 1.0E-130[AJ010230.1 1.0E-130 AF240698.1 1.0E-130 AB037756.1 ŝ 1.0E-130 M25140.1 1.0E-129 H83155.1 1.0E-130 X04092.1 1.0E-129 1.0E-130 1.0E-130 1.0E-129 1.0E-129 1.0E-129 1.0E-130 1.0E-130 1.0E-130 0.0E+00 Most Similar BLASTE (Top) Hit Value 2.04 2.49 44 44 3.68 3.52 2.04 2.04 6 32.43 2.49 5.17 9.4 1.87 1.88 6.81 6.81 2.06 8 7.48 80 1.07 4.77 1.57 4.77 Expression Signal 25715 26245 26286 28693 28993 21408 23560 24673 26322 19783 26286 28994 21409 22565 23243 22564 24674 27187 27392 28650 19782 19786 22565 ORF SEQ 24122 ID NO: 15614 16095 16132 16720 18424 18699 18960 19203 13446 13768 16165 16996 18385 9993 SEQ ID 18699 11547 11547 11835 12605 14333 14902 9991 16132 12777 12777 12777 14902 17190 ö 6229 8618 8888 1643 1940 2849 2849 3530 6301 7119 7314 8513 5706 6841 8554 8888 1643 2743 3703 3703 4438 5029 5029 4 SEQ ID 6267 9630 3857

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Oligie Exoli Flobes Explessed in Realt	Top Hit Descriptor	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA	Homo sapiens DCRR1 mRNA, partial cds	Homo sapiens DCRR1 mRNA, partial cds	Homo sapiens bela-tubulin mRNA, complete cds	Human heparin cofactor II (HCF2) gene, exons 1 through 5	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)	HUM516H08B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-516H08 5	HUM516H08B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-516H08 5'	Human ribosomal protein L7 (RPL7) mRNA, complete cds	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC cr48e07.3'	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC cr48e07.3'	Human von Willebrand factor pseudogene corresponding to exons 23 through 34	Human von Willebrand factor pseudogene corresponding to exons 23 through 34	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	on89e04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563870 3' similar to SW:TMOD_HUMAN P28289 TROPOMODULIN.;	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene	encoding mitochondrial protein, mRNA	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA	Homo sapiens actin, beta (ACTB) mRNA	Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds	HA1347 Human fetal liver cDNA library Homo sapiens cDNA	Homo sapiens mRNA for KIAA1363 protein, partial cds	H.sapiens nox1 gene (exon 2)	ts38b05.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.	ts38b05.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. :
שום באטוו ו וטי	Top Hit Database Source	F	님	L L	ΓN	F	FN	Ι	N	ΝΤ	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	NT	NT	Z	NT	IN	TN	EST_HUMAN		N	NT	1Ν	NT	EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN
5	Top Hit Acession No.	8923349 NT	8923349 NT	J83327.1	J83327.1	0.0E+00 AF141349.1	0.0E+00 M58600.1	6857825 NT	Y17151.2	Y17151.2	J78804.1			4W069534.1	4W069534.1	M60676.1	M60676.1	4758977 NT	4758977 NT	4758977 NT	4758977 NT	0.0E+00 AA953770.1		4501850 NT	450444 NI	5016088 NT	J89277.1	1114743.1	NB037784.1	(91213.1	A1623701.1	N623701.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 D83327.1	0.0E+00 D83327.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Y17151.2	0.0E+00 Y17151.2	0.0E+00 D78804.1	0.0E+00 D78804.1	· 0.0E+00 L16558.1	0.0E+00 AW06953	0.0E+00 AW06953	0.0E+00 M60676.1	0.0E+00 M60676.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00 U89277.1	0.0E+00 AI114743	0.0E+00 AB037784	0.0E+00 X91213.1	0.0E+00 AI623701	0.0E+00 AI623701.
	Expression Signal	1.34	1.34	2.45	2.45	5.57	76.0	2.41	1.4	1.4	1.22	1.22	4.14	8.1	8.1	5.8	2.75	1.77	1.77	1.49	1.49	42.13		1.09	14.77	47.55	13.39	1.46	1.03	6.13	1.39	1.88
	ORF SEQ ID NO:	19792	19793	19799	19800	19804	19816	19819	19845	19846	19847	19848	19849	19852	19853	19857		19869	19870	19869	19870	19875		19877		19886	19889	19895	19896	19901	19906	19906
	Exon SEQ ID NO:	10001	10001	10007	10007	10011	10020	10022	10038	10038	10039	10039	10040	10042	10042	10045	10047	10054	10054	10054	10054	10058		10000	10061	10070	10073	10079	10080	10085	10091	10001
	Probe SEQ ID NO:	15	15	20	20	24	33	35	51	51	52	52	53	55	55	59	61	69	69	71	71	74		192	77	86	88	94	95	102	110	1111

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Jugie Lyon Fronce Lypressed III realt	Top Hit Descriptor	yy01h09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5'	yy01h09.r1 Soares melanocyto 2NbHM Homo sapiens cDNA clone IMAGE:270017 5'	Homo sapiens neuropilin 2 (NRP2) mRNA	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA	801460375F1 NIH_MGC_66 Homo sapiens cDNA done IMAGE:3863803 5'	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'	zd62b05.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to	gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);	Homo saplens zinc finger protein mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C002	Homo sapiens chromosome 21 segment HS210002	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z CE22631;	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z	CE22631;	Homo sapiens mRNA for KIAA0784 protein, partial cds	Homo sapiens mRNA for KIAA0784 protein, partial cds	Human gamma-cytoplasmic actin (ACTGP9) pseudogene	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds	tq04f08.x1 NCL_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207847.3' similar to gb:J03191 PROFILIN I (HI IMAN):	tto4108.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN I,	(HUMAN);	Troing saprens DIVA mismach repair protein (MILTA) gene, complete cas
וום דייטוו ו וחד	Top Hit Database Source	EST_HUMAN	EST_HUMAN	TN	TN	LN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	LN L	FN	EST_HUMAN	EST_HUMAN		EST_HUMAN	NT	NT	NT	EST HUMAN		EST_HUMAN	NT	NT	NT	NT	NT	LN	NT	NAMIN TRE		ESI HUMAN	
ביים ביים	Top Hit Acession No.	136040.1	136040.1	4505458 NT	4505938 NT	4505938 NT		T56945.1	4504444	0.0E+00 BF036881.1	4504444 NT	2	1	1		V 73973.1	\F244088.1	NL163202.2	AL163202.2	3E018970.1		3E018970.1	.1	.1	050659.1	\F273045.1	1	1	VF167174.1	0.0E+00 A1587308.1			
	Most Similar (Top) Hit BLAST E Value	0.0E+00 N36040.1	0.0E+00 N36040.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF111168.	0.0E+00 BE295973.	0.0E+00 BE295973.		0.0E+00 W73973.1	0.0E+00 AF244088	0.0E+00 AL163202.	0.0E+00 AL163202.	0.0E+00 BE018970.		0.0E+00 BE018970	0.0E+00 AB018327	0.0E+00 AB018327	0.0E+00 D50659.1	0.0E+00 AF273045	0.0E+00 AF273045.	0.0E+00 AF167174.	0.0E+00 AF167174.	7 00+30 0		0.0E+00 AI58/308.	0.01.1001
	Expression Signal	1.83	1.83	0.86	3.17	3.17	1.49	1.49	9.05	2.42	15.84	1.36	1.1	1.18		2.99	1.51	18.37	18.37	4.25		4.25	1.98	1.98	130.42	2.83	2.83	2.92	26.2	6.33		9.33	16:1
	ORF SEQ ID NO:	19907	19908	19913	19921	19922	19929	19930		19943		19946	19947	19947		19948	19949	19952	19953	19960		19961	19964	19965	19976	19981	19982	19984	19985	19991		19992	19994
	Exon SEQ ID NO:	12636	12636	10094	10100	10100	10108	10108	10121	10125	10127	10130	10132	10132		10133	10134	10137	10137	10145		10145	10150	10150	10159	10164	10164	10166	10166	12661		12661	0/101
	Probe SEQ ID NO:	112	112	115	126	126	135	135	147	151	153	156	158	159		160	161	164	164	174		174	179	179	187	192	192	194	194	203		203	202

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Single Exon Probes Expressed in Heart	Most Similar Top Hit Acession (Top) Hit Top Hit Acession ID NO: Signal BLASTE No. Source Source	16.66 0.0E+00 4506632 NT	3.46 0.0E+00 AF132000.1 NT	19999 2.48 0.0E+00[AB018264.1 NT	19999 1.95	20000 1.61	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens	20005 3.43 0.0E+00 BE246780.1 EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens consequences as a consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the consequence of the 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sapiens cDNA
	· ————			19999	19999	20000	20004	20005	20006		20004		20005	90000	20007	20004	-	20005	90000	20023		2002	20032		20050	20051	20053	20066	20087	
	Exon SEQ ID NO:	10179	10180	10186	10186	10187	10195	10195	10195	L	10195		10195	200		10195		10195	10195		10208	, 10213	10215		3 10234	3 10234	10236			10247
	Probe SEQ ID NO:	208	209	215	216	217	224	224	224		225		225	300	77	226		226	226	238	240	247	249	257	269	269	270	281	281	282

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Table 4
Single Exon Probes Expressed in Heart

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Single Exon Propes Expressed in Heart	Top Hit Descriptor	Homo sapiens polassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens ribosomal protein S5 (RPS5) mRNA	Homo sapiens phosphoribosy/glycinamide formyltrans/erase, phosphoribosy/glycinamide synthetase, phosphoribosy/aminoimidazole synthetase (GART) mRNA	zv18c06.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753994 5'	Homo sapiens SON DNA binding protein (SON) mRNA	Homo sapiens SON DNA binding protein (SON) mRNA	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HAZ303)	Homo saplens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA	Homo sapiens moesin (MSN), mRNA	Homo sapiens X-box binding protein 1 (XBP1) mRNA	Human zinc finger protein zfp31 (zf31) mRNA, partial cds	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	Human mRNA for KIAA0184 gene, partial cds	Human mRNA for KIAA0184 gene, partial cds	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'	Homo sapiens mRNA for KIAA1019 protein, partial cds	qy81h05.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54199 PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (HUMAN):	RC2-CT0320-300100-016-a09 CT0320 Homo sapiens cDNA		Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
gie Exon Pro	Top Hit Database Source	NT	LN	NT	NT	NT	LN	EST_HUMAN	LZ LZ	N	NT	SWISSPROT	SWISSPROT	LN	NT	L	LN	LN LN	FZ	LN	LN⊤	LN	NT	LN	NT	IN	EST_HUMAN	LN	EST HUMAN	EST_HUMAN	NT	N
	Top Hit Acession No.	4557029 NT	4557029 NT	0.0E+00 AB028942.1	0.0E+00 AB028942.1	4506728 NT	4503914 NT	AA480002.1	4507152 NT	4507152 NT	l w l	014867	1 1	7657213 NT	7657213 NT	5174574 NT	4505256	4827057 NT	0.0E+00 U71600.1	AF231919.1	0.0E+00 AF231919.1	0.0E+00 AF231919.1	4507500 NT	4503854 NT	D80006.1	D80006.1	0.0E+00 AU134963.1	0.0E+00 AB028942.1	0.0E+00 Al363014.1	0.0E+00 AW754180.1	4503680 NT	4503680 NT
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00 O14867	0.0E+00 014867	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D80006.1	0.0E+00 D80006.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	5.26	5.26	. 4.03	3.11	5.3	1.99	2.03	13.28	9.68	2.23	6.0	6.0	4.18	2.31	3.67	0.86	3.76	0.8	2.15	2.15	3.4	0.89	1.4	1.37	1.52	1.13	5.35	1.01	3.43	1.38	2.04
	ORF SEQ ID NO:	20074	20075				20087		20088	20088			20102		20103	20115	20116	20120	20125	20129				20136				20188	20189		20159	20160
	Exon SEQ ID NO:	10254	10254	10265	10266	12664	10267	10268	10269	10269	10273	10285	10285	10286	10286	10300	10301	10304	10307	10311	10311	12665	10313	10315	10316	10316	10326	10365	10366	10334	10336	10337
	Probe SEQ ID NO:	290	290	301	302	303	304	305	306	307	311	324	324	325	326	341	342	345	348	353	353	354	356	358	359	360	372	381	382	387	390	391

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Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	H.sapiens gene for RNA pol II largest subunit, exons 23-29	H.sapiens gene for RNA pol II largest subunit, exons 23-29	Homo sapiens ribosomal protein L19 (RPL19) mRNA	yg09a02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE.31652.5'	Homo sapiens ribosomal protein S5 (RPS5) mRNA	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens SON DNA binding protein (SON) mRNA	Homo sapiens SON DNA binding protein (SON) mRNA	Mus musculus truncated SON protein (Son) mRNA, complete cds	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA	EST27054 Cerebellum II Homo sapiens cDNA 5' end	601111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA	Homo sapiens keratin 18 (KRT18) mRNA	Homo sapiens keratin 18 (KRT18) mRNA	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens mRNA for KIAA1209 protein, partial cds	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'	PM0-DT0065-130400-002-c06 DT0065 Homo sapiens cDNA	Novel human gene mapping to chomosome 1	Homo sapiens PC326 protein (PC326), mRNA	Homo sapiens chromosome 21 segment HS21C010	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA	601764858F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996998 5'
Jie Exon Pro	Top Hit Database Source	NT	NT	IN	TN	ΙN	LN	NT	NT	TN	EST_HUMAN	NT	TN	TN	NT	NT	NT	EST_HUMAN	EST_HUMAN	NT	NT	NT	NT	NT	NT	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	NT	EST_HUMAN	EST_HUMAN
ŽIIN I	Top Hit Acession No.	4503680 NT	(74870.1	(74870.1	4506608 NT		4506728 NT	\B028942.1	4507152 NT	4507152 NT	\F193607.1	4557879 NT	VA324262.1	3E254447.1	4504532 NT	4504532 NT	4557887 NT	4557887 NT	NL163246.2	NL163246.2	NL163246.2	0.0E+00 AB033035.1	0.0E+00 AU132898.1	3E385144.1	\W938825.1	AL117233.1	8923955 NT	0.0E+00 AL163210.2	3E081527.1	3F028005.1					
	Most Sımilar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X74870.1	0.0E+00 X74870.1	0.0E+00	0.0E+00 R17795.1	0.0E+00	0.0E+00 AB028942	0.0E+00	0.0E+00	0.0E+00 AF193607	0.0E+00	0.0E+00 AA324262	0.0E+00 BE254447	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AL163246	0.0E+00 AL163246.	0.0E+00 AL163246.	0.0E+00	0.0E+00/	0.0E+00 BE385144	0.0E+00 AW93882	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE081527	0.0E+00 BF028005.
	Expression Signal	2.04	1.17	1.64	1.64	2.43	6.0	0.84	0.84	43.09	1.31	2.61	2.42	4.7	4.7	3.51	2.01	86.0	0.91	3.15	3.15	1.27	1.27	2.26	7.05	7.05	2.59	1.64	2.17	1.05	1.07	1.64	3.91	1.97	1.13
	ORF SEQ ID NO:	20161	20162	20163	20164	20165	20166	20167	20168		19772		20190	20191	20192	20193	20206			20220	20221	20228	20229	20235	20236	20237	20242	20244	20250	20251	20253	20254			20273
	Exon SEQ ID NO:	10337	10338	10339	10339	10340	10341	10342	10342	10346	1866	10367	10368	10369	10369	10370	10382	10387	10388	10404	10404	10408	10408	10419	10420	10420	10428	10430	10438	12668	10440	10441	1	12669	10462
	Probe SEQ ID NO:	391	392	393	393	394	395	396	396	400	414	422	423	424	424	425	438	443	4	460	460	465	465	475	476	476	485	487	495	496	498	499	508	515	520

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Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens mRNA for KIAA1476 protein, partial cds	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TOEB1L) mRNA	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA	Homo saplens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	UI-H-BI1-acb-h-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE 2713951 3/	Homo sapiens RGH1 gene, retrovirus-like element	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), nuclear gene encoding mitochondrial protein, mRNA	Human apolipoprotein A-I (ApoA-I) gene, exon 1	601822627F1 NIH_MGC_75 Homo sapiens cUNA clone IMAGE:4045447 5	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo saplens low density lipoprotein-related protein 2 (LRP2), mKNA	zt60c07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726732 5'	Homo sapiens RGH2 gene, retrovirus-like element	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cUNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN):	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE 415567 5' similar to	gb:A21187 ALPHA-2-WACROGLOBULIN PRECURSOR (HUMAN);	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA	Homo sapiens glutamate receptor, ionotropic, N-methy D-aspartate 2B (GRIN2B) mRNA	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA	Human neutral amino acid transporter (ASCT1) gene, exon 8	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds	Homo saplens protein kinase, X-linked (PRKX) mRNA
jle Exon Prot	Top Hit Database Source	NT	N	NT	NT	N	EST HUMAN	N⊤	TN	LZ LZ	EST_HUMAN	N-	LN	TN	NT	NT	NT	NT	TN	NT	EST_HUMAN	N⊤	EST_HUMAN		EST HUMAN	NT	N	TN	INT	NT	LΝ	TN
Sing	Top Hit Acession No.	AB040909.1	E006030 NT	4504036 NT	4504036 NT	0.0E+00 AF003528.1	4.1	D10083.1	5174742 NT		-	4501854 NT		.1		6806918 NT	6806918 NT	6806918 NT	6806918	16918	3.1					4885526 NT	E009003 NT	5031624 NT		1	_	4826947 NT
	Most Similar (Top) Hit BLAST E Value		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AW13532	0.0E+00	0.0E+00	0.0E+00 J04066.1	0.0E+00 BF104898	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF149773	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D11078.1	0.0E+00 W78811.1		0.0E+00 W78811.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF108389	0.0E+00 AF108389.	0.0E+00
	Expression Signal	1.16	11.27	3.96	3.96	5.78	1.79	3.15	2.65	5.28	1.73	1.46	1.05	1.05	1.38	96.0	2.22	2.22	0.93	0.93	1.34	6.37	3.17		3.17	3.28	2.89	1.06	1.41	2.18	2.18	3.98
-	ORF SEQ ID NO:	20280	20283	20284	20285		20295		20318		20332	20336	20342	20343	20351	20354	20355	20356	20357	20358	20368	20372	20375		20376		20388	20391	20395	20398	20399	20404
	Exon SEQ ID NO:	10468		10472	10472	10477	10485	10495	10510	10522	10525	10529	10534	10534	10543	10546	10547	10547	10548	10548	10556	10560	10564		10564	10567	10574	10576	10579	10583	10583	10588
	Probe SEQ ID NO:	526	529	530	530	536	544	554	571	584	287	593	598	598	607	610	611	611	612	612	619	623	627		627	930	637	639	642	646	646	652

Page 363 of 413 Table 4 Single Exon Probes Expressed in Heart

		Τ		Γ	Γ			Τ	Γ	Τ	Τ	T	Γ	Γ			<u> </u>	Ī	Γ	<u> </u>	T	Γ	1	7	<u> </u>			Τ	Γ	Ť	T*	T	Π	
Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens protein kinase, X-linked (PRKX) mRNA	Human endogenous retrovirus pHE.1 (ERV9)	Homo saplens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA	Homo sapiens mRNA for KIAA1089 protein, partial cds	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA	np49d01.s1 NC_CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);	Human von Willebrand factor gene, exons 23 through 34	Human von Willebrand factor gene, exons 23 through 34	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo	sapiens cDNA clone TCAAP0779	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds	Homo sapiens chloride channel CLC4 (CIC4) mRNA, complete cds	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9	Homo sapiens mRNA for KIAA1339 protein, partial cds	Homo sapiens zinc finger protein 212 (ZNF212), mRNA	Homo sapiens mRNA for repressor protein, partial cds	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'	y69g08.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154046 5'	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA	Homo sapiens gene for AF-6, complete cds	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA	Human mRNA for KIAA0184 gene, partial cds	Human mRNA for KIAA0184 gene, partial cds	H.sapiens mRNA for interferon alpha/beta receptor (long form)	Homo sapiens mRNA for KIAA0910 protein, partial cds	Homo sapiens mRNA for KIAA0910 protein, partial cds	Homo saplens pericentrin (PCNT) mRNA
jie Exon Prop	Top Hit Database Source	L	NT	NT	NT	FZ	EST HUMAN	TN	N-	N.	L	LN.	NT		EST HUMAN	NT	NT	NT	NT	LN	NT	NT	NT	EST HUMAN	EST HUMAN	NT	L	NT	TN	NT	IN	NT	NT	N
Suis	Top Hit Acession No.	4826947 NT	X57147.1	4504424 NT	0.0E+00 AB029012.1	7657468 NT	<u>+-</u>		460675.1	5032192 NT	VF264750.1	1	11545800 NT		3E241577.1	0.0E+00 AF226990.2	AF226990.2	\F170492.1	103764.1	103764.1	AB037760.1	6912749 NT	330612.1	3E869735.1	348915.1	5032086 NT	AB011399.1	7661965 NT	080006.1	380006.1	(89772.1	AB020717.1	-	5174478 NT
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AA614537	0.0E+00 M60675.1	0.0E+00 M60675.1	0.0E+00	0.0E+00 AF264750.	0.0E+00 AF264750.	0.0E+00		0.0E+00 BE241577	0.0E+00	0.0E+00 AF226990.	0.0E+00 AF170492	0.0E+00 J03764.1	0.0E+00 J03764.1	0.0E+00 AB037760.	0.0E+00	0.0E+00 D30612.1	0.0E+00 BE869735.	0.0E+00 R48915.1	0.0E+00	0.0E+00 /	0.0E+00	0.0E+00 D80006.1	0.0E+00 D80006.1	0.0E+00 X89772.1	0.0E+00 AB020717	0.0E+00 AB020717	0.0E+00
	Expression Signal	3.98	0.95	4.56	4.35	2.03	19.46	7.66	7.66	1.45	3.89	3.89	9.78		1.7	1.12	1.12	2.4	1.55	1.55	0.78	1.12	0.81	2.17	3.38	2.4	1.58	2.97	1.17	1.17	2.64	2.37	2.37	6.84
	ORF SEQ ID NO:	20405		20419	20423		20450	20454		20464	20470	20471	20474		20481	20505	20506	20507	20510	20511	20512	20513	20514	20515	20519	20520	20529	20533	20544	20245				20560
	Exon SEQ ID NO:	10588	12672	10601	10606	10615	10625	10629	10629	10639	10644	10644	10646		10651	10670	10670	10671	10674	10674	10676	10677	12676	10678	10682	10683	10692	10696	10705	10705	10710	10714	10714	10718
	Probe SEQ ID NO:	652	658	299	672	682	692	969	969	200	712	712	714		719	739	739	740	743	743	745	746	747	748	752	753	762	765	775	775	780	784	784	789

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Single Exon Probes Expressed in Heart

Single Exoll Flobes Explessed in Free L	Top Hit Descriptor	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mixNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mKNA	Homo sapiens polassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mKNA	Homo sapiens serine-threonine protein Kinase (MNBH) mRNA, complete cds	Homo sapiens serine threonine protein kinase (MNBH) mKNA, complete cds	Homo sapiens GA-binding protein transcription factor, alpha subuhit (buki) (GABPA), mANA	Homo sapiens T-cell lymphoma Invasion and metastasis 1 (TIAM1) mKNA	Homo sapiens I -cell lymphoma invasion and metastasts I (TIAMI) mixtyA	Homo sapiens sodium/myo-inositol corransporter (SLCSAS) gene, complete cus	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens SON DNA binding protein (SON) mRNA	Homo sapiens mRNA for KIAA1019 protein, partial cds	Homo sapiens ribosomal protein S5 (RPS5) mKNA	Homo sapiens mRNA for KIAA0910 protein, partial cds	Homo sapiens mRNA for KIAA0910 protein, partial cds	nj66d07.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:99/453	nj66d07.s1 NCI_CGAP_Pr10 Homo sapiens cUNA clone IMAGE:99/453	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), miXNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu tumor-associated Knase (HONN), mKNA	Homo sapiens chromosome 21 segment HSZ1C003	QV0-BT0703-280400-211-g11 B10/03 Homo sapiens CUNA	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cLNNA	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 3]	protein C innibitor (numan, leukocytes, Genomic, 1216 nt, segment 2 of 3)
le Exoli Plone	Top Hit Database Source					LN	N	NT	닐	N	L	L'A	NT	NT	NT	NT	N.	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	NT	NT	본	NT	EST_HUMAN	EST_HUMAN	NT	TN	۲N	LN	NT	LN L	LZ.
Sing	Top Hit Acession No.	4507500 NT	7657213 NT	7657213 NT	57686	1	F108830.1	4503854 NT	4507500 NT	4507500 NT	0.0E+00 AF027153.1	\B028942.1	0.0E+00 AB028942.1	4507152 NT	0.0E+00 AB028942.1	4506728 NT	0.0E+00 AB020717.1	0.0E+00 AB020717.1	0.0E+00 AA533272.1	0.0E+00 AA533272.1	0.0E+00 BF677694.1	7657213 NT	7657213 NT	7657213 NT	7657213	0.0E+00 AL163203.2		0.0E+00 BE089592.1	0.0E+00 AL163203.2	4504958 NT	4504958 NT	0.0E+00 AF089747.1	0.0E+00 S69364.1	0.0E+00 S69364.1	0.0E+00 S69364.1
-	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF108830.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AB028942.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	7.06	1.51	4.43	3.91	1.24	1.24	1.14	1.55	1.55	1.57	3.37	3.37	7.38	3.03	2.02	1.25	1.25	1.97	1.97	7.39	1.3	1.3	2.16	2.16	0.87	1.85	1.85	3.93	7.45	3.29	1.5	0.99	66.0	0.99
	ORF SEQ ID NO:		20581	20582	20584	20590	20591	20596	20601	20602		20613			20616	20617		20621		20623		20624		20626		20650	20655		20665			20673	20674		20676
	Exon SEQ ID NO:	10719	10736	10737	10739	10744	10744	10749	10752	10752	10759	10763	10763	10764	10765	10766	10770	10770	10771	10771				10777	10777	10799	10806	10806	L	L	_		10829	10829	10829
	Probe SEQ ID NO:	790	807	808	810	816	816	821	825	825	832	836	836	837	838	839	843	843	844	844	845	849	849	850	850	873	880	880	890	900	903	904	906	902	905

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	Top Hit Descriptor	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds	Homo sapiens of cardiac alpha-myosin heavy chain gene	Homo sapiens of cardiac alpha-myosin heavy chain gene	Homo sapiens of cardiac alpha-myosin heavy chain gene	Homo sapiens of cardiac alpha-myosin heavy chain gene	Human ras inhibitor mRNA, 3' end	Human ras inhibitor mRNA, 3' end	Human ras inhibitor mRNA, 3' end	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA	os98e03.s1 NCI_CGAP_GC3 Homo saplens cDNA clone IMAGE:1613404 3'	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA	Homo sapiens mRNA for PSP24, complete cds	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA	Homo sapiens partial c-fgr gene, exons 2 and 3	Homo sapiens partial c-fgr gene, exons 2 and 3	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA	Human bela-tubulin (TUB4q) gene, complete cds	Human beta-tubulin (TUB4q) gene, complete cds	Human bela-tubulin (TUB4q) gene, complete cds	Homo sapiens 8q22.1 region and MTG8 (CBFA211) gene, partial cds	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo sapiens DKFZP586W0122 protein (DKFZP586W0122), mRNA	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA	aa86g07.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8;
	Top Hit Database Source	NT	LN	Ϋ́	N	NT	NT	TN	NT	NT	LN	EST_HUMAN	EST_HUMAN	LN	F	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	NT	LN	ΙN	TN	NT	NT	LN⊤	TN	LN	LN T	LN	LN	TN	EST_HUMAN
5	Top Hit Acession No.	L28101.1	Z20656.1	Z20656.1	Z20656.1	0.0E+00 Z20656.1	M37190.1	0.0E+00 M37190.1	0.0E+00 M37190.1	4507430 NT	4507430 NT	1	0.0E+00 Al001948.1	7657266 NT	0.0E+00 AB030566.1	0.0E+00 BF366974.1	0.0E+00 BF366974.1	0.0E+00 BF366974.1	X52207.1	X52207.1	4757969 NT	0.0E+00 U83668.1	0.0E+00 U83668.1	0.0E+00 U83668.1	0.0E+00 AF198490.1	0.0E+00 AF198490.1	0.0E+00 AF111170.3	0.0E+00 AF111170.3	AF111170.3	0.0E+00 AF111170.3	7661685 NT	5803114 NT	0.0E+00 AA458680.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00 L28101.1	0.0E+00 Z20856.1	0.0E+00 Z20656.1	0.0E+00 Z20656.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X52207.1	0.0E+00 X52207.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	2.14	105.13	105.13	167.64	167.64	36.3	13.25	53.71	1.9	1.9	2.46	2.46	7.21	2.52	4.64	4.64	4.64	1.27	1.27	1.25	1.05	7.48	69.9	1.99	3.49	0.84	1.43	1.81	2.23	2.28	2.66	1.94
	ORF SEQ. ID NO:	20677		20681	20682	20683	20706	20702			20710	20717	20718	20720	20730		20737	20738	20739				20756	20756	_		20761	20761	20761			20769	
	Exon SEQ ID NO:	10830	10833	10833	10834	10834	10860	10861	10862	10863	10863	12681	12681	10872	10882	10890	10890	10890	10891	10891	10900	10910	10911	10911	10914	10914	10917	10917	10917	10918	10921	10925	10927
	Probe SEQ ID NO:	906	606	606	910	910	935	936	937	938	938	946	946	948	959	296	296	296	896	896	226	886	686	990	993	994	266	866	566	1000	1003	1007	1009

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Single Exon Probes Expressed in Heart

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Top Hit Descriptor	EST51i24 WATM1 Homo sapiens cDNA clone 51i24 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p.)	EST51i24 WATM1 Homo sapiens cDNA clone 51i24 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p.)	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA	Homo sapiens hypothetical protein FLJ11196 (FLJ11196), mRNA	Homo sapiens heat shock 70kD protein 9B (mortalin-2) (HSPA9B) mRNA	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA	Homo sapiens alkylation repair, alkB homolog (ABH), mRNA	Homo sapiens Death associated protein 3 (DAP3) mRNA	MR0-BN0115-200300-003-h08 BN0115 Homo sapiens cDNA	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA	Homo sapiens protein kinase, X-linked (PRKX) mRNA	Homo sapiens protein kinase, X-linked (PRKX) mRNA	Homo sapiens ribosomal protein S27a (RPS27A) mRNA	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA	Homo sapiens DNA for Human P2XM, complete cds	Homo sapiens DNA for Human P2XM, complete cds	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA	qb22d10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697011 3'	Homo sapiens mRNA for KIAA0903 protein, partial cds	Homo saplens chromosome 12 open reading frame 3 (C12ORF3), mRNA	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA	Homo sapiens mRNA for KIAA1414 protein, partial cds
Top Hit Database Source	EST_HUMAN	EST HUMAN	トフ	La	トフ	トフ	الم	77	۲۲.	17	NT	7⊥	17	나	EST_HUMAN	ל⊤	上で	上,	Lγ	۲۲	4⊤	N⊤	NT	4⊤	11	11	T_HUMAN	LN	L,	1.7	1T	N
Top Hit Acession No.		_	4759249	4759249 NT	8922933 NT	4758569 NT	4826672 NT	4826672 NT	8923624 NT	8923624 NT	0.0E+00 AJ245922.1	8923087 NT	5174384 NT	4758117 NT	0.0E+00 BE005208.1	7706134 NT	7706134 NT	4826947 NT	4826947 NT	4506712 NT	8923290 NT		0.0E+00 AB002059.1	7657468 NT	7657468 NT	00290		0.0E+00 AB020710.1 N	9966844 NT	7305076 NT	7305076 NT	0.0E+00 AB037835.1 N
Most Similar (Top) Hit BLAST E Value	0.0E+00 N43182.1	0.0E+00 N43182.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AI147650.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Expression Signal	1.04	1.04	76.0	76.0	4.44	2.19	1.88	1.88	2.52	2.52	38.24	0.93	3.28	3.58	3.6	3.79	3.79	1.12	1.12	5.7	0.86	10.18	12.02	2.03	2.03	0.95	-	1.44	1.13	2.31	2.31	1.59
ORF SEQ ID NO:	20774	20775	20776	20777		20792	20807	20808	20812	20813	20814		20818	20827	20837	20861	20862	20872	20873	20874	20876	20878	20879	20880	20881	20884	20885	20887	20896	20908	20909	20911
Exon SEQ ID NO:	10930	10930	10931	10931	10935	10949	10966	10966	10970	10970	10971	10973	10975	10982	10996	11019	11019	11031	11031	11032	11034	11036	11038	ı	ı	11042	11043	11045	11054	11065	11065	11067
Probe SEQ ID NO:	1012	1012	1013	1013	1017	1031	1049	1049	1053	1053	1054	1056	1058	1066	1080	1103	1103	1116	1116	1117	1119	1121	1123	1124	1124	1128	1129	1131	1140	1152	1152	1154

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Single Exon Propes Expressed in Reali	Top Hit Descriptor	Homo sapiens keratin 18 (KRT18) mRNA	Homo sapiens mult. (E. coli) homolog 3 (MLH3), mRNA	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens chromosome 3 subtelomeric region	Homo saplens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA	Homo sapiens NF2 gene	Homo sapiens ribosomal protein S2 (RPS2) mRNA	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds	Homo sapiens mRNA for KIAA1507 protein, partial cds	Homo sapiens mRNA for KIAA1507 protein, partial cds	Homo sapiens Wolfram syndrome (WFS) mRNA	Homo sapiens Wolfram syndrome (WFS) mRNA	Homo sapiens Wolfram syndrome (WFS) mRNA	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA	Homo sapiens ring finger protein 9 (RNF9), mRNA	Homo sapiens zinc finger protein 173 (ZNF173) mRNA	Homo sapiens ring finger protein 9 (RNF9), mRNA	Homo sapiens mRNA for KIAA0577 protein, complete cds	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA	Human endogenous retrovirus HERV-K10	Homo sapiens mRNA for Familial Cylindromatosis cyld gene	Homo sapiens partial TTN gene for titin	qg38b06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:727A1.5 CE14213;	RAN, member RAS oncogene family-lomo sapiens RAN, member RAS oncogene family (RAN), mRNA
tie Exon Prop	Top Hit Database Source	NT	LN	FN	TN	LΝ	LN	NT	NT	NT	NT	NT	NT	NT	NT	NŢ	NT	L	LN	NT	LN	NT	NT	NT	NT	NT	NT	NT	LN	NT	LN	EST_HUMAN	NT
Juic	Top Hit Acession No.	4557887 NT	7657336 NT	0.0E+00 AF264750.1	0.0E+00 AF264750.1	0.0E+00 AF264750.1	0.0E+00 AF264750.1	0.0E+00 AF109718.1	4503098 NT	Y18000.1	4506718 NT	0.0E+00 AF084479.1	0.0E+00 AB040940.1	0.0E+00 AB040940.1	5174748 NT	5174748	5174748 NT	0.0E+00 AF096156.1	7657529 NT	7657529 NT	5803146 NT	4508004	5803146 NT	0.0E+00/AB011149.1	7661965 NT	7661965 NT	8567387 NT	8567387 NT	0.0E+00 M14123.1	0.0E+00 AJ250014.1	0.0E+00 AJ277892.1	0.0E+00 AI208756.1	6042206 NT
	Most Similar (Top) Hit BLAST E. Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	1.02	1.13	1.14	1.14	1.31	0.95	3.62	1.3	1.48	45.69	3.66	1.71	1.71	6.42	6.42	6.42	2.6	1.1	1.1	1.71	0,82	1.07	4.1	1.06	4.64	4.1	4.1	1.35	0.89	9.13	0.96	8.18
	ORF SEQ ID NO:	20920		20962	20963	20964	20965	20988	20989		21009	21018	21022	21023	21036	21037	21038		21050	21051	21057	21058	21059	21061	21062	21063	21064	21065	21078	21147	21156	21160	21161
	Exon SEQ ID NO:	11074	11101	11116	11116	11117	12687	11134	11135	11152	11160	11167	11173	11173	11186	11186	11186	11187	12689	12689	11202	11203	11205	11207	11208	11209	11210	11210	11221	11291	11298	11301	11302
	Probe SEQ ID NO:	1161	1191	1206	1206	1207	1208	1226	1227	1245	1253	1260	1266	1266	1278	1278	1278	1279	1289	1289	1295	1296	1298	1300	1301	1302	1303	1303	1315	1386	1393	1396	1397

Homo saplens ribosomal protein L5 (RPL5) mRNA

4507720 NT 4506654 NT

0.0E+00

5.75 10.12

21292

11435 12697

1530 1531

0.0E+00

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Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein Human von Willebrand factor pseudogene corresponding to exons 23 through 34 Human von Willebrand factor pseudogene corresponding to exons 23 through 34 Homo sapiens hHDC for homolog of Drosophila headcase (LOC51695), mRNA aa34a03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815116 5 Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA Homo sapiens KIAA1114 protein (KIAA1114), mRNA Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements Homo sapiens alpha1-6fucosytransferase (alpha1-6FucT) gene, exon Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA Top Hit Descriptor Homo sapiens transmembrane glycoprotein (GPNMB) mRNA Homo sapiens transmembrane glycoprotein (GPNMB) mRNA Homo sapiens KIAA0170 gene product (KIAA0170), mRNA Homo sapiens KIAA0170 gene product (KIAA0170), mRNA Cercopithecus aethiops cyclophilin A mRNA, complete cds Cercopithecus aethiops cyclophilin A mRNA, complete cds Homo sapiens KIAA0957 protein (KIAA0957), mRNA Homo sapiens KIAA1114 protein (KIAA1114), mRNA Homo sapiens RFB30 gene for RING finger protein Human transglutaminase mRNA, complete cds (L44L) and FTP3 (FTP3) genes, complete cds Human mRNA for KIAA0240 gene, partial cds Novel human gene mapping to chomosome Novel human gene on chromosome 20 Human nebulin mRNA, partial cds Human nebulin mRNA, partial cds Homo sapiens titin (TTN) mRNA Homo sapiens titin (TTN) mRNA Homo sapiens titin (TTN) mRNA Homo sapiens titin (TTN) mRNA Bovine mRNA for neurocalcin Single Exon Probes Expressed in Heart **EST HUMAN** Database Top Hit Source 눋 F 뉟 눋 F 늘 F 4505404 NT 4505404 NT 7662405 NT 7656972 NT Ξ 4507720 NT 뉟뉟 Z 6912457 NT 7706434 NT 7705565 NT Ξ z 4507720 NT 4507720 NT Ξ 4505646 NT 4505646 NT 7705565 7661965 7661965 Top Hit Acession 0.0E+00 AA481172.1 0.0E+00|AF023860.1 0.0E+00 AF038280.1 0.0E+00 AJ238093.1 0.0E+00 AL137764.1 0.0E+00 AL132999. 0.0E+00 M60676.1 M98478.1 Y07829.2 0.0E+00 M60676.1 0.0E+00 D10884.1 J35637.1 0.0E+00|U35637.1 0.0E+00 D87077.1 0.0E+00 U78027.1 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0户+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 Vost Similar (Top) Hit BLASTE Value 1.02 1.22 3.65 3.65 3.9 3.12 5.75 1.03 4.97 1.51 1.51 0.97 1.32 0.95 11.95 5.02 2.54 1.02 4.4 2.54 3.51 9.7 9.7 0.97 Expression Signal 21208 21209 21276 21289 21203 21214 21215 21220 21259 21273 21284 21285 21204 21223 21225 21226 21277 21291 21178 21180 21192 21231 21232 ORF SEQ 21177 io No 11399 11424 11425 11425 11426 11432 11435 11414 11420 11427 11312 11314 11342 11350 11352 11356 11420 11312 11327 11337 11342 11359 11361 11361 11422 SEQ ID 11314 11317 11337 11362 11367 11367 Exon ö 1519 1522 1530 1407 1409 1409 1412 1421 1432 1432 1437 1437 1445 1447 1451 1456 1456 1457 1462 1462 1495 1509 1515 1515 1520 1520 1527 1407 1454 1521 1517 SEQ ID

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Single Exon Probes Expressed in Hear	Top Hit Descriptor	Human laminin receptor (2H5 epitope) mRNA, 5' end	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA	H.sapiens hH2B/e gene	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5	Homo sapiens mRNA for KIAA1472 protein, partial cds	Homo saplens DNA polymerase zeta catalytic subunit (REV3) mKNA, complete cds	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA	Human sodium channel mRNA	yo76c05.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:183848 3'	Homo sapiens mRNA for KIAA1609 protein, partial cds	Homo sapiens mRNA for KIAA1609 protein, partial cds	wg81b07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR-062788 CXS2HIS2 7NC FINGER PROTEIN	Homo sapiens T-cell receptor gamma V1 gene region	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds	Homo sapiens keratin 18 (KRT18) mRNA	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone iMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);	H.sapiens H2B/h gene	H.sapiens H2B/h gene	Homo saplens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mKNA
e Exon Probe	Top Hit Database Source								HUMAN	T_HUMAN								EST HUMAN		IN LN	LIMANI	Τ		LZ				T_HUMAN	EST_HUMAN			
Sing	Top Hit Acession No.	M14199.1	4507720 NT	4507720 NT	4503098 NT		5921460 NT	21460	1	-		F157476.1	7662183 NT	7662183 NT	5729876	5729876 NT			1	Ţ	70.70				4557887 NT	7657065 NT	4557610 NT	130132.1				5031748 NT
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Z83738.1	0.0E+00	0.0E+00	0.0E+00 A	0.0E+00 AV690831.	0.0E+00 AB040905.	0.0E+00 AF157476.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M91803.1	0.0E+00 H26973.1	0.0E+00 AB046829	0.0E+00	00.1	0.0E+00 AF057177	0.0E+00 M29580.1	0.0E+00 M29580.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 H30132.1	0.0E+00 H30132.1	0.0E+00 Z80780.1	0.0E+00 Z80780.1	0.0E+00
	Expression Signal	11.11	5.81	5.81	12.91	1.66	1.38	1.38	5.5	5.5	1.5	0.98	2.49	2.49	14.05	14.05	0.94	4.67	4.1.4	1.4		3 33	1.56	1.56	1.22			2.99	2.99	1.21	1.21	7.85
	ORF SEQ ID NO:	21293	21306			21325	21326	21327		21329	21330	21331	21334	21335		21337	21339		21368			21410					21423				21430	
	Exon SEQ ID NO:	11436	11446	11446	11448	11467	11468	11468	11469	11469	12698	11474	11476	11476	11478	11478	11480	_	11507	11507		11548		L	11555	1_	丄	11561		11563		11566
	Probe SEQ ID NO:	1532	1541	1541	1543	1562	1563	1563	1564	1564	1566	1570	1572	1572	1574	1574	1576	1591	1602	1602		1040	1650	1650	1652	1653	1657	1659	1659	1661	1661	1664

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Table 4
Single Exon Probes Expressed in Heart

	Т	Г	T	1-	Т-	Т	η-	T	T	Τ-	Τ-		_	<u> </u>	T	1		<u>"</u>	*1 ₁₁₁ 1	T	·	<u></u>		41.,11			(t .1 <u>1</u> ,	alt 1	art that
Top Hit Descriptor	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA	Human hepatocyte growth factor gene, exon 15	Human hepatocyte growth factor gene, exon 15	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds	TCR zeta [human, Genomic/mRNA, 365 nt, segment 1 of 8]	Homo sapiens NOD2 protein (NOD2), mRNA	Homo saplens SMCY (SMCY) gene, complete cds	Homo sapiens ribosomal protein S2 (RPS2) mRNA	Homo sapiens E1A binding protein p300 (EP300) mRNA	Homo sapiens E1A binding protein p300 (EP300) mRNA	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds	zd66g09.r1 Soares_fetal_heart_NbHH19W_Homo sapiens cDNA clone IMAGE:345664 5	Homo saplens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA	Human ribosomal protein L21 mRNA, complete cds	Human mRNA for KIAA0333 gene, partial cds	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA	Homo sapiens activaling transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA	Homo sapiens immunoglobin superfamily, member 3 (IGSF3) mRNA, and translated products	Homo sapiens immunoglobin superfamily, member 3 (IGSF3) mRNA, and translated products	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA	Homo sepiens potassium voltage-gated channel. Shab-related subfamily member 1 (KCNR1) mRNA	Human retinal degeneration slow (RDS) gene, exon 1	Human retinal degeneration slow (RDS) gene, exon 1	UI-H-BI1-afin-f-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'	UI-H-BI1-afn-f-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
Top Hit Database Source	NΤ	LN	LZ	LN	TN	NT	NT	NT	١	L L	LZ	NT	EST HUMAN	۱.	LN	N	⊢ Z	٦	LN	ZT	Ę	トフ	トフ	LZ	F	N	LN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	8923841 NT			4826973 NT	0.0E+00 AB026542.1	394400.1	11545911 NT	0.0E+00 AF273841.1	4506718 NT	4557556 NT	4557556 NT			4505332 NT		0.0E+00 AB002331.1	4502264 NT	4502264 NT	4502264 NT	4504626 NT	4504626 NT	E005855 NT	6005855 NT	4826783 NT	4826783 NT			0.1	0.0E+00 AW207280.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 M75980.1	0.0E+00 M75980.1	0.0E+00	0.0E+00	0.0E+00 S94400.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U63963.1	0.0E+00 W76571.1	0.0E+00	0.0E+00 U14967.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U07147	0.0E+00 U07147.1	0.0E+00	0.0E+00
Expression Signal	4.55	1.02	1.02	1.43	2.59	2.6	0.87	1.75	13.81	6.0	6.0	1.23	1,13	3.89	7.25	4.6	4.34	4.34	4.34	1.04	1.04	10.22	10.22	3.19	3.19	4.52	4.52	1.47	1.47
ORF SEQ ID NO:	21442	21448	21449	21453	21460		21472	21481		21517	21518	21521		21525	21538	21541	21542	21543	21544	21558	21559	21566	21567	21576	21577	21578	21579	21584	21585
Exon SEQ ID NO:	11574	11579	11579	11582	11587	11589	12702	11611	12703	11649	11649	11651	11654	12704	11664	11666	11667	11667	11667	11680	11680	11691	11691	11701	11701	11702	11702	11706	11706
Probe SEQ ID NO:	1672	1677	1677	1680	1685	1687	1699	1710	1745	1749	1749	1751	1754	1755	1765	1767	1768	1768	1768	1781	1781	1793	1793	1804	1804	1805	1805	1809	1809

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Table 4
Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Hear	Top Hit Descriptor	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'	601179164F1 NIH_MGC_20 Homo saplens cDNA clone IMAGE:3547239 5	RC2-BN0126-200300-012-b04 BN0126 Homo sapiens cDNA	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds	Human transglutaminase mRNA, complete cds	Human transglutaminase mRNA, complete cds	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA	Homo saplens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	genes, comprete cos	numan robusci letase i pseudogene i	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA	Homo sapiens histidine ammonia-lyase (HAL) mRNA	Homo sapiens histidine ammonia-lyase (HAL) mRNA	Homo sapiens chromosome 21 segment HS21C052	Homo sapiens nebulin (NEB), mRNA	Homo sapiens nebulin (NEB), mRNA	Homo sapiens actinin, alpha 4 (ACTN4) mRNA	Homo sapiens actinin, alpha 4 (ACTN4) mRNA	Homo sapiens mRNA for KIAA0790 protein, partial cds	Homo sapiens mRNA for KIAA0790 protein, partial cds	Human TFEB protein mRNA, partial cds	Human TFEB protein mRNA, partial cds	x69b01.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679913 3'	x69b01.x1 NCL CGAP Pan1 Homo sapiens cDNA clone IMAGE.2679913 3'	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	H.saplens genes for semenogelin I and semenogelin II	H.sapiens genes for semenogelin and semenogelin I	Homo sapiens mRNA for KIAA1513 protein, partial cds	Homo sapiens SMCY (SMCY) gene, complete cds	Homo sapiens SMCY (SMCY) gene, complete cds
e Exon Propes	Top Hit Database Source			T HUMAN																			NT	NT Hor			EST HUMAN x69	EST_HUMAN X66				s.H . TN			NT
Buis	Top Hit Acession No.	0.0E+00 BE277465.1 E	0.0E+00 BE277465.1 E	92.1	4506384 NT	4506384 NT	1.			4507464 NT	4507464 NT			U.0E+00 M55632.1	5901905 NT	4809282 NT	4809282 NT	52.2	8400716 NT	8400716 NT	4826638 NT	4826638 NT		1	.1	:1	024.1	1.74.1	6912457	6912457 NT	.1	.1	0.0E+00 AB040946.1		0.0E+00 AF273841.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 BE0062	0.0E+00	0.0E+00	0.0E+00 AF1574	0.0E+00 M98478.1	0.0E+00 M98478.1	0.0E+00	0.0E+00	L	0.0E+00 AF-2407	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AL1632	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AB0183	0.0E+00	0.0E+00 M33782	0.0E+00	0.0E+00 AW193	0.0E+00 AW1930	0.0E+00	0.0E+00	0.0E+00 Z47556	0.0E+00 Z47556	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	2,08	2.08	0.99	3.52	3.52	1.65	4.06	4.06	2.28	2.28	L	5.25	1.9	0.94	1.97	1.97	1.12	1.15	1.15	8.13	8.13	1.21	1.21	2.01	2.01	1.33	1.33	8.4	8.4	0.92	0.92	2.31	0.86	0.86
	ORF SEQ ID NO:	21603	21604	21623	21651	21652		21661	21662	21669	21670				21678	21685			21700	21701	21702	21703	21715	21716	21720	21721	21722	21723		21725	21727	21728	21737		21760
	Exon SEQ ID NO:	11729	11729	11748	11777	11777	11785	12707	12707	11790	11790		- 1		12708	11808	11808	11819	11821	11821	11822	11822	11832	11832	11838	11838	11840	11840	<u> </u>	11841	11843	11843	11850		11868
	Probe SEQ ID NO:	1832	1832	1852	1881	1881	1889	1890	1890	1895	1895		1898	1903	1905	1913	1913	1924	1926	1926	1927	1927	1937	1937	1943	1943	1945	1945	1946	1946	1948	1948	1955	1975	1975

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Olige Extra Expressed in region	Top Hit Descriptor	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3833198 5	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia Β) (Fo) mRNA	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'	Homo sapiens KIAA1114 protein (KIAA1114), mRNA	Homo sapiens KIAA1114 protein (KIAA1114), mRNA	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mKNA	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mKNA	HSC0IC021 normalized Infant brain cDNA Homo sapiens cDNA clone c-0tc02	qvg0f08.x1 NCI_CGAP_Ut2 Home sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repotitive	ANTARTARET NIH MGC 69 Homo saciens cDNA clone IMAGE:3887747 5	POLICOS AND AND SERVICE FOR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A WILL MACE TO THE WAY A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR A FIRM IN A CETATA FAR 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CETATA FAR A FIRM IN A FIRM	6019U2004FT NIT INICO 19 TOILO Septens COIN COINE INVACE: 413520 5	OU BUZGOATE INITIALIZAÇÃO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL 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COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DELA COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DE	RC3-C 10413-Z/0700-0ZZ-d10 C 10413 Homo Sapiens CLIVA	RC3-C10413-270700-022-d10 C10413 Homo saplens CLINA	Human plasma membrane calcium A I Pase isotom 2 (AP I 282) mKNA, comiete cds	Human plasma membrane calcium ATPase isotorm 2 (APT2B2) mKNA, comiete cds	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA	QV1-CN0065-140800-318-c10 GN0065 Homo sapiens cDNA	Homo sapiens X-linked juvenile retinoschisis protein (XLRS1) gene, exon 6 and complete cds	601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	genes, complete cds	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA	QV-BT065-020399-092 BT065 Homo sapiens cDNA	QV-BT065-020399-092 BT065 Homo saplens cDNA	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNMB3L), mRNA	Human DNA-binding protein mRNA, 3'end
וב רעמון ומק	Top Hit Database Source	EST_HUMAN	EST_HUMAN	E N	EST HIMAN	-'	Į,	EST_HUMAN	EST_HUMAN	NT	NT	EST_HUMAN	144441111111111111111111111111111111111	EST HOMAN	TOT TOWN	EST HUMAN	ES! HOMAN	EST HUMAN	EST_HUMAN	N	NT	NT	EST_HUMAN	TN	EST_HUMAN	N		NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	NT
3,112	Top Hit Acession No.		0.0E+00 BE743215.1	010001	4503046 IN I	7705565	7705565 NT	A077589.1	A077589.1	7657468 NT	4585863 NT	742399.1		NI244247.1)CO11773.1	0.0E+00 BF315325.1	3F315325.1	3E697125.1	3E697125.1	.00620.1	.00620.1	4758489 NT	0.0E+00 BE767964.1	0.0E+00 AF018963.1	0.0E+00 BF027562.1	4503756 NT		0.0E+00 AF240786.1	AW752708.1	0.0E+00 AI904640.1	Al904640.1	7657252 NT	
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	L	0.05 +00	0.00+30.0	0.0E+00	0.0E+00 AA07758	0.0E+00 AA07758	0.0E+00	0.0E+00	0.0E+00 Z42399.1		0.0E+00 AI244247	0.0E+00 DEB/1/22	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE69712	0.0E+00 L00620.1	0.0E+00 L00620.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00 AW7527	0.0E+00	0.0E+00 A1904640		
	Expression Signal	1.09	1.89		0.96	2.40	10.	1.95	1.95	2.34	1.6	0.92		1.94	7.59	1.5	1.5	2.42	2.42	2.53	2.53	1.32	2.63	1.13	3.09	2		0.99	1.16	1.96		1.19	1.6
	ORF SEQ ID NO:	21793	21794			21/30	21178					21802					21814		21820	21826	21827				21854	L	L	21856					
	Exon SEQ ID NO:	11903	11903		11905		11314		11908	11910	11912							11926	11926	11931	11931	11936	11957	11958	11960			11963		l	_	1	1 1
	Probe SEQ ID NO:	2011	2011		2013	2014	2015	2017	2017	2019	2021	2022		2024	2029	2031	2031	2035	2035	2040	2040	2045	2067	2068	2070	2071		2073	2074	2076	2076	2112	2132

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Single Exon Probes Expressed in Heart

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Single Exult Plobes Expressed in Rear	Top Hit Descriptor	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346688 5'	Human mRNA for KIAA0244 gene, partial cds	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'	0032e01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567895 3'	Human apolipoprotein B-100 (apoB) gene, exons 22 through 29	602014829F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150734 5'	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA	601900261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129622 5'	bb84e02.yf NIH_MGC_10 Forno sapiens cDNA clone IMAGE:3049082.5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTFIN	2k53c07.s1 Spares pregnant uterus NbHPU Home saniens cDNA clone MAAGE 486540 3' cimilar to	gb.X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);	2k3s07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN)	Homo sapiens chromosome 21 segment HS210004	Homo sapiens chromosome 21 segment HS21C004	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	Human beta-prime-adaptin (BAM22) gene, exon 16	Homo sapiens E1A binding protein p300 (EP300) mRNA	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5	Homo sapiens mRNA for KIAA 1363 protein, partial cds	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA	oz09c07.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE.1674828 3'	zv/8a11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5	zv/8a11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'	602021846F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157339 5
lle Exull Pion	Top Hit Database Source	EST_HUMAN	L	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN		EST_HUMAN	EST HUMAN	TN	NT	N	TN	NT	NT	NT T	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	NT	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN
JIIC	Top Hit Acession No.	0.0E+00 BE274696.1	J87685.1	0.0E+00 AV738288.1	0.0E+00 AV738288.1	0.0E+00 AA931691.1	J19828.1	1	1.	.1	0.0E+00 BF377897.1	0.0E+00 BF313617.1	0.0E+00 BE018750.1		0.0E+00 AA042813.1	0.0E+00 AA042813.1	2	0.0E+00 AL163204.2	7662401 NT	7662401 NT	U36264.1	4557556 NT	362401	1	0.0E+00 BE905563.1	-	0.0E+00 AB037784.1	11545748 NT	45748		1	1	0.0E+00 BF347039.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 D87685.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M19828.1	0.0E+00	0.0E+00	0.0E+00 BF377897	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	1.02	1.09	10.46	10.46	1.4	0.9	17.1	11.29	2.35	2.35	1.77	1.92		0.92	0.92	2:32	2.32	2.63	2.63	1.04	7.56	1.44	1.09	0.87	0.87	1.36	4.16	4.16	2.51	2.21	2.21	2.23
	ORF SEQ ID NO:	21922	21925	21926	21927	21929		21933	21934	21937	21938	21943	21946		21947	21948	21956.	21957	21958	21959		21984	21988	21996	21999	22000	22002	22034	22035	22036	22038	22039	22041
	Exon SEQ ID NO:	12026	12028	12029	12029	12031	12033	12036	12037	12040	12040	12714	12046		12047	12047	12055	12055	12056	12056	12061	12080	12086	12093	12096	12096	12098	12137	12137	12138	12140	12140	12142
	Probe SEQ ID NO:	2138	2140	2141	2141	2143	2145	2148	2149	2152	2152	2156	2159		2160	2160	2168	2168	2169	2169	2174	2193	2199	2206	2209	2209	2212	2253	2253	2254	2256	2256	2258

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Table 4
Single Exon Probes Expressed in Heart

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	Top Hit Descriptor	Homo sapiens potassium channel Kv2.1 mRNA, complete cds	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA	7f22a02.xt NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:094939 094939 KIAA0857 PROTEIN	Homo sapiens phosphorylase kinase alpha subunit (PHKA2) gene, exon 32	ty57c08.x1 NCI_CGAP_Ut2 Homo saplens cDNA clone IMAGE:2283182 3'	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA	Homo saplens titin (TTN) gene, alternative spilce products, partial cds	Homo sapiens titin (TTN) gene, alternative splice products, partial cds	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5	601586843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'	MR1-SN0033-120400-002-a04 SN0033 Homo sapiens cDNA	Homo sapiens KIAA0244 protein (KIAA0244), mRNA	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds, cytochrome P450 polypeptide	4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450	polypeptide 5 (CYP3A5) gene, partial cds	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'	MRo-BN0070-090600-029-d12 BN0070 Homo sapiens cDNA	AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'	ox60b02.x1 Soares_NHHMPu_S1 Homo septiens cDNA clone IMAGE:1660683 3' similar to TR:008662	xx15f07.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR O54924	054924 EX084.;	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'	AB005622 HeLa cDNA (T.Noma) Homo sapiens cDNA similar to adenyate kinase isozyme 2	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA	Homo sapiens gene for cholecystokinin type-A receptor, complete cds	Homo sapiens gene for chalecystokinin type-A receptor, complete cds
אור בייטוו ו וטיי	Top Hit Database Source	IN	N	EST HUMAN	F	EST_HUMAN	NT	NT	LN	LN	TN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	IN	NT			NT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	MANUEL FOR	NO.	EST HUMAN	EST HUMAN	EST_HUMAN	IN	NT	닏
<u></u>	Top Hit Acession No.	0.0E+00 L02840.1	6325466 NT	0.0E+00 BE676095.1	-	0.0E+00 AI6255421		5803178 NT	0.0E+00 AF058332.1	0.0E+00 AF058332.1	5174678 NT	1	0.0E+00 BE794026.1	AW867076.1	7662017	4758497 NT	4758497 NT			0.0E+00 AF280107.1	0.0E+00 AU118082.1	0.0E+00 AU118082.1	0.0E+00 AU118082.1	0.0E+00 BE814424.1	0.0E+00 AU119582.1	0 0E 100 A 104202E 1	71042020	0.0E+00 AW303998.1	0.0E+00 BE895605.1	0.0E+00 AB005622.1	6006002 NT	0.0E+00 D85606.1	0.0E+00 D85606.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00			0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	007100	0.0L.100	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	1.19	2.03	-	10.08	2.72	1.76	1.76	4.26	4.26	2.88	1.75	5.71	0.98	1.97	1.44	1.44			2.31	7.57	7.57	7.57	0.96	1.34	ď	50.0	0.98	2.03	1.69	5.63	2.48	2.48
-	ORF SEQ ID NO:		22048			22057						22083			22085		22087	i			22088	22089	22090		22138			22141				22162	
	Exon SEQ ID NO:	12147	12148	12155	12158	12159	12164	12164	12173	12173	12182	12185	12186	12187	12188	12189	12189				12191	12191	12191	12208	12243		0477	12249	12251		12265	Шl	12268
	Probe SEQ ID NO:	2263	2264	2271	2274	2275	2280	2280	2291	2291	2300	2304	2305	2306	2307	2308	2308			2309	2310	2310	2310	2327	2363	000	7300	2369	2371	2382	2386	2390	2390

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Single Exon Probes Expressed in Heart

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Single Exoli Flobes Expressed in Healt	Тор Hit Descriptor	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA	CM0-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA	CM0-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA	602184558T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE.4300383 3'	ha04h04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'	UI-HF-BP0p-ais-c-07-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA	601592530F1 NIH_MGC_7 Homo sapiens cDNA done IMAGE:3946518 5'	Homo sapiens death receptor 6 (DR6), mRNA	UI-H-BI4-aoz-b-08-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'	Homo sapiens mRNA for membrane transport protein (XK gene)	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mRNA	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA	RC4-HT0276-160200-013-d05 HT0276 Homo sapiens cDNA	Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA	Human Sec62 (Sec62) mRNA, complete cds	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5	601489241F1 NIH_MGC_69 Homo saplens cDNA clone IMAGE:3891371 5	Homo sapiens adlican mRNA, complete cds	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'	601105312F1 NIH_MGC_15 Hamo sapiens cDNA clone IMAGE:2987955 5	7q27h12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE: 3' similar to TR: O00246 C00246 HYPOTHETICAL 9.3 KD PROTEIN	Homo sapiens adlican mRNA, complete cds	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5'
gie Lauri riu	Top Hit Database Source	NT	EST_HUMAN	INT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	TN.	EST_HUMAN	NT	N-	EST_HUMAN	NT	EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HIMAN	NT	EST_HUMAN
	Top Hit Acession No.	0.0E+00 AF106275.1	0.0E+00 BF345274.1	5729777 NT	0.0E+00 BE831003.1	0.0E+00 BE831003.1	0.0E+00 BF569144.1	0.0E+00 AW466922.1	0.0E+00 AW 501010.1	5453965 NT	5453965	0.0E+00 AW813853.1	0.0E+00 BE795542.1	7657038,NT	0.0E+00 BF509482.1	232684.2	5453871 NT	0.0E+00 BE910378.1	7657468 NT	BE150865.1	8923340 NT	J93239.1	0.0E+00 BE886490.1	0.0E+00 BE875511.1	0.0E+00 BE875511.1	0.0E+00 AF245505.1	0.0E+00 BE536921.1	0.0E+00 AU143277.1	0.0E+00 AU143277.1	0.0E+00 BE292896.1	0.0E+00 BE292896.1	0.0E+00.BE223041.1	0.0E+00 AF245505.1	0.0E+00 BE296613.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Z32684.2	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U93239.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0 0F+00	0,0E+00	0.0E+00
	Expression Signal	2.28	0.98	3.95	0.87	0.87	2.27	2.66	3.45	2.08	2.08	2.35	16.13	1.18	1.8	2.25	5.57	1.99	1.96	55.78	1.14	3.21	1.64	4.39	4.39	26.0	1.27	3.8	3.8	1.19	1.19	G C	7.65	1.05
	ORF SEQ ID NO:	22172			22188	22189				22219	22220		22233	21671	22234			22239							22256			22274	22275		22277	22278		22304
	Exon SEQ ID NO:	12276	12279	12287	12291	12291	12296	12305	12307	12321	12321	12334	12339	11792	12340	12343	12345	12347	12348	12349	12350	12351	12357		- 1		12379	12383	12383	12384	12384	12385	12388	12414
	Probe SEQ ID NO:	2398	2402	2410	2414	2414	2419	2428	2430	2444	2444	2457	2462	2463	2464	2467	2469	2471	2472	2473	2474	2475	2481	2486	2486	2488	2504	2509	2509	2510	2510	2511	2514	2540

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Table 4
Single Exon Probes Expressed in Heart

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Onlight Event Topics Expension and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and t	Top Hit Descriptor	Homo sapiens mRNA for KIAA1415 protein, partial cds	Homo sapiens mRNA for KIAA1415 protein, partial cds	UI-H-BW1-amp-f-12-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'	602152653F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293612 5	601279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621786 5	Homo saplens mRNA for KIAA1321 protein, partial cds	tn19b08.x1 NCI_CGAP_Brn25 Horno sapiens cDNA clone IMAGE:2168055 3' similer to 9b.L20977 cALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN);	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kD (TAF2I)	mRNA	Homo sapiens mRNA for KIAA1438 protein, pertial cds	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5	601590108F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3944304 5'	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051389 5	601584930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds	Homo sapiens guanylate cyclase activating protein 2 (GUCA1B) gene, exon 1	Homo sepiens mRNA for KIAA0536 protein, partial cds	AU 133385 NT2RP4 Homo saplens cDNA clone NT2RP4001964 5'	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'	RC1-OT0086-220300-011-d07 OT0086 Homo sapiens cDNA	7h15h05.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316089 3'	601298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5	Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA	EST188414 HCC cell line (matastasis to liver in mouse) Il Homo septens cDNA 5' end similar to ribosomal	protein L29	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:394359′5'	Human beta-prime-adaptin (BAM22) gene, exon 5
מסון ווסעים אול	Top Hit Database Source	NT	NT	EST HUMAN	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN		N⊤	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	LΝ	. LN	LN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N		EST_HUMAN	EST_HUMAN	NT
2	Top Hit Acession No.	0.0E+00 AB037836.1	0.0E+00 AB037836.1	0.0E+00 BF513835.1	0.0E+00 BF672818.1	0.0E+00 BE616695.1	0.0E+00 AB037742.1	AI571737.1		5032150 NT	AB037859.1	3E795445.1	0.0E+00 BE795445.1	0.0E+00 BE293328.1	3E792472.1	4504686 NT	4507720 NT	J78027.1	AF173227.1	0.0E+00 AB011108.1	AU133385.1		0.0E+00 AU130403.1	3.1	AW887015.1	0.0E+00 BF000018.1	0.0E+00 BE383165.1	BE531263.1	8922843 NT		0.0E+00 AA316723.1	0.0E+00 BE794884.1	U36253.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AI571737		0.0E+00	0.0E+00	0.0E+00 BE79544	0.0E+00	0.0E+00	0.0E+00 BE79247;	0.0E+00	0.0E+00	0.0E+00 U78027.1	0.0E+00 AF173227	0.0E+00	0.0E+00 AU13338	0.0E+00 M69225.1	0.0E+00	0.0E+00 AU13040	0.0E+00 AW88701	0.0E+00	0.0E+00	0.0E+00 BE53126	0.0E+00		0.0E+00	0.0E+00	0.0E+00 U36253.1
	Expression Signal	2.37	2.37	3.85	2.8	1.16	1.34	0.97		2.27	5.78	1.03	1.03	1.1	10.42	2.46	7.02	1.09	5.19	1.17	86.0	1.41	1.21	1.21	1.29	1	3.25	2.74	1.74		8.72	0.88	3.59
	ORF SEQ ID NO:	22318	22319		22325		22332	22333		22334	22336			22339		22358			22369	22370			22376	22377	22380		22386		22413				22452
	Exan SEQ ID NO:	12654	12654	12426	12432	12434	12440	12441		12442	12444	12445	12445	12448	12456		1	12476	12477	12481	1	l _	12487		12490	İ	1	12496	12523			12556	12562
	Probe SEQ ID NO:	2553	2553	2554	2560	2562	2569	2570		2571	2573	2574	2574	2577	2585	2595	2601	2608	2609	2613	2616	2617	2619	2619	2622	2626	2627	2628	2656		2690	2691	2698

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Single Exon Probes Expressed in Heart

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Olligie Exoli Plobes Expressed iii neart	Top Hit Descriptor	Homo sapiens neuregulin 1 (NRG1), transcript variant SMDF, mRNA	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds	601591991F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3945983 5'	602155923F1 NIH_MGC_83 Homo sapiens cDNA clone IWAGE:4297132 5'	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'	AV721647 HTB Homo saplens cDNA clone HTBBYE09 5'	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds	AV651066 GLC Homo sapiens cDNA clone GLCCLD07 3'	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5	RC4-HT0587-170300-012-d11 HT0587 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C001	UI-H-BW1-amw-e-07-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'	AV725534 HTC Homo saplens cDNA clone HTCCCA03 5'	au55d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW:R13A HUMAN P40429 60S RIBOSOMAI PROTFIN 13A	602071957F1 NCL CGAP Brn67 Homo sapiens cDNA clone IMAGE:4214679 5	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5'	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'	glycoprotein D=Duffy group antigen [human, blocd, Genomic DNA, 3068 nt]
	Top Hit Database Source	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	IN	IN	IN	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	IN	EST_HUMAN	EST_HUMAN		EST_HUMAN	IN	EST_HUMAN	LN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	L
0	Top Hit Acession No.	7669517 NT	0.0E+00 AF110763.1	0.0E+00 BE796376.1	0.0E+00 BF680632.1	0.0E+00 BE563433.1	0.0E+00 AV721647.1	5174486 NT	5174486 NT	8923441 NT	8923441 NT	0.0E+00 AF290195.1	0.0E+00 AV651066.1	3F377897.1	3F377897.1	47,57963 NT	4757963 NT	0.0E+00 BE747193.1	0.0E+00 BE176836.1	0.0E+00 AL163201.2	0.0E+00 BF514110.1	4503098 NT	0.0E+00 BF677694.1	7427522 NT	0.0E+00 AV725534.1	4V725534.1	1879163.1	0.0E+00 BF530661.1	3E872768.1	0.0E+00 AU131494.1	0.0E+00 AU131494.1	0.0E+00 BE300344.1	0.0E+00 BE300344.1	376830.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BF377897	0.0E+00 BF377897	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE872768	0.0E+00	0.0E+00	0.0E+00	0.0E+00 E	0.0E+00 S76830.1
	Expression Signal	1.08	10.23	10.37	3.2	13.51	1.28	2.17	2.17	6.0	6.0	2.2	15.67	1.72	1.72	3.21	3.21	2.2	0.97	1.3	3.47	1.07	4.95	1.73	9.56	9.56	11.15	1.97	2.91	1.11	1.11	10.1	10.1	4.6
	ORF SEQ ID NO:	22454	22455	22462	22463	22467		22470	22471	22472	22473	22474		22475	22476	22479	22480	22485	22488		22498		22507	22513	22515	22516		22521	22522	22523	22524	22525	22526	19966
	Exon SEQ ID NO:	12564	12565	12571	12572	12731	12575	12577	12577	12578	12578	12579	12580	12581	12581	12585	12585	12589	12592	12603	12604	12610	12616	12620	12623	12623	12625	12628	12629	12631	12631	12632	12632	10151
	Probe SEQ ID NO:	2700	2701	2708	2709	2712	2713	2715	2715	2716	2716	2717	2718	2719	2719	2723	2723	2727	2730	2741	2742	2748	2754	2758	2761	2761	2763	2766	2767	2769	2769	2770	2770	27.75

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Single Exon Probes Expressed in Heart

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Top Hit Descriptor	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds	Homo sapiens ALR-like protein mRNA, partial cds
 | PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA | PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA | H.sapiens Id3 gene for HLH type transcription factor | Homo sapiens chromosome 21 segment HS21C068 | Human transglutaminase mRNA, complete cds | Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene | Homo sapiens gammna-cytoplasmic actin (ACTGP3) pseudogene

 | Novel human mRNA from chromosome 1, which has similarities to BAT2 genes | H.sapiens mRNA for nuclear DNA helicase II | Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds | Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
 | Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA | Homo sapiens serine/threonine kinase 9 (STK9) mRNA | DKFZp586G0621_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586G0621 | Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA | Homo sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
 | QV2-BT0636-130400-138-h03 BT0636 Hamo sapiens cDNA | QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA | Homo sapiens chromosome 21 segment HS21C006 |
| Top Hit
Database
Source | NT | NT | L | LN | TN | NT | N | NT | LN | NT | NT
 | EST_HUMAN | EST_HUMAN | FZ | LN. | LΝ | NT | NT

 | NT | NT | NT | NT
 | NT | NT | EST_HUMAN | NT | NT | NT
 | EST_HUMAN | EST HUMAN | N |
| Top Hit Acession
No. | AB033281:1 | AF264750.1 | 4F264750.1 | 4503202 | 4503202 | X85980.1 | AF068624.1 | AB040960.1 | 4J238852.1 | AL163201.2 | V80902.1
 | 3E154504.1 | 3E154504.1 | X73428.1 | 4L163268.2 | M98478.1 | J50657.1 | J50657.1

 | AL096857.1 | r/10658.1 | AF152303.1 | 4503470
 | 4503470 | 4507280 | AL047599.1 | 7661883 | 7661883 | 4503098
 | 3E081896.1 | 3E081896.1 | 0.0E+00 AL163206.2 |
| Most Similar
(Top) Hit
BLAST E
Value | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00
 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00

 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00
 | 0.0E+00 | 0.0E+00 | | 0.0E+00 | 0.0E+00 | 0.0E+00
 | 0.0E+00 | 0.0E+00 | 0.0E+00/ |
| Expression
Signal | 1.94 | 1.37 | 1.37 | 3.58 | 3.58 | 2.39 | 1.27 | 1.1 | 1.07 | 2.24 | 5.94
 | 1.58 | 1.58 | 1.38 | 2.84 | 2.58 | 43.46 | 43.46

 | 45. | 4.62 | 96.0 | 25.08
 | 25.08 | 2.42 | 1.35 | 1.25 | 1.25 | 3.42
 | 4.95 | 4.95 | 1.64 |
| ORF SEQ
ID NO: | | 20479 | 20480 | 20784 | 20785 | | | | | 22538 | 22541
 | 22543 | 22544 | | | 22547 | 22551 |

 | | - | | 22556
 | 22557 | 22568 | 22572 | | |
 | | 22577 | 22588 |
| Exon
SEQ ID
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 | 12751 | 12751 | 12753 | 12755 | 12757 | 12761 | 12761

 | 12765 | 12766 | 12767 | 12768
 | 12768 | 12779 | 12782 | 12783 | 12783 | 12784
 | 12786 | 12786 | 12794 |
| Probe
SEQ ID
NO: | 2778 | 2784 | 2784 | 2789 | 2789 | 2805 | 2806 | 2808 | 2814 | 2815 | 2819
 | 2822 | 2822 | 2824 | 2826 | 2828 | 2833 | 2833

 | 2837 | 2838 | 2839 | 2840
 | 2840 | 2851 | 2854 | 2855 | 2855 | 2856
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Table 4
Single Exon Probes Expressed in Heart

Single Extri Flobes Explessed III fredit	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C006	zr96b11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683517 3' similar to contains Alu	repetitiva element;	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9	Homo sapiens EphA4 (EPHA4) mRNA	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	br/18d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247 O16247 F44E7.2 PROTEIN.;	th18d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247	016247 F44E7.2 PROTEIN.;	ZINC FINGER PROTEIN 132	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds	Homo sapiens mRNA for KIAA1267 protein, partial cds	Homo sapiens mRNA for KIAA1267 protein, partial cds	Homo sapiens mRNA for KIAA1508 protein, partlal cds	Homo sapiens mRNA for KIAA1508 protein, partial cds	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4	(MLLT4) mRNA	7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1 Q9VLN1 CG17293 PROTEIN.;	7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1	Q9VLN1 CG17293 PROTEIN.;	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA	Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA	Homo sapiens v-erb-a avian erythroblastic leukernia viral oncogene homolog-like 4 (ERBB4) mRNA	Homo sapiens neurexin III (NRXN3) mRNA	H.sapiens NF-H gene, exon 4	H.sapiens NF-H gene, exon 4	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
JIE EXUIT FIUD	Top Hit Database Source	NT		EST_HUMAN	NT	IN	NT	EST HUMAN		EST_HUMAN	SWISSPROT	LZ	TN	NT	NT	NT	TN	IN	Į.		N	EST HUMAN		EST HUMAN	IN	TN	NT	NT	TN	LN	Z	L
Sillo Sillo	Top Hit Acession No.	0.0E+00 AL163206.2		0.0E+00 AA215579.1		4758279	4503470 NT	0.0E+00 AI561002.1		N561002.1	52740	NF152338.1	7.	.1	0.0E+00 AB040941.1	0.0E+00 AB040941.1	7661903 NT	7661903 NT	5174574 NT		5174574 NT	0.0E+00 BF110702.1		0.0E+00 BF110702.1	4505084 NT	4505084 NT	4885214 NT	4885214 NT	4758827 NT	X15309.1	X15309.1	0.0E+00 AF106275.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00		0.0E+00	0.0E+00 Y19210.1	0.0E+00	0.0E+00	0.0E+00		0.0E+00 AI561002	0.0E+00 P52740	0.0E+00 AF152338.	0.0E+00 AB033093	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X15309.1	0.0E+00 X15309.1	0.0E+00
	Expression Signal	1.64		1.08	3.09	1.16	18.66	1.25		1.25	1.87	1.5	1.34	1.34	4.98	4.98	2.66	2.66	3.23		3.23	1.27		1.27	2.03	2.03	0.94	0.94	1.6	1.3	1.3	7.93
	ORF SEQ ID NO:	22589		22590		22599	22600	22601		22602	22604	22605	22617	22618	22619	22620	22623	22624	22625		22626	22630			22642		22645				22655	
	Exan SEQ ID NO:	12794		12795	12801	12804	12805	12806	1_	12806	12808	12809	12824	12824	12825	12825	12828	12828	12829	<u> </u>	12829	12833			12842	12842	12844	12844		12854		12856
	Probe SEQ ID NO:	2866		2867	2874	2877	2878	2879		2879	2881	2882	2897	2897	2898	2898	2901	2901	2902		2902	2907		2907	2915	2915	2917	2917	2924	2927	2927	2929

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Table 4
Single Exon Probes Expressed in Heart

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Top Hit Descriptor	qf43f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA	Homo sapiens mRNA for PKU-alpha, partial cds	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA	Homo sapiens chromosome 21 segment HS21C046	Human displacement protein (CCAAT) mRNA	Homo sapiens semenogelin I (SEMG1) mRNA	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA	Isoform 2 of a novel human mRNA from chromosome 22	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds	Homo sabiens transcription factor IGHM enhancer 3. IM41 protein. IM4 protein. IM5 protein. TE4 protein.	JM10 protein. A4 differentiation-dependent protein, frince I IM domain protein, 3 and supprotein, 134 protein,	complete cds; and L-type calcium channel a>	Homo sapiens interleukin 2 receptor, beta (IL2RB) mRNA	Human germline gene 16.1 for Ig lambda L-chain C region (IgL-C16.1)	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA	Homo sapiens offactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds	Homo sapiens potassium voltago-gated channel. Shab-related subfamily member 1 (KCNB1) mRNA	Human ferritin heavy chain mRNA, complete cds	Homo saplens mRNA for KIAA0549 protein, partial cds	Homo sapiens mRNA for KIAA0549 protein, partial cds	ye32f03.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:S29539 S29539 BASIC PROTEIN, 23K - ;
Top Hit Database Source	EST_HUMAN		NT		F	TN						LN				TN			LN		L	NT		INT	TN		NT		LN	LN	L	EST_HUMAN (
Top Hit Acession No.	0.0E+00 AI149880.1	0.0E+00 AF281074.1	0.0E+00 AF281074.1	4506118 NT	0.0E+00 AB004884.1	7662273 NT	5729755 NT	5729755	0.0E+00 AL163246.2		4506882 NT	0.0E+00 AF195953.1	5579469 NT	5579469 NT	0.0E+00 AL359403.1	0.0E+00 AF017433.1			0.0E+00 AF196779.1	4504664 NT					0.0E+00 AF149773.1	7662139 NT	0.0E+00 AF042075.1	4826783 NT	L20941.1		0.0E+00 AB011121.1	
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00,	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00(0.0E+00 M74099.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00			0.05+00	0.0E+00	0.0E+00 X03529.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 /	0.0E+00	0.0E+00	0.0E+00 ≠	0.0E+00	0.0E+00 T94870.1
Expression Signal	1.13	0.84	0.84	76.0	2.15	1.33	1.59	1.59	0.89	1.04	0.82	4.85	7.86	7.86	5.08	2.02			1.74	0.99	2.79	1.85	1.89	2.85	3.97	4.21	1.64	3.45	19.64	1.79	1.79	9.41
ORF SEQ ID NO:		22677	22678	22679	22680	22689	22690	22691		22714	22721		22730	22731		22735				22739	22760		22767	. 22786	22787	22791	22792	22824	22832	22836	22837	22845
Exon SEQ ID NO:	12870	12879			12881		12892				12929	12934	12937	12937	12939	12942		_		12947	12966	12970	12974	12995	12996	13001	13002		13036	13040	13040	13048
Probe SEQ ID NO:	2943	2952	2952	2953	2954	2964	2962	2965	2990	2992	3001	3006	3009	3009	3011	3014			3017	3019	3038	3043	3047	3068	3069	3074	3075	3102	3111	3115	3115	3123

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Table 4
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חושים ביים ביים ביים ביים ביים ביים ביים ב	Top Hit Descriptor	601878507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5	wu12h10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516803 3'	H.saplens mRNA for gamma-glutarnyltransferase	H.sapiens mRNA for gamma-glutarnyltransferase	Homo sapiens neurexin III (NRXN3) mRNA	Homo sapiens neurexin III (NRXN3) mRNA	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC2545), nuclear gene encoding mitochondrial protein, mRNA	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CRE9BP) mRNA	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA	ae87b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'	Homo sapiens angiostatin binding protein 1 mRNA, complete cds	Homo sapiens angiostatin binding protein 1 mRNA, complete cds	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA	Homo sapiens titin (TTN) mRNA	Human connexin 43 processed pseudogene	Homo saplens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-	Injuryayaya (CTTZID), complement component C4 (C4D) CTT, nearbase (CMZY), TVD, complement navior D ((8f), and complement component C2 (C2) genes,>	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA	tr58f08.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2222535 3' similar to SW:RL11_RAT P25121 60S RIBOSOMAL PROTEIN L11.;contains Alu repetitive element;	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6	Homo sapiens hormonally upregulated neu tumor-associated kinasc (HUNK), mRNA	Homo sepiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
אור בייטון ווסף	Top Hit Database Source	EST_HUMAN	EST HUMAN	NT	NT	NT	NT	IN	NT	NT	LN	LN.	NT	N	EST_HUMAN	LN⊤	LN L	NT	NT	NT		۲N	۲	LN T	NT	NT	LN1	EST_HUMAN	F	NT	NT	INT
	Top Hit Acession No.	3F243336.1	0.0E+00 Al968086.1	K98922.1		4758827 NT	4758827 NT	. 4504658 NT	4507720 NT	4507720 NT	M28699.1	4502098 NT	4758055 NT	4758055 NT	0.0E+00 AA774783.1	AF286598.1	0.0E+00 AF286598.1	4557590 NT	4507720 NT	M65189.1		AF019413.1	AF055084.1	4502014 NT	4502014 NT	AF265208.1	8923624 NT	0.0E+00 AI589294.1	0.0E+00 AF128893.1	0.0E+00 AF128893.1	7657213 NT	7657213 NT
	Most Similar (Top) Hit BLAST E Value	0.0E+00 BF243336	0.0E+00	0.0E+00 X98922.1	0.0E+00 X98922.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M28699.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF28659	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M65189.		0.0E+00 AF01941	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF26520	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	1.1	1.03	3.99	3.99	1.5	1.5	7.73	3.26	3.26	2.44	2.23	0.82	0.82	26.3	4.53	4.53	1.56	3.35	4.39		1.19	4.15	3.46	3.46	2	0.89	4.86	2.98	2.98	-	1
	ORF SEQ ID NO:	22862	22863	22870	22871	22883	22884	22892	22893	22894	22910	22912					22929	22935				22949		22959	22960		22974	23003				23014
	Exon SEQ ID NO:	13063	13065	13070	13070	13081	13081	13088	13089	13089	13105	13108	13113	13113	13115	13123	13123	13134	13139	13148		13149	13151	15066	15066		13176	13203		L	13212	13212
	Probe SEQ ID NO:	3138	3140	3145	3145	3156	3156	3163	3164	3164	3180	3183	3188	3188	3190	3198	3198	3210	3215	3224		3225	3227	3237	3237	3252	3253	3282	3289	3289	3290	3290

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Table 4
Single Exon Probes Expressed in Heart

Top Hit Descriptor	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA	lomo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA	Homo sapiens pyrln (MEFV) gene, complete cds	Homo sapiens mRNA for KIAA1507 protein, partial cds	601464995F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3858246 5	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM2000735 5'	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA	Homo sapiens T-typc calcium channel alpha1 subunit Alpha11-a isoform (CACNA11) mRNA, complete cds	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	Homo sapiens KIAA0852 protein (KIAA0952), mRNA	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA	Homo saplens leukocyte immunoglobulin-ilke receptor, subfamily A (with TM domain), member 2 (LILRA2),	пRNA	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds	Homo sapiens death receptor 6 (DR6), mRNA	Homo sapiens mRNA for rapa-2 (rapa gene)	Homo sapiens mRNA for rapa-2 (rapa gene)	Bacteriophage P1 replication region including repA, parA, and parB genes and incA, incB, and incC incompatibility determinants	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA	wp14d10.x1 NOL_CGAP_Lu19 Homo sepiens cDNA clone IMAGE:2464819 3' similar to TR 073634 C73634 NEURAL CELL ADHESION MOLECULE.	1014d10 x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:073634 C73634	NEURAL CELL ADHESION MOLECULE;	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA	Human endogenous retrovirus HERV-K10	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds	Homo sapiens hypothetical protein (AF038169), mRNA	Homo sapiens hypothetical protein (AF038169), mRNA
Top Hit Database Source					EST_HUMAN	T_HUMAN				Z.									LN	L L		EST HUMAN	Γ	EST_HUMAN					LN LN		
Top Hit Acession No.	4502582 NT	4502582	0.0E+00 AF111163.1 NT	0.0E+00 AB040940.1	0.0E+00 BE779039.1		7363436 NT	7363436 NT	7706239 NT	0.0E+00 AF211189.1	7662401 NT	7662401 NT	4502398 NT		5803067 NT	AF110763.1	7657038 NT	AJ277276.1	0.0E+00 AJ277276.1		7427522	0.CE+00 A(935159.1			0.0E+00 AJ278120.1	6552332	6552332 NT	M14123.1		9558718 NT	9558718 NT
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 K02380.1	0.0E+00	0.0E+00	-	0.0E+00 /	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M14123.1	0.0E+00 U43293.1	0.0E+00	0.0E+00
Expression Signal	1.01	1.01	11.07	96.0	0.99	3.01	1.66	1.66	1.43	0.99	1.35	1.35	96.0		1.71	6.04	2.08	1.53	1.53	5.53	1.21	3.68		3.68	2.67	2.86	2.86	1.14	6.18	1.01	1.01
ORF SEQ ID NO:	23015	23016	23019	23021	23026	23073	23076	23077	23079	23080	23094	23095	23096		23098	22455	23111	23115	23116	23118	23120	23126		23127	23132	23141	23142	23148	23153		23158
Exan SEQ ID NO:	13214	13214	13218	13220	13224	13270	13276	13276	13279	13280	13295	13295	13296		13299	12565	13312	13315	13315	13317	13319	13326		13326	13330	13337	13337	13343	13348	13353	13353
Probe SEQ ID NO:	3292	3292	3296	3298	3303	3350	3357	3357	3360	3361	3377	3377	3378		3381	3390	3395	3398	3398	3400	3402	3409		3409	3413	3420	3420	3426	3431	3436	3436

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Single Exon Probes Expressed in Heart	Тор Hit Descriptor	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds	Homo sapiens chromosome 21 unknown mRNA	ab51f12.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'	ab51112.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'	ab51f12.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'	mo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45) mRNA	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA	te35g12.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:000498 000498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN;	Human endogenous retroviral DNA (4-1), complete retroviral segment	Homo sapiens semenogelin II (SEMG2) mRNA	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds	Novel human gene mapping to chomosome X	Homo sapiens mRNA for KIAA1476 protein, partial cds	ox77c11xt Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1662356 3' similar to WP:T19B4.4 CF13742	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA	QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds	602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE.4248596 5'	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE;2979024 3'	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'	Homo saplens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA	Homo saplens midline 1 (Opitz/BBB syndrome) (MID1) mRNA	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
le Exon Probe	Top Hit Database Source	NT.	NT	H	EST_HUMAN (a		EST_HUMAN a		T_HUMAN	EST_HUMAN 6		EST HUMAN C	Г		T LN	NT	H H	O NAMIN TSE		EST_HUMAN C	TN	EST_HUMAN 6		EST_HUMAN h	T HUMAN							TN T
Sing	Top Hit Acession No.	0.0E+00 AF045452.1				0.0E+00 AA626677.1		4508028 NT	0.0E+00 BE304791.1	0.0E+00 BE304791.1	4826795 NT	0.0E+00 Al384007.1	M10976.1	4506884 NT	0.0E+00 AF078868.1	0.0E+00 AL133204.1	0.0E+00 AB040909.1	0 0E+00 A1081907 1	25463	0.0E+00 AW852217.1	0.0E+00 AF118846.1	0.0E+00 BF676393.1	26967	0.0E+00 AW664693.1	0.0E+00 AW664693.1	4826763 NT	7662319 NT	4557752 NT	4557752 NT	D87327.1	389491	0.0E+00 AB026542.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00/	0.0E+00	0.0E+00 /	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	$\overline{}$	0.0E+00	0.0E+00
	Expression Signal	2.06	2.06	1.23	0.94	0.94	0.94	1.11	2.23	2.23	1.43	0.92	96.0	0.82	1.3	1.39	96.0	80 0	1.26	4.53	0.95	7.43	1.1	0.98	0.98	1.13	0.98	0.79	0.79	1.51	28.67	4.26
	ORF SEQ ID NO:	23163	23164	23172	23175	23176	23177	23180	23182	23183	23185	23191	23194	23217		23225	23226		23242			23250		23269	23270	23274	23277	23282	23283	23297		23316
	Exan SEQ ID NO:	13357	13357		13371	13371	13371	13374		13377	13379	13386	13389	13412	13414	13422	13423	13443	13445	13449	13456	13457		13480	13480	13483	13485					13530
	Probe SEQ ID NO:	3440	3440	3448	3455	3455	3455	3458	3461	3461	3463	3470	3473	3495	3497	3505	3507	3597	3529	3533	3540	3541	3564	3566	3566	3569	3571	3578	3578	3596	3600	3616

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds	Homo saplens SH2-containing protein Nsp2 mRNA, complete cds	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09	Homo sapiens chromosome 21 segment HS210004	Homo saplens chromosome 21 segment HS21C004	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA	Homo sapiens mRNA for KIAA0796 protein, partial cds	UI-H-BW0-ajs-e-12-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'	UI-H-BW0-ajs-e-12-0-UI.s1 NCI_CGAP_Sub6 Homo saplens cDNA clone IMAGE:2733022 3'	Human gene for Type XIX collagen a1 chain, exon 6	aa06g01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4. [1] ;	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA	Homo sapiens mRNA for KIAA1414 protein, partial cds	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo sapiens ribosomal protein S2 (RPS2) mRNA	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA	Homo sapiens soluble neuropilin-1 mRNA, complete cds	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds	Pan troglodytes olfactory receptor (PTR208) gene, partial cds	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds	Mus musculus junctophilin 1 (Jp1-pending), mRNA	te62f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
le Exon Probe	Top Hit Database Source	LN	LN	EST HUMAN	EST_HUMAN	IN	NT				EST_HUMAN (EST HUMAN								TN	NT					EST HUMAN	TN			
Sing	Top Hit Acession No.	1	1	Ψ.	Ψ.	0.0E+00 AL163204.2	0.0E+00 AL163204.2	5729928 NT			0.0E+00 AW 298134.1	1	0.0E+00 AA463659.1	357468	0.0E+00 AB037835.1	7662183 NT	4506718 NT	7657065 NT	7657065 NT	0.0E+00 AF145712.1	1	0.0E+00 AF179733.1	7657468 NT	7657468 NT	0.0E+00 AF020091.1	10181139 NT	0.0E+00 Al377699.1	0.0E+00 AF152496.1	4758199 NT	S78685.1	7710148 NT
	Most Similar (Top) Hit BLAST E Value	0.0E+00 AF124250	0.0E+00 AF124250.	0.0E+00 AA852743	0.0E+00 AA852743	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AB004630	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00
	Expression Signal	3.26	3.26	1.5	75.	2.2	2.2	1.79	1.25	3.53	3.53	66.0	1.03	3.35	0.91	3.88	7.88	1.02	1.02	1.13	1.01	2.3	1.69	1.69	1.45	1:1	1:1	1.7	4.46	11.67	2
	ORF SEQ ID NO:	23318	23319	23323	23324	23326	23327	23331	23333	23344	23345	23369	23370		23387	23397	23399	23401		23441		23442	23446	23447	23448	23453	23455		23456		
	Exon SEQ ID NO:	13533	13533	13537	13537	13540	13540	13544	13546	13559	13559	13582	13583	13591	13600	13613	13615	13618	13618	13659	13660	13661	13664	13664	13665	13669	13671	13672	13673	13676	13677
	Probe SEQ ID NO:	3619	3619	3623	3623	3626	3626	3630	3632	3645	3645	3668	3669	3677	3687	3699	3701	3705	3705	3746	3747	3748	3751	3751	3752	3756	3758	3759	3760	3763	3764

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										-,-									21	*1444	ر	1.4	9.	. de . e.		4			-14.	41 -11-	all 4	N
	Top Hit Descriptor	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo sapiens myosin light chain kinase Isoform 2 (MLCK) mRNA, complete cds	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds	Homo sapiens 5-hydroxydryptamine (serotonin) receptor 1D (HTR1D) mRNA	Homo sapiens chromosome 21 segment HS21C079	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA	Human zinc finger protein ZNF134 mRNA, complete cds	Homo sapiens potassium voltage-gated charnel. Shab-related subfamily member 1 (KCNIR1) mBNA	Homo sapiens familial mental retardation prolein 2 (FMR2) gene axon 11	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA	Homo sapiens amphiphysin gene, partial cds	wk01f01.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:O43340 O43340 R28830 2, contains element PTR7 repetitive element	Homo sabiens ribosomal protein S8 (RPS8), mRNA	DKFZp434N0413_r1 434 (synonym: htes3) Homo sapiens cl7NA clone DKF7p434Nn413 5'	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA	Homo sapiens AP1 gamma subunit binding protein 1 (AP1 GBP1), mRNA	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds	Homo sapiens ryanodine receptor 3 (RYR3) mRNA	Homo sapiens zinc finger protein (KIAA0412) mRNA	RC3-HT0860-170800-011-e12 HT0860 Homo sapiens cDNA	cDNA clone Incyte 1996726 similar to MXRA5	sion library Homo sapiens cDNA clone Incyte 1996726 similar to MXRAS		Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds	601236966F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'	601153727F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509743 5'	PM3-LT0031-100100-003-h09 LT0331 Homo sapiens cDNA
9.0	Top Hit Database Source	LZ LZ	Z	LN	LN	N	F	LN LN	LN LN	NT	LN	LNT	LN	NT	EST HUMAN	LN	EST HUMAN	LN	LN	LN	NT	LN	NT	NT	EST_HUMAN	EST_HUMAN		EST_HUMAN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	7662183 NT	0.0E+00 AF069601.2	0.0E+00 AF069601.2	4504534 NT	4L16327	6912735 NT	4503178 NT	4503178 NT	J09412.1	4826783 NT	AF012615.1	4759171 NT	AF099117.1	0.0E+00 AI864727.1	4506742 NT	+	E005887 NT	E005887 NT	4504138 NT	4505078 NT	0.0E+00 AF149412.1	4506758 NT	4585642 NT	0.0E+00 BF355295.1	\W888221.1		W888221.1	1	1	1	0.0E+00 AW580740.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U09412.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF099117	0.0E+00	0.0E+00	0.0E+00 AL040338	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 /	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AW888221		0.0E+00 AW888221	0.0E+00 AF129533.	0.0E+00 BE378602	0.0E+00 BE313146,	0.0E+00
	Expression Signal	2.39	1.31	1.31	1.97	1.61	1.12	2.67	29.67	3.93	1.63	0.99	1.87	0.82	2.54	6.08	1.41	1	-	2.45	1.8	0.87	1.27	1.62	1.75	1.4		4.1	1.78	3.2	1.27	0.97
	ORF SEQ ID NO:	23460	23462	23463	23464	23467	23470	23478	23479	23482	23483	23486	23487	23489	23498	23502	23508	23515	23516	23518		23521	23534	23537	23544	23546		23547	23552	23557	23558	23563
	Exon SEQ ID NO:	13678	13681	13681	13682	13685	13687	13692	13692	13694	13696	13699	13700	13702	13711	13714	13719	13725	13725	13727	13728	13732	13742	13745	13751	13753		13753	13759	13764	13765	13771
	Probe SEQ ID NO:	3765	3768	3768	3769	3773	3775	3780	3780	3782	3784	3787	3788	3790	3799	3802	3807	3813	3813	3815	3816	3820	3830	3833	3840	3842		3842	3848	3853	3854	3860

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Table 4
Single Exon Probes Expressed in Heart

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Single Exon Plopes Expressed in Heart	Top Hit Descriptor	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2	Homo sapiens chromosome 21 segment HS21C103	Novel human gene mapping to chomosome 20	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens chromosome 21 segment HS21C068	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Human zinc finger protein ZNF133	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (IRNA48 gene)	Homo sapiens mRNA for rapa-2 (гара депе)	Homo sapiens mRNA for rapa-2 (rapa gene)	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA	Homo sapiens phosphoribosylglyclnamide formyltransferase, phosphoribosylglycinamide synthetase,	phosphoribosylaminoimidazole synthetase (GART) mRNA	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA	Homo sapiens mRNA for KIAA0287 gene, partial cds	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds	Homo saplens protein kinase, X-linked (PRKX) mRNA	Homo sapiens protein kinase, X-linked (PRKX) mRNA	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA	Home sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	wu04d04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE.251597537	w104d04.x1 NCI_CGAP_GC6 Homo sepiens cDNA clone IMAGE:25159753'
Jie Exon Pro	Top Hit Database Source	TN	NT	FZ	NT	NT	LΝ	IN	LN	LN	NT	NT	N-	NT	NT	N	TN		μ	L	NT	TN	TN	NT	LN	⊢N	TN	LV	FZ	FZ	۲ ₂	LZ.	片	I⊢'I	EST_HUMAN
	Top Hit Acession No.	VF116195.1	5.1	A23910.1	3.2	1.1	1.2	0.0E+00 AL163268.2	4503470 NT	7662183		5.1	7.1	3.1	5.1	5032026 NT	5032026 NT		4503914 NT	4885306	AB006625.1	4758807 NT	11419297 NT	.1	7.1	5.1	4826947 NT	. 4826947 NT	5901905 NT	4503854 NT	4503854 NT	8922391 NT	8922391 NT	.1	
	Most Similar (Top) Hit BLAST E Value	0.0E+00 AF11619	0.0E+00	0.0E+00 M23910.	0.0E+00 AL16330;	0.0E+00	0.0E+00 AL16328	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U09366.1	0.0E+00 AB01561	0.0E+00 AJ23861	0.0E+00 AJ27727	0.0E+00 AJ27727	0.0E+00	0.0E+00		0.0E+00		_	0.0E+00	0.0E+00	0.0E+00 AL096857	0.0E+00 AF16552	0.0E+00 AF15747	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AI982597	0.0E+00 AI982597
	Expression Signal	4.6	4.6	3.93	5.44	1.53	2.89	1.46	25.75	1.18	2.05	6.24	3.79	3.28	3.28	5.63	5.63		0.81	4.89	1.94	1.28	6.1	1.58	2.7	0.85	0.8	0.8	66.0	1.16	1.16	1.05	1.05	4.59	4.59
	ORF SEQ ID NO:		23588				23605	23613		23623	23624	23645		23658	23659	23663	23664		23677	23682	23683	23684	23685	23686	23695	23697	20872	20873	23707	23708	23709	23711	23712	23722	23723
	Exon SEQ ID NO:	13803	13803	13813	13815	13822	13825	13833	13844	13847	13848	13867	13875	13883	13883	13888	13888		13900	13906	13907	13909	13910	13911	13919	15071	11031	11031	13931	13932	13932	13935	13935	13944	13944
	Probe SEQ ID NO:	3893	3893	3903	3905	3912	3916	3924	3935	3939	3940	3960	3968	3976	3976	3981	3981		3993	4000	4001	4003	4004	4005	4013	4017	4022	4022	4028	4029	4029	4032	4032	4041	4041

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Online LAbiesseu in near	Most Similar Top Hit Acession (Top) Hit Acession Signal BLASTE No. Signal Value Top Hit Descriptor Signal Value Top Hit Acession (Top) Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descri	1 EST HUMAN	23726 0.88 0.0E+00 BE184856.1 EST_HUMAN MR1-HT0707-100500-001-a02 HT0707 Home sapiens cDNA		Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamytransferase) (TGM3) mRNA mRNA	23734 1.98 0.0E+00 5729725 NT Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA	T_HUMAN	23748 1.52 0.0E+00 AW408788.1 EST_HUMAN UI-HF-BM0-adx-c-02-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5	1.33 0.0E+00 8922466 NT	23752 1.33 0.0E+00 8922466 NT Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA	Zu08h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197.3' similar to contains Alu	1.02 0.0E TOO AA TO 14.00.1	23776 7.82 0.0E+00 AA401438.1 EST_HUMAN repetitive element; contains element; contains element; contains element; contains element; contains element;	23791 3.79 0.0E+00 4507720 NT Homo sapiens titin (TTN) mRNA	23/92 3.79 0.0E+00 450/720 NT Homo sapiens titin (TTN) mRNA		8.21 0.0E+00	8.21 0.0E+00 4758199 NT	0.88 0.0E+00[AL163303.2 NT	23837 1.13 0.0E+00 AJ003145.1 NT Homo sapiens mRNA for olfactory receptor protein, pseudogene	7.84 0.0E+00 J02610.1 NT	0.95 0.0E+00{AW9366	0.88	0.0E+00 4826827 NT	5.73 0.0E+00 AF174590.1 NT	1.92 0.0E+00 A1189844.1 EST HUMAN similar to contains MER20.b2 MER20 repetitive element:			0.87 0.0E+00 6563384 NT
				1.9			6.1				1.9															3	9.1	4.0		
	ORF SEQ ID ID NO:			950			998				83																105	108		
	B Exon D SEQ ID NO:	4044 13946	4044 13946	4048 13950	4055 13957	4056 13958	34 13966	39 13971	71 13973	71 13973	31 13983	43008		98 13998	13 14013	13 14013	26 14026	30 14030	30 14030	37 14037	33 14063	76 14076	30 14090		36 14096	14098	14105	10 14108		30 14128
	Probe SEQ ID NO:	8	8	9	40	40	4064	4069	4071	4071	4081	5	\$	4098	4113	4113	4126	4130	4130	4137	4163	4176	4190	4196	4196	4198	4206	4210	4224	4230

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Table 4
Single Exon Probes Expressed in Heart

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onigie Exori Plobes Expressed in near	Top Hit Descriptor	Homo sapiens protein kinase C, nu (PRKCN), mRNA	Human G2 protein mRNA, partial cds	Human G2 protein mRNA, partial cds	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds	Human Ig light chain VL1 region germline (humIv1c2c) gene, partial cds	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products,	partial cds	H.sapiens H2B/h gene	H.sapiens H28/h gene	H.sapiens H4/d gene for H4 histone	H.sapiens H4/d gene for H4 histone	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA	Homo sapiens mRNA for KIAA1360 protein, partial cds	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10	Homo saplens ACTN2 gene fcr alphe-Actinin 2, exon 10	Homo sapiens HPS1 gene, intron 5	xx68e08.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW:AHNK_HUMAN C098666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete	sds.	Homo sapiens chromosome 21 segment HS21C007	PM1-HT0305-101199-002-d03 HT0305 Homo sapiens cDNA	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds	H.sapiens pancreatic polypeptide receptor PP1 gene	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
le Exon Pror	Top Hit Database Source	NT	NT	NT	TN	LN	NT		NT	NT	LN	NT	NT	Z	LN LN	NT	IN	NT	NT	LN	NT	LN	EST HUMAN	LZ		Nī	N⊤	EST_HUMAN	NT	N	LN	NT	NT	N
3116	Top Hit Acession No.	6563384 NT			6912281 NT	7.2	03901.1							7662091 NT	7662091 NT	4885126 NT	1.1	7019456 NT		0.0E+00 AJ249765.1	0.0E+00 AJ249765.1	.F200629.1	0.0E+00 AW084964.1	8051619 NT		0.0E+00 AF016050.1		0.0E+00 AW381570.1		0.0E+00 AJ278120.1	4758467 NT	F108830.1	66526.1	78684.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 U10991.1	0.0E+00 U10991.1	0.0E+00	0.0E+00 AF15304	0.0E+00 U03901.1		0.0E+00 L14561.1	0.0E+00 Z80780.1	0.0E+00 Z80780.1	0.0E+00 X60483.1	0.0E+00 X60483.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AB03778	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF20062	0.0E+00 A	0.0E+00		0.0E+00	0.0E+00 A	0.0E+00	0.0E+00 AJ278120	0.0E+00	0.0E+00	0.0E+00\AF10883	0.0E+00 Z66526.1	0.0E+00
	Expression	0.87	1.17	1.17	10.2	1.15	1.59		5.17	2.78	2.78	1.58	1.58	8.95	8.95	10.81	86.0	1.1	5.85	8.1	8.1	1.92	40.23	1.91		1.38	7.5	1.29	1.83	1.83	3.91	2.3	1.47	1.12
	ORF SEQ ID NO:	23905	23911	23912	23917		23943		23950	23955	23956	23962	23963	23969	23970	23982	23984	24012		24025	24026	_	24080			24083		24087	24094	24095	24097	24098		24111
	Exan SEQ ID NO:	14128	14135	14135	14144	14162	14167		14173	14177	14177	14183	14183	14187	14187	14197	14200	14230	14238	14243	14243	14264	14296	15073		14299	14302	14304	14310	14310	14312	14313	14318	14324
	Probe SEQ ID NO:	4230	4237	4237	4245	4263	4268		4274	4278	4278	4284	4284	4289	4289	4299	4302	4333	4341	4346	4346	4368	4401	4403		4405	4408	4410	4416	4416	4418	4419	4424	4429

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Table 4
Single Exon Probes Expressed in Heart

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Single Explicased III near	Top Hit Descriptor	Homo sapiens pyrin (MEFV) gene, complete cds	Homo sapiens pyrin (MERV) gene, complete cds	Homo sapiens zinc finger protein 195 (ZNF195), mRNA	Homo sapiens syncytin precursor, mRNA, complete cds	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds	Homo sapiens zinc finger protein 211 (ZNF211), mRNA	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens PTEN (PTEN) gene, exons 3 through 5	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility	complex)	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)	Homo sapiens DNA for amyloid precursor protein complete cds	zp18008.s1 Stratagene fetal retina 937202 Homo sanjans cDNA clone IMAGE 600864.3*	Homo sapiens odz (odd Ozlten-m, Drosophila) homolog 1 (ODZ1), mRNA	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds	Homo sapiens chromosome 21 segment HS21C100	Homo sapiens gene for natriuretic protein, partial cds	Homo saplens keratin 18 (KRT18) mRNA	Homo sapiens keratin 18 (KRT18) mRNA	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene. exon 2 and complete eds	Mus musculus E-cadherin binding protein E7 mRNA, complete cds	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
JIE LAUII FIUL	Top Hit Database Source	N	닐	LN.	TN	NT	NT	NT	NT	N	NT	N	N	N		NT	FN	LN	EST HUMAN	1	LZ	NT	NT	NT	NT	NT	NŢ	Ä	L	N	NT	N
	Top Hit Acession No.	0.0E+00 AF111163.1	0.0E+00 AF111163.1	TN 8265009	0.0E+00 AF208161.1	0.0E+00 AF152337.1	5454175 NT	4503470 NT	4503098 NT	4502556 NT	L35485.1	7662091 NT	7662091 NT	0.0E+00 AF143314.1		17245418.1	0.0E+00 A.1245418 1	087675.1	0.0E+00 AA174072.1	7657410 NT	NL163284.2	0.0E+00 AF184110.1	0.0E+00 AL163300.2	AB037521.1	4557887 NT	4557887 NT	\F153819.1	NF153819.1	0.0E+00 AF167441.1	4507720 NT	4507720 NT	18890.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00 AJ245418.	0.05	0.0E+00 D87675.1	0.0E+00/	0.0E+00	0.0E+00 AL163284.	0.0E+00	0.0E+00	0.0E+00 AB037521	0.0E+00	0.0E+00	0.0E+00 AF153819.	0.0E+00 AF153819.	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Y18890.1
	Expression Signal	1.95	1.95	3.08	5.37	1.92	1.36	15.15	1.47	1.58	2.78	9.78	9.78	2.04		8.67	8 67	0.84	1.5	1.55	1.22	1.71	4.37	1.89	1.91	1.91	1.3	1.3	1.18	7.43	7.43	21.96
	ORF SEQ ID NO:	24112	24113	24123		24135	24139	24147	24156	24161		24163	24164			24179	24180					24205	24206		24216	24217	24218	24219	24220	23791	23792	24238
	Exon SEQ ID NO:	14325	14325	15074	14338	14343			14367	14371	14375	14377	14377	14392		14394	14394		14416		14421	14422	14423	14424	14434	14434	14435	14435	14436	14013	14013	14452
	Probe SEQ ID NO:	4430	4430	4439	4444	4449	4452	4462	4473	4477	4481	4483	4483	4498		4500	4500	4511	4523	4526	4528	4529	4530	4531	4541	4541	4542	4542	4543	4554	4554	4560

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Single Exon Probes Expressed in Heart

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Snigle Exori Propes Expressed in Hear	Top Hit Descriptor	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA	Homo sapiens fruncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint	uoibal	Homo sapiens mRNA for KIAA1399 protein, partial cds	Homo sapiens mRNA for KIAA1399 protein, partial cds	Human displacement protein (CCAAT) mRNA	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE :68310 5	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE 68310 5	601158935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505521 6'	601285246F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607067 5	Human AHNAK nucleoprotein mRNA, 5' end	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA	Human CYP2D7AP pseudogene for cytochrome P450 2D6	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA	Homo sapiens bromodomain adjacent to zinc finger domain, 28 (BAZ28), mRNA	Homo sapiens alpha-3 type IX collegen (COL9A3) gene, promoter region, and excus 1-26	Homo sapiens proteinx0008 (AD013), mRNA	Homo sapiens proteinx0008 (AD013), mRNA	UI-H-Bi3-ajw-c-04-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds	Homo saplens HSPC024-iso mRNA, complete cds	Human connexin 43 processed pseudogana	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	genes, complete cds	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
Jie Exon Proj	Top Hit Database Source	EST_HUMAN		LN L	NT	INT	LN-	Z	LZ	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	LN L	NT	N	LN LN	NT.	LN	LN LN	N	NT.	LN		EST_HUMAN	NT	NT	NT	ļ	LN	N	LN	NT		5
	Top Hit Acession No.	BE081527.1		.1		0.0E+00 AB037820.1		6453812 NT	6453812 NT)	0.0E+00 AF184110.1	7662181 NT		7304922 NT	7304922 N	.F026801.1	7019320 NT	019320	7.1	+	1			1.1		1	_	4503766 NT	4885048 NT
	Most Similar (Top) Hit BLAST E Value	0.0E+00		0.0E+00	0.0E+00 AB037820	0.0E+00	0.0E+00 M74099.1	0.0E+00	0.0E+00	0.0E+00 T56945.1	0.0E+00 T56945.1	0.0E+00	0.0E+00	0.0E+00 M80902.1	0.0E+00 M69197.1	0.0E+00 M69197.1	0.0E+00	0.0E+00	0.0E+00 X58467.1	0.0E+00	0.0E+00	0.0E+00 AF026801	0.0E+00	0.05+00	0.0E+00 AW44463	0.0E+00 A	0.0E+00 AF083242.	0.0E+00 M65189.1	i i	0.0E+00 AF240785	0.0E+00 X87205.1	0.0E+00 AF084479	0.0E+00 AF097416.	0.0E+00	0.0E+00
	Expression Signal	2:32		2.01	2.65	2.65	2.55	1.82	1.82	1.03	1.03	0.99	1.11	37.36	3.14	3.14	1.12	1.34	1.54	0.95	0.95	1.09	0.92	0.92	1.78	1.11	1.8	2.04	(2.83	2.79	1.3	1.47	3.51	61.82
	ORF SEQ ID NO:	24246			24257	24258	24259	24262	24263	19929	19930		24267	24290	24293	24294	24297	24298		24319	24320	24327	24330	24331	24355	24363			· · _		24408	24410	24411	24412	24414
	Exon SEQ ID NO:	14458		14465	14470	14470	14471	14474	14474	10108	10108	14475	14481	14502	14505	14505	14508	14509	14524	14532	14532	14538	14541	14541	14562	14567	14572	14583	0	14620	7794-1	14624	14625	14626	14528
	Probe SEQ ID NO:	4566		4574	4580	4580	4581	4585	4585	4586	4586	4587	4593	4614	4617	4617	4620	4621	4636	4644	4644	4652	4655	4655	4676	4681	4686	4697	100	4/35	4/3/	4/39	4740	4/41	4/43

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Table 4
Single Exon Probes Expressed in Heart

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olligie Exori Probes Expressed in near	Top Hit Descriptor	ZING FINGER PROTEIN 132	Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), mRNA	Homo sapiens chromosome 21 segment HS21C003	Homo sepiens hypothetical protein FLJ20073 (FLJ20073), mRNA	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tor-alpha) gene, J1-	J61 segments; and Tcr-C-alpha gene, exons 1-4	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tor-alpha) gene, J1- J61 segments; and Tor-C-alpha gene, exons 1-4	H.sapiens MeCP-2 gene	H.sapiens MeCP-2 gene	Human collagenase type IV (CLG4) gene, exon 2	Homo sapiens chromosome 21 segment HS21C080	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kJ (TAF2I) mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	H.sapiens MICA gene	Homo saplens zinc finger protein (KIAA0412) mRNA	Homo sapiens mRNA for KIAA0633 protein, partial cds	Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA	Homo sapiens meningioma expressed antigen 6 (colled-coll proline-rich) (MGEA6), mRNA	Hano sapiens desmoplakin (DPI, DPII) (DSP) mRNA	Homo saplens gene encoding filensin, exon 8	Homo sapiens zinc-finger DNA-binding protein (HUMHOXY1), mRNA	Homo sapiens mRNA for immunog obulin kappa light chain, anti-RhD, therad 7	Homo sapiens MHC class 1 region	Homo saplens opioid receptor, delta 1 (OPRD1) mRNA	Homo saplens splice variant AKAP350 mRNA, partial cds	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo saplens partial TTN gene for titin	Homo sapiens titin (TTN) mRNA	Homo sapiens COL4A6 gene for a6(IV) collagen, exon 44 and partial cds
Jie Exori Pro	Top Hit Database Source	SWISSPROT	Z	NT	NT	L		NT	L L	L	NT	NT	N	٦N	LN TN	L	TN	NT	LNT	N⊤	N⊤	LN⊤	LN-	NT	TN	LN	NT	LN	NT	NT	N-	N.
Sillo	Top Hit Acession No.	P52740	8922180 NT	AL163203.2	8923080 NT	7661979 NT		1	-	_		1	0.0E+00 AL163280.2	5032150 NT	6806918 NT		4585642 NT	AB014533.1 NT	6677648	5174560 NT	4758199	τ-	7705546			4505508 NT	AF091711.1	4507720 NT	4507720 NT	AJ277892.1	4507720	1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00		0.0E+00	0.0E+00		0.0E+00 M94081	0.0E+00 M94081	0.0E+00 X94628.	0.0E+00 X94628.	0.0E+00 M55582.	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X92841.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Y16723.	0.0∈+00	0.0E+00 AJ01044;	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.DE+00	0.0E+00 D63562
-	Expression Signal	1.4	76.0	8.0	7.78	0.95		1.66	1.66	1.69	1.69	1.08	3.22	0.99	0.82	1.44	1.97	1.18	2.26	1.05	8.64	1.2	1.61	1.33	24.91	2.43	2.46	5.48	5.48	0.86	12.01	0.95
-	ORF SEQ ID NO:	24415	24417	24419	24424	24428		24429	24430	24432	24433	24436	24437	24447	24458	24460	24463	24464	24466	24467	24469	24471	24472		24477		24480	23791	23792	24484	24490	24493
	Exon SEQ ID NO:	14629	14631	14633	14637	14641		14642	14642	14644	14644	14647	14648	14660	14671	14673	14678	14677	14679	14680	14682	14684	14685	14686	14690	14692	14693	14013	14013	14697	14706	14709
	Probe SEQ ID NO:	4744	4746	4748	4752	4756		4757	4757	4759	4759	4762	4763	4776	4786	4788	4791	4792	4794	4795	4797	4799	4800	4801	4806	4808	4809	4812	4812	4814	4824	4827

Page 392 of 413 Table 4 Single Exon Probes Expressed in Heart

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| Top Hit Descriptor | Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallytranstransferase, geranytransferase) (FDPS) mRNA | Homo sapiens sialytransferase 8 (alpha-N-acetylneuraminate: alpha-2,8-sialytransferase, GD3 synthase)
(SIAT8) mRNA | Human mRNA for transcription factor AREB6, complete cds | Human mRNA for transcription factor AREB6, complete cds | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) | Homo sapiens chromosome 21 segment HS21C084 | UI-H-BI3-alv-f-02-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3038691 3' | Homo sapiens hypothetical protein FLJ11190 (FLJ11190), mRNA | Homo sapiens titin (TTN) mRNA | Homo sapiens titin (TTN) gene, alternative splice products, partial cds | Homo sapiens titin (TTN) gene, alternative splice products, partial cds | Homo sapiens titin (TTN) mRNA | Human ribosomal protein L21 mRNA, complete cds | 601303729F1 NIH_MGC_21 Homo capiens cDNA clone IMAGE:3638118 5'

 | Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA | Homo sapiens mRNA for KIAA1043 protein, partial cds

 | Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
 | Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA | Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI> | Homo sapiens chromosome Xq28 metanoma antigen family A2a (MAGEA2A), metanoma antigen family A12 (MAGEA12), metanoma antigen family A2b (MAGEA2B), metanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogonase like protein (NSDHL), and L1> | Homo sapiens titin (TTN) mRNA
 | Homo sapiens titin (TTN) mRNA | Homo sapiens titin (TTN) mRNA | Homo sapiens titin (TTN) mRNA | Homo sapiens E2F transcription factor 2 (E2F2) mRNA | Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 3 | Homo sapiens chromosome 21 segment HS21C009 |
| Top Hit
Database
Source | L | LN LN | ۲ <u>۷</u> | LN | Ł | LZ. | EST_HUMAN | LΝ | NT | NT | Z | LY. | Z | EST_HUMAN

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LN | LN. |
| Top Hit Acession
No. | 4503684 | 4506952 | | | | .2 | | 8922926 | 4507720 | | | 4507720 | | 3.1

 | 4758199 | 5.1

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 | 8923441 | | |
 | 4507720 | 4507720 | 4507720 | 4758225 | | 0.0E+00 AL163209.2 |
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(Top) Hit
BLAST E
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 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00/ | 0.0E+00 |
| Expression
Signal | 1.52 | 1.06 | 1.31 | 1.31 | 0.86 | 1.34 | 1.45 | 1.2 | 7.99 | 2.81 | 2.81 | 2.95 | 4.34 | 2.58

 | 5.37 | 66.0

 | 1.66
 | 1.66 | 1.06 | 1.06 | 5.81
 | 5.81 | 3.51 | 7.76 | 1.17 | 1.35 | 1.33 |
| ORF SEQ
ID NO: | 24496 | 24105 | 24508 | 24509 | 24515 | 24530 | 24536 | 24542 | 24490 | 24544 | 24545 | 24552 | |

 | 24569 | 24574

 | 24584
 | 24585 | 24596 | 24597 | 23791
 | 23792 | 24602 | 24603 | | 24619 | |
| Exon
SEQ ID
NO: | 14713 | 14319 | 14726 | 14726 | 14734 | 14751 | 14759 | 14766 | 14708 | 14768 | 14768 | 14774 | 14777 | 14789

 | 14794 | 14804

 | 14817
 | 14817 | 14830 | 14830 | 14013
 | 14013 | 14834 | 14835 | 14843 | 14853 | 14862 |
| Probe
SEQ ID
NO: | 4831 | 4837 | 4845 | 4845 | 4854 | 4871 | 4879 | 4885 | 4886 | 4888 | 4888 | 4894 | 4897 | 4910

 | 4915 | 4925

 | 68617
 | 4939 | 4953 | 4953 | 4957
 | 4957 | 4959 | 4960 | 4968 | 4978 | 4987 |
| | Exan ORF SEQ Expression (Top) Hit Acession Signal No: Signal Value Source | Exan ORF SEQ Expression (Top) Hit Acession Database No. Signal Value 14713 24496 1.52 0.0E+00 4503684 NT | Exan
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Single Exon Probes Expressed in Heart

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Single Extended Expressed in Hear	Top Hit Descriptor	Homo sapiens gammna-cytoplasmic actin (ACTGP3) pseudogene	Homo sapiens partial TTN gene for titin	Homo saplens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo saplens titin (TTN) mRNA	Bacillus amyloliquefaciens sacB gene for levansucrase (EC 2.4.1.10)	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds	Homo sapiens vascular endothellal cadherin 2 mRNA, complete cds	Homo sapiens cyclophilin (USA-CYP) mRNA	Homo sapiens G-protein coupled receptor (RE2), mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (1 TN) mRNA	Homo saplens titin (TTN) mRNA	Homo sapiens PR domain containing 1, with ZNF domain (PRDM1) mRNA	Human cellular fibronectin mRNA	Human cellular fibronectin mRNA	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphale transporter (NPT3) name, complete add	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Human offactory receptor-like gene, complete cds	Human olfactory receptor-like gene, complete cds	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds	Homo sapiens glypican 3 (GPC3) mRNA	Escherichia coli K-12 MG1655 section 217 of 400 of the complete genome	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
le Exoli Pio	Top Hit Database Source	NT	LN	LZ	L	N	N	N	LN ⊢N	N	Ę	L'A	۲N	LZ	N-		Z-	N	NT	N	5	<u></u>	۲ <u>۷</u>	TN	LN	トフ	ラ	NT	ト	NT	ا حا	トフ	トフ
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	Most Similar (Top) Hit BLAST E Value	0.0E+00 D50657.1	0.0E+00 AJZ77892	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X52988.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M10905.1	0.0E+00 M10905.1	0.0E+00\U91328.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AE00032	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	37.78	2.29	3.02	4.23	2.89	2.89	2.43	1.84	1.84	1.01	1.22	11.22	11.22	14.9	14.9	1.33	1.03	1.03	1.06	3.04	6.27	6.27	1.34	1.34	9:38	9.38	0.94	1.35	0.8	1.06	0.96	1.59
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	Exan SEQ ID NO:	14865	14875	14876	14878	14013	14013	14892	14909	14909	14912	14926	14013	14013	14013	14013	14935	14940	14940	14941	14950	14013	14013	14967	14967	14013	14013	14992	14993	14997	15007	15026	15028
	Probe SEQ ID NO:	4990	2000	5001	5003	5005	5005	5018	5037	5037	5040	5054	5055	5055	5056	5056	5065	5070	5070	5071	2080	5096	5096	5098	5098	5099	5099	5124	5126	5130	5140	5159	5162

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Single Exon Probes Expressed in Heart

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Onigio Exono Explication in reality	Top Hit Descriptor	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds	Homo sapiens placental growth hormone isoform hGH-V3 (hGH-V) mRNA, complete cds	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens chromosome 21 segment HS21C085	Homo sapiens titin (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA	Homo sapiens aconitase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15	Homo sapiens keratin 12 (KRT12) gene, complete cds	Homo sapiens keratin 12 (KRT12) gene, complete cds	Homo sapiens protocadherin alpha 13 (PCDHA13), mRNA	RC3-GN0076-310800-013-b03 GN0076 Homo saplens cDNA	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds	H.saplens Immunoglobulin heavy chain gene, variable region	H.sapiens immunoglobulin heavy chain gene, variable region	7f10c06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294250 3'	ht99a02.X1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3165194 3' similar to SW:Y054_HUMAN_	P42094 HTPUINE HOAL PROTEIN NIAAUU34.	OU (2004ZZF) NIT MOU, / HOMO Septens CUINA CIONE IMAGE: 3943804 5	601589422F1 NIH_MGC_7 Homo saprens cDNA clone IMAGE:3943804 5	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7	oh68a09.y5 NCI_CGAP_Kid5 Homo sapiens cDNA clone (MAGE:1472152 5' similar to gb:M185121G HEAVY CHAIN PRECLIFSOR VLI REGION (HLIMAN)	Homo sabiens Sp4 transcription factor (SP4), mRNA	602118928F1 NIH MGC 56 Homo seniens CDNA clone IMAGE 4275254 5	601061489F1 NIH MGC 10 Homo sapiens cDNA clone IMAGE:3447839 5	601105891F1 NIH MGC 15 Homo sapiens cDNA clone IMAGE:2988310 5	602071372F1 NCI CGAP Brn64 Homo saplens cDNA clone IMAGE:4214272 67	602071372F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE: 4214272 5	Homo sapiens Bloom syndrome (BLM) mRNA
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<u></u>	Top Hit Acession No.	0.0E+00 AF245703.1	0.0E+00 AF245703.1	0.0E+00 AF006061.1	4507720 NT	4507720 NT	4507720 NT	AL163285.2	4507720 NT	4507720 NT	4502398 NT	0.0E+00 AF093093.1	0.0E+00 AF137286.1	0.0E+00 AF137286.1	9256579 NT	0.0E+00 BE931080.1	AF182034.1	0.0E+00 AF182034.1	X56163.1	X56163.1	0.0E+00 BE675498.1		0.0E+00 BE220/53.1	0.0E+00(BE/94412.1	0.0E+00 BE794412.1	M29908.1	0 0E+00 A1701363 1	11421038 NT	O OF + OO BERESSARS 1	0.0E+00 BE538857.1	0.0E+00 BE292784.1	0.0E+00 BF526328.1	BF526328.1	4557364 NT
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	Expression Signal	1.12	1.12	1.72	10.43	10.43	6.75	1.38	3.97	3.97	96.0	15.66	2.25	2.25	2.99	3.82	3.12	3.12	1.92	1.92	5.8		1.//	1.67	1.67	5.46	ά,	5 42	2 94	1 92	1.31	1.8	1.8	1.71
	ORF SEQ ID NO:	24797	24798	24814	23791	23792	24816		24822	24823			24830	24831	24917	24926	24930	24931	24940	24941	25032			25034	25035	25037	25038			25052		_	25081	26122
	Exan SEQ ID NO:	15031	15031	15050	14013	14013	15052	15056	15058	15058	15059	15086	15137	15137	15150	15158	15162	15162	15168	15168	15228			15230	15230	15232	15237	19442	15244	15247	15253	15257	15257	15987
	Probe SEQ ID NO:	5165	5165	5186	5187	5187	5189	5193	5195	5195	5196	5208	5214	5214	5226	5234	5238	5238	5245	2745	5307		2308	6055	5303	5311	5313	5319	5324	5327	5333	5337	5337	5348

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Table 4
Single Exon Probes Expressed in Heart

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onigie Lyon I robes Lypiessed III realt	Top Hit Descriptor	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	Human gene for dlhydrollpoamide succinyltransferase, complete cds (exon 1-15)	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), niRNA	602042322F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179988 5'	602042322F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179988 5'	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA	IMR0-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'	601105291F1 NIH_MGC_15 Homo saplens cDNA clone IMAGE:2987903 5'	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds	Homo sapiens Surf-5 and Surf-6 genes	Homo sapiens Surf-5 and Surf-6 genes	EST02238 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCM48	UI-HF-BL0-adh-d-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5'	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA	Human beta-prime-adaptin (BAM22) gene, exon 13	4p95b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);	Homo sapiens KVLQT1 gene	Ното sapiens KVLQT1 gene	HA2981 Human fetal liver cDNA library Homo sapiens cDNA	Homo sapiens protocadherin beta 2 (PCDHB2), mRNA	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'	Mus musculus aczonin (Acz), mRNA	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, excn 13B and isoform beta-1B, complete cds
gie Lauit iu	Top Hit Database Source	L	LN	NT	NT	. 1	EST HUMAN	EST_HUMAN	9.1 EST HUMAN	LN	EST_HUMAN	EST HUMAN	EST_HUMAN	LN	NT	LN	LN	LN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	LN⊤	EST_HUMAN	FN	۲N	6.1 EST_HUMAN	NT	EST_HUMAN	LNT.	Ŋ
בֿ <u>ס</u>	Top Hit Acession No.	AF257737.1	0.0E+00 AF257737.1	D26535.1	D26535.1	11420819 NT	0.0E+00 BF529931.1	0.0E+00 BF529931.1	0.0E+00 BF313139.1	11434392	AW867316.1	0.0E+00 BE292889.1	0.0E+00 BE292889.1 ES	11420818	11420B19 NT	AF064254.1	0.0E+00 AF064254.1	AJ224639.1	AJ224639.1	M85719.1	AW 405472.1	AW361877.1	AW361877.1	0.0E+00 AW361877.1	U36261.1	0.0E+00 AA195905.1	AJ006345.1	AJ006345.1	0.0E+00 AI207616.1	1141680	0.0E+00 BE560082.1	10048478 NT	U86961.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00 AF25773	0.0E+00	0.0E+00 D26535.	0.0E+00 D26535.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AW8673	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AJ22463	0.0E+00 AJ22463	0.0E+00 M85719.	0.0E+00 AW 4054	0.0E+00 AW3618	0.0E+00 AW3618	0.0E+00	0.0E+00 U36261.	0.0E+00	0.0E+00 AJ00634	0.0E+00 AJ00634	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00 U86961.1
	Expression Signal	5.24	5.24	1.45	1.45	1.67	3.26	3.26	2.35	4.21	2.43	3.05	3.05	1.31	1.31	5:35	5:35	2.9	2.9	69'9	3.67	5.74	5.74	5.74	1.88	3.26	1.5	1.5	2	3.98	6.76	1.58	3.03
	ORF SEQ ID NO:	25101	25102	25114	25115	25141	25158	25159		25362		25405	25406	25420	25421		25430	25435	25436	25453	25459	25471	25472	25473	25475	25515	25516	25517	25524		25542		25544
	Exan SEQ ID NO:	15272	15272	15282	15282	15294	15305	15305	15308	15315	15341	15351	15351	15365	15365	15372	15372	15376	15376	15390	15394	15408	15408	15408	15410	15448	15449	15449	15454	15464	15471	15472	15473
	Probe SEQ ID NO:	5352	5352	5362	5362	5374	5386	5386	5389	5396	5420	5431	5431	5444	5444	5451	5451	5455	5455	5470	5474	5489	5489	5489	5491	5531	5532	5532	5537	5548	5555	5556	5557

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Only e Lyon Clobes Lybressed in real	Top Hit Descriptor	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds	602036272F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184321 5'	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'	Homo saplens cadherin 20 (CDH20) mRNA, complete cds	RC5-ET0027-210600-022-G10 ET0027 Homo sapiens cDNA	601645287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930453 5'	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14	601158515F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3505323 5'	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'	Homo saplens KIAA0735 gene product, synaptic vesicle protein 2B homolog (KIAA0735), mRNA	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA	Homo saplens potassium voltage gated channel, Shal-related subfamily, member 2 (KCND2), mRNA	zł 40h01.r1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;	2r40h01.r1 Soares, NhHMPu, S1 Homo sapiens cDNA clone IMAGE 665905 5' similar to SW:YY05 HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5.	Human T cell surface glycoprotein CD-6 mRNA, complete cds	Human T cell surface glycoprolein CD-6 mRNA, complete cds	AU137772 PLACE1 Homo sapiens cDNA clone PLACE1007201 5'	Human G protein-coupled receptor GPR-9-6 gene, complete cds	zq81d03.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN.	Homo sapiens xylosyltransferase II (XT2), mRNA	Homo sapiens xylosyltransferase II (XT2), mRNA	601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5	Human anion exchanger (AE1) gene, exons 1-20	Homo sapiens peptide transporter 3 (LOC51296), mRNA
אוב בצמון בוחר	Top Hit Database Source	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LNT	EST_HUMAN	EST HUMAN	1N	LN	LN⊤	EST_HUMAN	EST HUMAN	LN	LN	EST_HUMAN	LN⊤	EST HUMAN	L	N	EST_HUMAN	LN	N
Sillo Sillo	Top Hit Acession No.	J86961.1	0.0E+00 BF338835.1	0.0E+00 BE273983.1	0.0E+00 BF569905.1	0.0E+00 AF217289.1			0.0E+00 BF031742.1	3F031742.1	.1	1	8.1	0.0E+00 BE280197.1	3E889610.1	11433071 NT	11433071 NT	9789986 NT	0.0E+00 AA193506.1	0.0E+00 AA193506.1	J34625.1	J34625.1	2.1		0.0E+00 AA204740.1	11545913 NT	11545913 NT	3E257173.1	.35930.1	11435630 NT
	Most Similar (Top) Hit BLAST E Value	0.0E+00 U86961.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 W33069	0.0E+00 W33069	0.0E+00 AF01261	0.0E+00	0.0E+00 BE88961	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U34625.	0.0E+00 U34625.1	0.0E+00	0.0E+00 U45982.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE25717	0.0E+00 L35930.1	0.0E+00
	Expression Signal	3.03	2.1	2.93	1.74	2.47	1.89	1.41	1.66	1.66	1.54	1.54	2.16	3.57	2.74	1.63	1.63	10.66	1.29	1.29	13.03	13.03	1.41	3.4	4.14	3.57	3.57	2.8	1.47	1.38
	ORF SEQ ID NO:	25545	25553	25555	25566	25588		25593	25613	25614	25633	25634		25636	25642	25654	25655	25668	25671	25672	25690		25742	25756	25770	25771	25772			25811
	Exen SEQ ID NO:	15473	15480	15482	15489	15510	15511	15515	15530	15530	15545	15545	15546	15548	15551	15561	15561	19450	15574	15574	15589	15589	15638	15649	15663	15664	15664		15690	15701
	Probe SEQ ID NO:	2999	5564	5566	5574	5596	2629	5601	5615	5615	5631	5631	5632	5634	5638	5649	5649	5660	5663	5663	5680	2680	5730	5741	5729	5756	5756	5775	5784	5795

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Table 4
Single Exon Probes Expressed in Heart

Oligie Lyoll Fores Lybressed III real	Top Hit Acession Databasco Top Hit Descriptor Source	0.0E+00 AV650020.1 EST_HUMAN AV650020 GLC Homo sapiens cDNA clone GLCCAD09 3'	0.0E+00 AW575598.1 EST_HUMAN UI-HF-BL0-acc-g-12-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone iMAGE:30567513	0.0E+00 H01255.1 EST_HUMAN y/27b03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149933 5'	N	HUMAN	0.0E+00 BE735989.1 EST_HUMAN 601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5	0.0E+00 AU119245.1 [EST_HUMAN AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5/	0.0E+00 AU119245.1 EST_HUMAN AU119245 HEMBA1 Homo sepiens cDNA clone HEMBA1005360 5		0.0E+00 BE293153.1 EST_HUMAN 601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE;2987963 5/	0.0E+00 BE293153.1 EST_HUMAN 601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5'	HUMAN	0.0E+00 AW406348.1 EST_HUMAN UI-HF-BLO-acc-h-02-0-UI.11 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'	0.0E+00 AV719444.1 EST_HUMAN AV719444 GLC Homo sapiens cDNA clone GLCEHC06 5'	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT.1a (CACNA1G)	0.0E+00 AF190860.1 NT mRNA, complete cds	0.0E+00 AW 163640.1 EST_HUMAN TR:015390 015390 GT24. [3] TR:043840 TR:043206;	EST_HUMAN	0.0E+00 BE799873.1 EST_HUMAN 601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5	0.0E+00 BE889813.1	0.0E+00 BE889813.1 EST_HUMAN 601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'	0.0E+00 L24493.1 NT Human antigen CD27 gene, exons 1-2	0.0E+00 AL163204.2 NT Homo sapiens chromosome 21 segment HS21C004	0.0E+00 AL163204.2 NT Homo sapiens chromosome 21 segment HS21C004	6 6005983 NT Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA	TEST HOMAN	Z	EST_HUMAN	5.1 EST_HUMAN	HUMAN	
Olligie LAC							EST			.1	3.1	3.1 EST	EST	EST			.1		_					.2	.2	FN 5865009	1		EST	EST	9.1 EST	
	Most Similar (Top) Hit BLAST E Value	0.0E+00 A1	0.0E+00 AV	0.0E+00 HC	0.0E+00 X15377.1	0.0E+00 BE	0.0E+00 BE	0.0E+00 At	0.0E+00 At			0.0E+00 BE	0.0E+00 AV	0.0E+00 AV	0.0E+00 A\		0.0E+00 AF	0.0E+00 A1			0.0E+00 BE	0.0E+00 BI	0.0E+00 に			00+30.0				0.0E+00 B	0.0E+00	
	Expression Signal	8.1	2.81	4.21	1.89	4.25	4.25	11.57	11.57	1.56	4.81	4.81	1.36	1.36	1.69		2.24	3.45		4.79	7.23	7.23	3.71	2.15	2.15	3.54	4.13	1.79	3.58	1.48	1.44	
	ORF SEQ ID NO:		25848		25857	25862	25863	25869	25870	_		25883	25931	25932	25951		25958	25964		25978	25981	25982	25988	25991	25992	25999						
ı	Exon SEQ ID NO:	15732	15736	15738	15744	15749	<u> </u>	15753	15753	15760	15765	15765	15807	15807	15826		15835	15841	 _	15856	15860	15860	15866	15869	15869	15875						
i	Probe SEQ ID NO:	5826	5830	5832	5838	5843	5843	5847	5847	5854	5859	5859	5901	5901	5921		2930	5936	5936	5951	5955	5955	5961	5964	5964	5970	56/5	5974	5980	5991	6011	

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Table 4
Single Exon Probes Expressed in Heart

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Single Exoll Flobes Explessed III leaf	Top Hit Descriptor	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA	zp88e03.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627292 5'	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA	Homo sapiens CD6 antigen (CD6), mRNA	601339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3882267 5'	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'	601443867F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95.;	7b49f03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN OOR 379 GOL GIN-95.	CM1-HT0877-060900-397-g11 HT0877 Homo sapiens cDNA	23403.rl Soares NhHMPu S1 Homo sabiens cDNA clone IMAGE 655332 5	Homo saplens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)	(CTNND2), mRNA	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'	Human MYCL2 gene, complete cds	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA	601148954F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501829 5/	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	Homo sapiens NALP1 mRNA, complete cds	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 51	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds	EST366876 MAGE resequences, MAGC Homo sapiens cDNA	601113958F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354566 5'
JIE LAUII FIU	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	H HAAN	EST HUMAN	EST HUMAN		NT	EST HUMAN	NT	NT	LN	NT	EST_HUMAN	NT	NT	NT	NT	TN	EST_HUMAN	IN	EST HUMAN	ΤΝ	EST HUMAN	EST_HUMAN
CIIC	Тср Hit Acession No.	3F085667.1	0.0E+00 AA190755.1	41940621.1	A1940621.1	11435626 NT	3E566381.1	0.0E+00 BE867889.1	0.0E+00 BE867889.1	0.0E+00 BE550162.1	1 1 1 1 1 1 1 1				11034810 NT	0.0E+00 BF569905.1	103069.1	0.0E+00 AF217289.1	AF217289.1	11420775 NT	3E262941.1	237976.1	237976.1	AF257737.1	AF257737.1	AF310105.1	0.0E+00 BF569905.1	_01978.1	0.0E+00 BF306996.1	U41302.1	0.0E+00 AW954805.1	BE254103.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00 BF085667	0.05+00	0.0E+00 AI940621	0.0E+00 AI940621	0.0E+00	0.0E+00 BE566381	0.0E+00	0.0E+00	0.0E+00	0 0E+00 BE55016	0.0	00+H00		0.0E+00	0.0E+00	0.0E+00 J03069.1	0.0E+00,	0.0E+00 AF217289	0.0E+00	0.0E+00 BE26294	0.0E+00 Z37976.1	0.0E+00 Z37976.1	0.0E+00 AF25773	0.0E+00 AF25773	0.0E+00 AF31010	0.0E+00	0.0E+00 L01978.1	0.0E+00	0.0E+00 U41302.1	0.0E+00	0.0E+00
	Expression Signal	1.81	3.15	80.9	6.08	3.07	1.98	13.15	13.15	2.07	200	1,46	3.84		10.28	2.57	2:32	2.8	2.8	2.75	5.63	2.32	2.32	2.83	2.83	1.35	2.18	3.58	5.61	1.76	1.34	1.41
	ORF SEQ ID NO:	26077	26191	26201	26202	26208	24867	24872	24873	26130	26121	26150	26153			26118		26157	26158	24876	24842	24843	24844	24845	24846	24851	26213	26217	26224	26227	26241	26242
	Exon SEQ ID NO:	[16046	16054	16054	16059	15104	15109	15109	15995	1 5005	16012	16015		15973	15982	15990	16019	16019	15112	15125	15126	15126	15127	15127	15132	16064	16067	16075	16078	16091	16092
	Proba SEQ ID NO:	6042	6063	6071	6071	9209	6094	6609	6609	6101	6404	6118	6121		6126	6135	6142	6146	6146	6154	6168	6169	6169	6170	6170	6175	6178	6181	6130	6183	6225	6226

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| Top Hit Descriptor | AU133213 NT2RP4 Homo sepiens cDNA clone NT2RP4001556 5' | AU143706 Y79AA1 Homo sapiens cDNA clone Y79AA1002365 5' | 601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5' | 601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5 | Homo sapiens keratin 12 (KRT12) gene, complete cds | Homo sapiens keratin 12 (KRT12) gene, complete cds | Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA | Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA | qc67a07.x1 Soares_placenta_BtoSweeks_ZNbHPBto9W Homo sapiens cDNA clone IMAGE:17146443' similar to SW:ARSD_HUMAN P51689 ARYLSULFATASE D PRECURSOR; contains clement HGR repetitive element; | qc67a07 x1 Soares_placenta_8to9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:1714644 3' | similar to SW:AKSU_HUMAN P51689 ARYLSULFATASE D PRECURSOR ;contains element HGR
repetitive element : | Homo sapiens mycsin, heavy polypeptide 8. skeletal muscle, perinatal (MYH8) mRNA | Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8) mRNA | 602035089F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE 4182839 5
 | zn60f09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:G806562 G806562 NEBULIN. | Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds | Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds | H.sapiens DNA for ZNGP2 pseudogene, exon 4 | Human P2x1 receptor mRNA, complete cds
 | Human P2x1 receptor mRNA, complete cds
 | EST368573 MAGE resequences, MAGD Homo saplens cDNA | EST362586 MAGE resequences, MAGA Homo sapiens cDNA

 | xb39a05.y1 NCI_CGAP_Lu31 Homo sapiens cDNA clone IMAGE.2578640 5' similar to TR:Q08050 Q08050 HNF3/FH TRANSCRIPTION FACTOR GENESIS | AU117553 HEMBA1 Homo sapiens cDNA clone HEMBA1001661 5' | Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA | zn56f02.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE.562203 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN); | ะn17d05.x1 Normai Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC cn17d05 random
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| Top Hit
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 | | HUMAN | | HUMAN | EST_HUMAN
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| Top Hit Acession
No. | AU133213.1 | 4U143706.1 | 3E891286.1 | 3E891286.1 | 4F137286.1 | 4F137286.1 | 11436699 | 11436699 | AI128344.1 | | N128344.1 | 11426392 | 11426392 | 3F337375.1
 | AA128453.1 | 4F005213.1 | AF005213.1 | C70172.1 | J45448.1
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 | 1W 239326.1 | \U117553.1 | 11427135 | \A211663.1 | N752561.1
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| Most Similar
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 | |
| Expression
Signal | 6.9 | 2.44 | 1.31 | 1.31 | 1.97 | 1.97 | 3.63 | 3.63 | 25.51 | | 25.51 | 18.73 | 18.73 | 14.06
 | 5.1 | 6.72 | 6.72 | 7.55 | 11:09
 | 11.09
 | 1.43 | 2.54

 | 1.67 | 8: | 3.64 | 54.65 | 4.25
 | |
| ORF SEQ
ID NO: | 26253 | | | | 24830 | 24831 | 26305 | 26306 | 26323 | | 26324 | 26326 | 26327 |
 | 26329 | 26353 | 26354 | 26360 | 26362
 | 26363
 | 26372 | 26374

 | 26411 | | 26422 | 26434 | 26486
 | |
| Exon
SEQ ID
NO: | 16103 | 16119 | 16126 | 16126 | 15137 | 15137 | 16150 | 16150 | 16166 | | 16166 | 16168 | 16168 | 16170
 | 16172 | 16191 | 16191 | 16200 | 16202
 | 16202
 | 16210 | 16212

 | 16251 | 16261 | 16262 | 16272 | 16321
 | |
| Probe
SEQ ID
NO: | 6237 | 6253 | 6260 | 6260 | 6273 | 6273 | 6286 | 6286 | 6302 | | 6302 | 6304 | 6304 | 9069
 | 6308 | 6328 | 6328 | 6337 | 6339
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 | 6347 | 6349

 | 6386 | 6400 | 6401 | 6411 | 6462
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| | Exon ORF SEQ Expression (Top) Hit Top Hit Acession Signal BLASTE No. Source | Exon
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Database 16103 26253 5.9 0.0E+00 AU133213.1 EST_HUMAN 16119 26253 5.9 0.0E+00 AU133213.1 EST_HUMAN 16119 26280 1.31 0.0E+00 BE801286.1 EST_HUMAN 16120 26280 1.37 0.0E+00 AF137286.1 NT 16130 26306 3.63 0.0E+00 AF137286.1 NT 16150 26306 3.63 0.0E+00 AF137286.1 NT 16150 26306 3.63 0.0E+00 AF137286.1 NT 16150 26306 3.63 0.0E+00 AF137286.1 NT 16160 26324 25.51 0.0E+00 AF137286.1 NT 16161 26325 3.63 0.0E+00 AF137286.1 NT 16162 26323 3.63 0.0E+00 AF138344.1 EST_HUMAN 16163 26324 18.73 0.0E+00 AF128344.1 EST_HUMAN</td><td>Exon
NO:: ORF SEQ
Signal Expression
Signal (Top) Hit
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16103 ORF SEQ
26263 Expression
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161103 (Top) Hit
26262 Top Hit Accession
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No:
161103 Top Hit Accession
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161104 Top Hit Accession
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161105 Top Hit Accession
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161106 Top Hit Accession
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NO: ORF SEQ
ID NO: Expression
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Database Top Hit Acession
Source Top Hit Acession
Database 16103 26253 5.9 0.0E+00 AU133213.1 EST_HUMAN 16119 26253 5.9 0.0E+00 AU133213.1 EST_HUMAN 16119 26280 1.31 0.0E+00 BE801286.1 EST_HUMAN 16120 26280 1.37 0.0E+00 AF137286.1 NT 16130 26306 3.63 0.0E+00 AF137286.1 NT 16150 26306 3.63 0.0E+00 AF137286.1 NT 16150 26306 3.63 0.0E+00 AF137286.1 NT 16150 26306 3.63 0.0E+00 AF137286.1 NT 16160 26324 25.51 0.0E+00 AF137286.1 NT 16161 26325 3.63 0.0E+00 AF137286.1 NT 16162 26323 3.63 0.0E+00 AF138344.1 EST_HUMAN 16163 26324 18.73 0.0E+00 AF128344.1 EST_HUMAN</td> <td>Exon
NO:: ORF SEQ
Signal Expression
Signal (Top) Hit
BLASTE
Value Top Hit Acession
No: Top Hit
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16103 ORF SEQ
26263 Expression
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26262 Top Hit Accession
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Source Top Hit Acession
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Table 4
Single Exon Probes Expressed in Heart

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onigie Exori Flobes Expressed in Realt	Top Hit Descriptor	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC cn17d05 random	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete ods	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete ods	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA	601885465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5	AU129622 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5'	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'	601593156F1 NIH_MGC_9 Home sapiens cDNA clone IMAGE:3947365 5'	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'	601481713F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3884258 5	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'	zo01c06.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566410 5'	601305658F1 NIH MGC_39 Homo sapiens cDNA clone IMAGE:3639903 5'	Human amylold-beta protein (APP) gene, exon 11	Human amyloid-beta protein (APP) gene, exon 11	zf81b04.r1 Stratagene schizo brain S11 Homo saplens cDNA clone IMAGE:728719 5' similar to 1R:G300482	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT)	AU142402 Y79AA1 Homo sapiens cDNA clone Y79AA1000277 5'	602153008F1 NIH_MGC_81 Homo sepiens cDNA clone IMAGE:4294128 5	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5	601485254F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887773 5	UI-HF-BN0-akj-f-01-0-UI.r1 NIH_MGC_50 Homo saplens cDNA clone IMAGE: 3077496 5	au93b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to TR:060463 060463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOLYNDOL ACE 131	601578195F1 NIH MGC 9 Homo saplens cDNA clone IMAGE:3926998 5'	601578195F1 NIH_MGC_9 Hamo sapiens cDNA clone IMAGE:3926998 5'
gie Exori rion	Top Hit Database Source	EST_HUMAN	LZ TZ	NT	LN TN	LN	EST_HUMAN	EST_HUMAN	TN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	TN	L		EST_HUMAN		EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	T	EST_HUMAN
0	Top Hit Acession No.	AI752561.1	0.0E+00 AF064205.1	0.0E+00.AF064205.1	11417342 NT	6912735 NT	0.0E+00 BF217905.1	0.0E+00 AU129622.1	4501848 NT			0.0E+00 AU120424.1	0.0E+00 AU120424.1	0.0E+00 BE787610.1	0.0E+00 BE787610.1	AA149791.1	0.0E+00 BE736046.1	M34872.1	M34872.1		4A397551.1	0.0E+00 AU142402.1	0.0E+00 BF673096.1	4L120124.1	0.0E+00 AL120124.1	0.0E+00 BE877693.1	4W500549.1	0.0E+00 AW157233.1	3E745597.1	3E745597.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00 AI752561	0.0E+00	0.0E+00.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 /	0.0E+00	0.0E+00	0.0巨+00	0.0E+00 AA149791	0.0E+00	0.0E+00 M34872.1	0.0E+00 M34872.1		0.0E+00 AA397551	0.0E+00/	0.0E+00.0	0.0E+00 AL120124	0.0E+00	0.0E+00	0.0E+00 AW50054	0.0E+00	0.0E+00 BE745597	0.0E+00 BE745597
	Expression Signal	4.25	1.59	1.59	1.3	1.98	5.37	2.98	6.49	4.97	4.97	60.88	60.88	1.52	1.52	1.29	3.72	3.97	3.97	-	1.65	7.54	8.73	1.96	1.96	1.31	1.35	14.35	1.16	1.16
	ORF SEQ ID NO:	26487	26530	26531	26551	26569	26571	26576	26586					26614	26615	26690	26719	26729	26730		26749	26750		26783	26784		26810	26813	26842	26843
	Exan SEQ ID NO:	16321	16358	16358	16374	16389	16392	16397	16408	16413	16413	16414	16414	16432	16432	16502	16525	16534	16534		16554	16557	16568	16594	16594	16610	16621	16626	16654	16654
	Probe SEQ ID NO:	6462	6488	6488	6515	6530	6534	6539	6550	6555	6555	6556	6556	6574	6574	6622	6645	6654	6654		65/4	6677	6588	6714	6714	6730	6742	6747	6775	6775

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Table 4

Single Exon Probes Expressed in Heart

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Single Exon Probes Expressed in Heart	Top Hit Descriptor	Homo sapiens Xq pseudoautosomal region, segment 1/2	7d76a04.x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:3278862 3' similar to TR:O95793 O95793 STAUFEN PROTEIN.;	WI80b10.x1 NCI_CGAP_Em25 Homo saplens cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN P50281 MATRIX METALL OPROTEINASE-14 PRECURSOR:	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	#73a08.s1 Soares_tests_NHT Homo saplens cDNA clone IMAGE:727958 3' similar to gb:S85655 PROHIBITIN (HUMAN);	QV3-DT0045-221299-046-007 DT0045 Homo sapiens cDNA	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone (MAGE:3856179 5'	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens chromosome 21 segment HS21C009	601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA	H.sapiens mRNA for gamma-glutamytransferase	H. sapiens mRNA for gamma-glutamyltransferase	H.sapiens mRNA for gamma-glutamyltransferase	xc46e01.x1 NCI_CGAP_Utt Home sapiens cDNA clone IMAGE:2707032:3' similar to gb M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);	HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02	ري. دي	801236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5	2522604.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724062 5:	601900571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744 5'	UI-H-BI1-adr-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'	UI-H-BI1-adr-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3	601150051F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502836 5'	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542.5
gle Exon Pro	Top Hit Database Source	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	Z	LZ LZ	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LZ	니	EST_HUMAN	N	NT	Ľ	NT	NT	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Sin	Top Hit Acession No.	0.0E+00 AJ271735.1	0.0E+00 BE674157.1	A1885671.1	0.0E+00 BE563650.1	0.0E+00 BE563650.1	11427235 NT	11427235 NT	AA398511.1	0.0E+00 AW364874.1	0.0E+00 AW364874.1	0.0E+00 BE612586.1	0.0E+00 BE612586.1	0.0E+00 AL163209.2	0.0E+00 AL163209.2	0.0E+00 BE890797.1	4758695 NT	4758695 NT	X98922.1	X98922.1	X98922.1	0.0E+00 AW513513.1		D52650.1	0.0E+00 BE378495.1	0.0E+00 AA410545.1	0.0E+00 BF313946.1	0.0E+00 AW139673.1	0.0E+00 AW139673.1	0.0E+00 BE260272.1	0.0E+00 BF700165.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 AI88567	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AA39851	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X98922	0.0E+00 X98922.1	0.0E+00 X98922.	0.0E+00	i	0.0E+00 D52650.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	2.72	2.2	1.36	1.31	1.31	1.44	1.44	3.89	1.45	1.45	1.21	1.21	1.25	1.25	2.01	2.4	2.4	2.85	2.85	2.85	1.36	,	3.64	4.46	1.31	4.32	1.41	1.41	2.39	1.83
	ORF SEQ ID NO:	26852	26878	26879	26887	26888	26897	26898		26928	26929	26942	26943	26956	26957		26984	26985	27026	27027	27028		9	27083	27081	27083		27088	27089	27104	27106
	Exon SEQ ID NO:	16662	16689	16690	16696	16696	16703	16703	16730	16735	16735	16748	16748	16758	16758	16778	16791	16791	16833	16833	16833	16870		16872	16888	16892	16893	16898	16898	16915	16917
	Probe SEQ ID NO:	6783	6810	6811	6817	6817	6824	6824	6851	9589	9589	6989	6989	6839	6829	6899	6913	6913	6955	6955	6955	6993	1	6995	7011	7015	7016	7021	7021	7038	7040

Page 402 of 413 Table 4 Single Exon Probes Expressed in Heart

Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part Part			7	\neg	1 -			$\overline{}$	7		_	_	_	$\overline{}$	_	_	_		_			-	٠, -	-	1 41	الهست		- Barr	1		1	.41.19	11.1	#771 P
Exon ORF SEQ Expression Signal (Top) Hit Top Hit Access SEQ ID ID NO: Signal Most Similar Parameter No. 16917 27107 1.83 0.0E+00 BF700165.1 No. 16917 27108 1.83 0.0E+00 BF700165.1 No. 16917 27108 1.83 0.0E+00 BF700165.1 10947 16918 27142 3.54 0.0E+00 CA00 AND ADD ADD ADD ADD ADD ADD ADD ADD ADD	bes Expressed in Heart	Top Hit Descriptor	602127664F1 NIH MGC 36 Homo sapiens cDNA clone IMAGE-4284542 5	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284547 5	or80g02.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072.63S RIBOSOMAL PROTEIN L7A (HUMAN)	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1 mRNA	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1 mRNA	Homo sapiens ITGB4 gene for integrin beta 4 subunit. exons 3-41	AV718377 FHTB Homo sapiens cDNA clone FHTBAAF11 5'	xw/3c07.xt NCL CGAP_Par1 Homo sapiens cDNA clone IMAGE.2833644 3' similar to gb.X53587 INTEGRIN BETA-4 SUBUNIT PRECURSOR (HIMAN)	AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001575 5'	Homo sapiens mRNA for KIAA0454 protein pertial cds	hf48a09.x1 Soares NFL T GBC S1 Home sahiens CDNA clone IMAGE: 2035606.3	hf48a09.x1 Soares NFL T GBC S1 Home sahiens cDNA clans (MACE: 2025605.2)	DKFZp434C1814 s1 434 (synonym: htes3) Homo seniens cDNA clone DKFZp434C1814 s1	DKFZp434C1814_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814_3	Homo saplens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes,	partial cds	Homo sapiens mRNA for KIAA1512 protein, partial cds	Homo sapiens furnor protein p73 (TP73), mRNA	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region	Homo sapiens mRNA for KIAA0823 protein, partial cds	Homo sapiens mRNA for KIAA0823 protein, partial cds	AV660739 GLC Homo sapiens cDNA clone GLCGKG123'	Homo sapiens polycystin-L (PKDL), mRNA	601141119F1 NIH MGC 9 Homo sapiens cDNA clone IMAGE: 3140740 5.	601141119F1 NIH, MGC 9 Homo sapiens cDNA clone IMAGE:3140740 5	Human mRNA for GABA-A receptor, alpha 1 subunit	wq34a12.x1 NOI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473150 3' sImilar to SW:MGB3_HUMAN	015480 MELANOMA-ASSOCIATED ANTIGEN B3;	Homo sapiens protocadherin alpha 8 (PCDHA8), mRNA	EST370381 MAGE resequences, MAGE Homo sapiens cDNA	Human endogenous retrovirus, complete genome	Homo sapiens MAP-kinase activating death domain (MADD), mRNA
Exon No.: ORF SEQ Expression Signal (Top) Hit Top Hit Aces: SEQ ID NO. Most Similar Signal Most Similar Value No. 16917 27107 1.83 0.0E+00 BF700165.1 No. 16917 27107 1.83 0.0E+00 BF700165.1 16917 27108 1.83 0.0E+00 BF700165.1 16950 27142 3.54 0.0E+00 CA962527.1 16950 27143 3.54 0.0E+00 CA11377.7 16950 27143 3.54 0.0E+00 CA11377.7 16970 27171 1.25 0.0E+00 AV337277.1 16972 27218 2.64 0.0E+00 AV13377.7 17024 27278 3.64 0.0E+00 AV337277.1 17025 27218 2.64 0.0E+00 AV337277.1 17026 27218 2.64 0.0E+00 AV337277.1 17027 27218 2.64 0.0E+00 AV337277.1 17024 27278 3.84 0.0E+00 AV350233.1 17065 27242 2.84 0.0E+00 AV360233.1 17065 27242 2.	gle Exon Pro	Top Hit Database Source	EST HUMAN	EST_HUMAN	EST HUMAN	NT	NT	NT	EST_HUMAN	EST HUMAN	EST_HUMAN	TN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	, i	Z	N⊤	LN⊥	NT	ΝΤ	LN	 	N	EST HUMAN		TN		EST_HUMAN	NT	EST_HUMAN	LZ	L
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		ORF SEQ ID NO:		27108		27142				27169	27171	27218	27219	27220	27241	27242	27242	27217	27244	27261	27268	27272	27273	27277	27280	27298	27299	27313	00000	2/320	2/324	27333	2/340	27352
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		Probe SEQ ID NO:	7040	7040	7069	7073	7073	7088	7095	7099	7102	7147	7148	7148	7176	7176	7177	74.70	1/8	285	7204	/207	7207	7210	7213	7231	7231	7241	7050	1207	4627	7,263	607/	1.280

Page 403 of 413
Table 4
Single Exon Probes Expressed in Heart

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NIH MGC 71 Homo sapiens CDNA clone IMAGE -3041086 F1	601510247F1 NIH MGC 71 Homo sapiens CDNA clone IMAGE 2011086 E1	EST50505 Gall bladder I Homo sapiens cDNA 5' end	EST50505 Gall bladder I Homo sapiens cDNA 5' end	ba09f05.yt NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus Bc-x. mRNA complete refs (MOLSE)	602023150F1 NCI CGAP Brn67 Home services CDNA place NA CELLAFORCE EL	OV2-HT0608-25/2700-382-bos 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11 434 (swnotym: hises) Home caniens cDNA	ow60h01xt Soares_NSF_89W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to	Homo sanione hundholing Colloging	Homo sapiens himphofical C2H2 and financial C2H2 and financial C2H2 C2H2 C2H2 C2H2 C2H2 C2H2 C2H2 C2H	THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE 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cDNA clone IMAGE:3027548 F	Homo sapiens solute carrier family 21 (organic anion transporter) member 0 (SI C2140) mDNA	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
Exon NO: 17166 ORF SEQ 27365 Expression Signal (Top) Hit Value (Top) Hit Value Top Hit Aces No: Value 17166 27365 1.44 0.0E+00 BE94823.1 17174 27374 1.24 0.0E+00 BE883843.1 17174 27374 1.24 0.0E+00 BE883843.1 17174 27375 1.24 0.0E+00 BE883843.1 17784 27384 1.6 0.0E+00 BE883843.1 17727 27375 1.38 0.0E+00 BE207063.1 17282 27457 3.0 0.0E+00 BE207063.1 17282 27457 3.0 0.0E+00 BE712515.1 17282 27457 3.0 0.0E+00 BE7207063.1 17282 27551 2.71 0.0E+00 BE738013.1 17282 27553 1.27 0.0E+00 AL042278.1 16442 26629 2.06 0.0E+00 AL042278.1 16444 26632 2.06 0.0E+00 AL042278.1 1	gle Exon Pro	Top Hit Database Source	NT	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HIMAN	EST HUMAN	FOT HIMAN	I N	L	EST HIMAN	EST HIMAN	EST HUMAN	L L	1	1	1		П	T		HUMAN		
Exon ORF SEQ ID ID NO: Expression of ID NO: Mode NO: 17166 27365 1.44 17167 27366 2.56 17174 27374 1.24 17184 27383 1.6 17184 27384 1.6 1727 27426 1.38 1727 27427 1.38 1727 27427 1.38 1727 27479 1.181 1727 27479 1.27 17242 27551 2.71 17243 27629 2.06 16444 26632 8.86 16445 26633 8.86 16445 26634 1.69 17324 27529 1.37 17323 27529 1.37 17324 27531 7.21 17325 27541 2.85 17326 27563 3.98 17358 27563 3.98 17360 27564 <td< td=""><td>Sin</td><td>Top Hit Acession No.</td><td>AB011150.1</td><td></td><td></td><td></td><td>AA344601.1</td><td>AA344601.1</td><td>BE207063.1</td><td>BE207063.1</td><td>BF348013.1</td><td>BE7125151</td><td>AL042278.1</td><td></td><td>60151</td><td>11560151</td><td>A1290909.1</td><td></td><td>T</td><td>Γ</td><td></td><td></td><td></td><td>9.1</td><td></td><td></td><td></td><td>.1</td><td>11437282</td><td>11437282</td></td<>	Sin	Top Hit Acession No.	AB011150.1				AA344601.1	AA344601.1	BE207063.1	BE207063.1	BF348013.1	BE7125151	AL042278.1		60151	11560151	A1290909.1		T	Γ				9.1				.1	11437282	11437282
Exon ORF SEQ Expression NO: IO NO: Signal NO: 17166 27365 1.44 17167 27366 2.56 17174 27374 1.24 17184 27384 1.6 17184 27384 1.6 1727 27426 1.38 1724 27551 2.71 1725 27457 3 1727 27457 1.38 1727 27457 1.181 17292 27553 1.27 17244 26632 2.06 16444 26632 8.86 16444 26634 1.69 17324 27529 1.37 17323 27529 1.37 17324 27531 1.37 17325 27529 1.37 17326 27529 1.37 17325 27529 1.37 17326 27563 3.98 17		Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	00+H00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 (0.0E+00	0.0E+00 E	0.0E+00	0.0E+00
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		ORF SEQ ID NO:	27365	27366	27374	27375	27383	27384	27426	27427	27551	27457	27479	27503	26628	26629	26632	26633	26634	27464		27529	27530	27531	27541	27562	27563	27566	27574	27575
Probe NC: NC: 7290 7290 7308 7308 7308 7300 7425 7429 7431 74453 7463 7463 7463 7463 7463 7463 7463 746		Exon SEQ ID NO:		_:	_ [_	17184	17227	172271	17346	17252	17273	17292	16442	16442	16444	16444	16445	17259	17321	17323	17323	17324	17335	17358	17358	17360	17369	17369
		Probe SEQ ID NO:	7290	7291	7298	7298	7308	7308	7360	7360	7368	7383	7406	7425	7429	7429	7431	7431	7432	7450	7461	7463	7463	7464	7475	7488	7488	7490	7499	/499

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Table 4
Single Exon Probes Expressed in

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Single Exon Probes Expressed in Heart	Top Hit Descriptor		From Saptens soute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA	OU 10/34/2017 NIH MGC_21 Home sapiens cDNA clone IMAGE:3956238 5'	noning septems Keratin Ze (KK 2E) gene, complete cds	nomo sapiens keratin 2e (KRT2E) gene, complete cds	RCZ-B10642-130300-017-g01 BT0642 Homo sapiens cDNA	UI-HT-BNO-4Kg-b-12-0-UI:r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5	GTT - CNO-CANG-D-12-U-UTT NIH MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5	nomo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tronsingen gone families	UI-HT-BN0-akj-c-07-0-UI.r1 NIH MGC_50 Homo sapiens cDNA clone IMAGE:3077364 5	iviutippe scierosis associated retrovirus polyprotein (pol) mRNA, partial cds	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt. segment 5 of 5]	O DO MONTAGO IN TO THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF	RO13346n7E4 NIH MCC 36 11	3E:3688680 5'	VMZ-C-103 T1-30 T199-043-n11 C10311 Homo sapiens cDNA	AL143246 NT2NDD2 U.	R04505555524 NILL 1900 Sapiens CUIVA clone N12RP3004260 5	ANT-SOCKER AND MICH SAPIENS CONA Clone IMAGE 3949383 5	Homo saniens KIAAAAA East American Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Constant Cons	A[1132349 NT-2009 LD.	Homo saniene profosodkoji od k. 12 7000 NT2RP3004260 51	Homo saniens lettocath immin 12 (PCDH-alpha12) mRNA, complete cds	Homo sanians largesty immunoglobulin-like receptor-1 mRNA, complete cds	MR4-TN0114-11000 404 - 01 TN0116 Teceptor-1 mRNA, complete cds	601155227F1 NIH MGC 21 Homes in Paris Saplens cDNA	And 2501 xt NCI CGAP CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to chixons and the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the	HOWE CONTROLLE DEHYDROGENASE M CHAIN (HUMAN);	Promo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5
ngle Exon Pro	Top Hit Database Source	NIT	EST DIMAN	NIT	FIN	EST LIMAN	EST LIMAN	EST HIMAN	H.	<u> </u>		EST HUMAN		L	_ <u>\</u>	EST HIMAN	EST HIMAN	EST HIMAN	EST HIMAN	FST HIMAN	EST HIMAN	N	EST HUMAN	LN	NT	NT	EST HUMAN	Т		NAWA!	T_HUMAN
iš	Top Hit Acession No.	11437282 NIT	0.0E+00 BF900549 1	0.0E+00 AF019084 1	0.0E+00/AE019084 1	0.0E+00 RF082977 1	0.0E+00 AW500293 4	0.0E+00 AW500293.1	AE020308 4	0 0 E + 0 0 E + 0 0 E + 0 0 E + 0 E + 0 E + 0 E + E +	0.0E-00 At 029300.1	0.0E+00 AF009668 4		378466.1	378466.1	0.0E+00 BE563320.1	W363135 1	0.0E+00 AU132349.1	0.0E+00 AU132349.1			2067	0.0E+00 AU132349.1	9.1	1.1					0.0E+00 11427235 NT	3
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0F+00 AF0203(1	0.05+00	0.0E+00		0.0E+00 S78466.	0.0E+00 S78466.	0.0E+00	0.0E+00 AW3631	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 A	0.0E+00.A	0.0E+00 AF009220	0.0E+00 AF009220.1	0.0E+00 BF092898.1	0.0E+00 BE28079;	0.0E+00 A	0.0E+00	0.0E+00 AU143673.1
	Expression Signal	1.93	1.47	2.59	2.59	1.47	1.76	1.76	1.25	2,74	2.45	1.34		2.56	2.56	2.57	1.62	2.17	2.17	7.73	7.73	1.76	2.22	1.86	2.72	2.72	1.65	2.44	1.74	1.91	5.98
	ORF SEQ ID NO:	27576	27509	27591	27592	27812	27626	27627	27629	27630	27645	27673	10070	169/7	27692	27693	27701	27722	27723	27734	27735	27743	27756	27757	27776	27777	27784	27795	27800	27810	27826
	Exon SEQ ID NO:	17369		17381	17381	17399	17410	17410	17414	17414	17431	17458	17472	7/4/1	17472	17473	17481	17500	17500	17509	17509	17516	17532	17533	17551	17551	17558	17570	17578	17586	17603
	Probe SEQ ID NO:	7499	7514	7530	7530	7548	7559	7559	7563	7563	7580	7607	7621		7621	7622	/630	7650	7650	/659	7659	7666	/682	7683	//01	//01	90/	7720	7728	7736	7753

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Table 4
Single Exon Probes Expressed in Heart

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Olligie Lauri Fodes Lapressed III Fear	Top Hit Descriptor	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4	Homo sapiens HEF like Protein (HEFL), mRNA	Homo sapiens HEF like Protein (HEFL), mRNA	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene	Homo sapiens partial RANBP7 gene for RanBP7//mportin7 and partial ZNF143 gene	平97h11.r1 Stratagene muscle 937209 Homo sapions cDNA clone IMACE:628197 5'	z31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'	231f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5	Homo sapiens KIF4 (KIF4) mRNA, complete cds	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sapiens mRNA for actin binding protein ABP620, complete cds	Homo saplens mRNA for estrogen receptor beta, complete cds	Homo sapiens mRNA for estrogen receptor beta, complete cds	zq06h11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628965 5' similar to TR:G407097 G407097 165KD PROTEIN	602037045F1 NCI CGAP Brn64 Homo sapiens cDNA clone IMAGF 4184939 5'	602037045F1 NC CGAP Brn64 Homo sapiens cDNA clone IMAGE:4184939 5	FB23A4 Fetal brain, Stratagene Homo sapiens cDNA clone FB23A4 3'end	nab45e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'	AV654765 GLC Homo sapiens cDNA clone GLCDZC07 3'	xu74b01.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:M69066 MOESIN	(HUMAN);	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'	601467419F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870700 5'	RC2-BT0642-150200-012-d03 BT0642 Homo sapiens cDNA	RC2-BT0642-150200-012-d03 BT0642 Homo sapiens cDNA	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
gie Lauri i iu	Top Hit Database Source	EST HUMAN	LN	LN.	NT	EST_HUMAN	EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST HUMAN	EST_HUMAN	NT	NT	LN	LN	FST HIMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN
5	Top Hit Acession No.	AU143673.1	0.0E+00 AF072408.1	11421001 NT	11421001 NT	AU136637.1	4U136637.1	0.0E+00 AJ295844.1	0.0E+00 AJ295844.1	0.0E+00 AA196387.1	0.0E+00 AA131248.1	4A131248.1	0.0E+00 AF179308.1	3E730772.1	3E730772.1	11560151 NT	AB029290.1	AB006590.1	0.0E+00 AB006590.1	0.0F+00 AA194770.1	0.0E+00 BF340331.1	3F340331.1	T03078.1	0.0E+00 BF436218.1	0.0E+00 AV654765.1		0.0E+00 AW517950.1	0.0E+00 BE549213.1	0.0E+00 BE781742.1		3E082720.1		-	_
	Most Similar (Top) Hit BLAST E Value	0.0E+00 AU14367.	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AU136637	0.0E+00 AU13663	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AA131248	0.0E+00	0.0E+00 BE73077	0.0E+00 BE73077	0.0E+00	0.0E+00 AB029290	0.0E+00 AB006590	0.0E+00/	0.07	0.0E+00	0.0E+00 BF340331	0.0E+00 T03078.1	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE082720	0.0E+00	0.0E+00	0.0E+00 AV711075
	Expression Signal	5.98	7.52	2.48	2.48	2.96	2.96	2.13	2.13	4.01	1.17	1.17	1.46	3.45	3.45	1.24	1.64	5.19	5.19	3.27	5.43	5.43	1.37	2.35	2.05		3.55	90.9	1.65	2.23	2.23	1.69	1.69	2.33
	ORF SEQ ID NO:	27827	27830	27832	27833	27868	27869	27879	27880	27892	27915	27916	27937	27959	27960	27985	27987	27991	27992	27993	27994	27995	28036	28065			28072	28074	28092	28101	28102	28111	28112	28170
	Exon SEQ ID NO:		17606	17608	17608		17635	17645	17645	17654	17673	17673	17692	17715	17715	17742	17747	17753	17753	17754	17755	17755	17796	17822	17823		17832	17834	17851	17858	17858	17865	17865	17924
	Probe SEQ ID NO:	7753	7756	7758	7758	7785	7785	7795	7795	7804	7823	7823	7842	7865	7865	7892	7897	7903	7903	7904	7905	7905	7946	7972	7973		7982	7984	8001	8008	8008	8015	8015	8032

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Table 4
Single Exon Probes Expressed in Heart

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Cirgle Lyon Flobes Cypressed in Dealt	Top Hit Descriptor	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA	EST375636 MAGE resequences, MAGH Homo sapiens cDNA	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA	wy61f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553065 3' similar to TR:Q60566 Q60566 VDX;	TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0917	wb28a12.x1 NCI_CGAP_GC6 Homo saplens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 mSR1 repetitive element:	wb28a12.x1 NCI_CGAP_GC6 Homo sepiens cDNA clone IMAGE:2306974 3' similar to contains element	MSK1 MSK1 repetitive element;	Hamo sapiens NOD2 protein (NOD2), mRNA	Homo sapiens NOD2 protein (NOD2), mRNA	UI-HF-BL0-acm-d-04-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA	wu32b06.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:25217153	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906865 5	601434522F1 NIH_MGC_72 Homo sepiens cDNA clone IMAGE:3919636 5'	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'	2995b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN):	601588829F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'	xy04g10.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852226 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S16 (HUMAN);	AU135741 PLACE1 Homo sapiens cDNA clone PLACE1002794 5'
שוני בייסון ו זיסי	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	100	ES HOMAN	LN.	IN	EST_HUMAN	LN	IN	LN	EST HUMAN	EST_HUMAN	EST HUMAN	LN	LN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
5	Top Hit Acession No.	VV711075.1	4W813783.1	\W963563.1	11431124 NT	11431124 NT	1W057621.1	3E243270.1	0.0E+00 AI652239.1		0.0E+00 AI652239.1	11545911 NT	11545911 NT	\W404795.1	11424829 NT	4504536 NT	4504536 NT	1991827.1	0.0E+00 BE882109.1	0.0E+00 BE891630.1	R923939 NT	8923939	4.1				0.0E+00 AV727362.1	0.0E+00 AW516055.1	0.0E+00 AU135741.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00 AV71107	0.0E+00 AW8137	0.0E+00 AW96356	0.0E+00	0.0E+00	0.0E+00 AW0576	0.0E+00 BE24327	0.0E+00	L	0.0E+00/	0.0巨+00	0.0E+00	0.0E+00 AW4047	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AI991827	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE90330	0.0E+00 A	0.0E+00 E	0.0E+00	0.0E+00 A	0.0E+00	0.0E+00
	Expression Signal	2.33	6.11	6.43	2.5	2.5	1.99	1.92	4.86		4.80	2.91	2.91	2.01	4.8	9.16	9.16	2.73	3.04	10.56	22.36	22.36	1.91	4.05	4.69	6.8	6.8	17.96	2.17
	ORF SEQ ID NO:	28171		28178	28191	28192	28195	28200	28201	0000	70797				28224	28225	28226	28227	28231	28233	28234	28235	28247	25515	28269	28277	28278	28296	28301
	Exon SEQ (D NO:	17924	17926	17931	17942	17942	17945	17950	17951	12064	108/1	17959	17959	17972	17975	17976	17976	17977	17980	17984	17986	17986	18000	15448	18022	18031	18031	18044	18049
	Probe SEQ ID NO:	8032	8034	8040	8051	8051	8054	8059	8060	000	OGO OGO OGO OGO OGO OGO OGO OGO OGO OGO	8068	8068	8081	8084	8085	8085	8086	8089	8093	8095	8095	8110	8113	8134	8143	8143	8156	8161

Page 407 of 413
Table 4
Single Exon Probes Expressed in Heart

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| Top Hit Descriptor | hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:29454753' similar to contains element MSR1 repetitive element; | hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element; | hg13d02x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element: | H.sapiens mRNA for H1 histamine receptor | HSC3IC031 normalized Infant brain cDNA Homo sapiens cDNA clone c-3ic03 | Homo sapiens RGH1 gene, retrovirus-ilke element | xw66f01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' similar to gb:X17115 IG MU CHAIN C REGION (HUMAN): | UI-H-BI3-alh-a-01-0-UI st NCI CGAP Sith5 Home canions CDNA class MAACE 12226 40 21 | UI-H-BI3-alh-a-01-0-UI.s1 NCI CGAP Sub5 Homo saniens cDNA clone IMAGE 2736646 3 | Homo sapiens ribosomal protein L31 (RPL31) mRNA | Homo saplens mRNA for KIAA0667 protein, partial cds | 601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5

 | Homo sapiens mRNA for KIAA0545 protein, partial cds
 | Homo saplens of cardlac alpha-myosin heavy chain gene | 601582046F1 NIH MGC 7 Homo sabiens cDNA clone IMAGE 3036530 5 | 602141405F1 NIH MGC 46 Homo sapiens cDNA clone IMAGE 4307432 51 | AU118386 HEMBA1 Homo sapiens cDNA clone HFMBA1003486 5 | xn72b01.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb.X02152_cds1 L- | LACTATE DEHYDROGENASE M CHAIN (HUMAN); | qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772.3* | qf43c03.x1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772.3

 | QV4-ST0234-121199-032-b06 ST0234 Homo sapiens cDNA | AU116908 HEMBA1 Homo saplens cDNA clone HEMBA1000255 5. | Homo sapiens insulin receptor (INSR), mRNA | QV0-UM0093-170400-191-d06 UM0093 Homo seniens CDNA

 | QV0-UM0093-170400-191-d06 UM0093 Homo saniens CDNA | 502037014F1 NCI CGAP Brn64 Homo saniens cDNA clone IMA CE: 4484070 E | 501148357F1 NIH MGC 19 Homo sapiens cDNA clone IMAGE 3463340 F | Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17 | Homo sapiens of cardiac alpha-myosin heavy chain gene
 |
| Top Hit
Database
Source | EST_HUMAN | EST_HUMAN | | | EST_HUMAN | NT | EST HUMAN | EST HUMAN | EST HUMAN | IN | NT | EST HUMAN

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| Top Hit Acession
No. | AW 59333.1 | AW 59333.1 | AW 59333.1 | 234897.1 | -13069.1 | J10083.1 | | | | 4506632 | AB014567.1 | 3E298449.1

 | AB011117.1
 | 720656.1 | 3E792155.1 | 3F684061.1 | VU118386.1 | | W 236269.1 | 1149809.1 | V149809.1

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 | 0.0E+00
 | 0.0E+00 | 0.0E+00 | 0.0E+00 | 0.0E+00 / | 1 | 0.0=+00 | 0.05+00 | 0.0=+00

 | 0.0E+00 A | 0.0E+00 | 0.0E+00 | 0.0E+00

 | 0.0E+00 | 0.0E+00 B | 0.0E+00 B | 0.0E+00 | 0.0E+00 Z20656.1
 |
| .Expression
Signal | 3.45 | 3.45 | 3.45 | 1.82 | 2.8 | 2.12 | 2:92 | 5.64 | 5.64 | 14.21 | 2.03 | 2.35

 | 1.88
 | 59.52 | 3.47 | 25.37 | 6.16 | 6 | 27.7 | 0.77 | 0.77

 | 3.05 | 4.62 | 18.63 | 1.78

 | 1.78 | 2.14 | 49.5 | 2.53 | 68.7
 |
| ORF SEQ
ID NO: | 28304 | 28305 | 28306 | | 28308 | 28313 | 28328 | 28329 | 28330 | | 28332 | 28346

 | 28359
 | 28363 | 28371 | | 28374 | | 00000 | 2027.0 | 2007

 | 78380 | | 28386 | 28392

 | 28393 | 28394 | 28395 | 28403 | 28404
 |
| Exon
SEQ ID
NO: | 18054 | 18054 | 18054 | | | ı | 18077 | 18078 | 18078 | 10179 | 18081 | 18092

 | 18106
 | 18109 | 18120 | 18121 | 18124 | 10406 | 10120 | 10130 | 10130

 | 18131 | 18142 | 18145 | 18151

 | 18151 | 18152 | 18153 | 18161 | 18162
 |
| Probe
SEQ ID
NO: | 8166 | 8166 | 8166 | 8168 | 8169 | 8176 | 8191 | 8192 | 8192 | 8194 | 8196 | 8208

 | 8224
 | 8227 | 8240 | 8241 | 8244 | 27.00 | 8250 | 0250 | 0000

 | 1079 | 8262 | 8265 | 8271

 | 8271 | 8272 | 8273 | 8282 | 8283
 |
| | Exon ORF SEQ .Expression (Top) Hit Acession No. Signal BLASTE No. Source | Exon
SEQ ID
NO: ORF SEQ
Signal
NO: Expression
Signal
Value Most Similar
(Top) Hit
BLAST E
Value Top Hit Acession
No. Top Hit Acession
No. Top Hit Acession
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SEQ ID
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ID NO: Top Hit Acession
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Page 408 of 413 Table 4 Single Exon Probes Expressed in

Only e Exort Plobes Expressed in Heart	Top Hit Descriptor	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA	ob32e07.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element MSR1 repetitive element:	Homo sapiens signaling lymphocytic activation molecule /St AAA)	C05089 Human heart cDNA (YNakamira) Homo saniens cDMA ก่อกราชมเบิดของ	0856h01.r1 NCI CGAP GCB1 Home saniens (DNA Alexa MACCASOSOS	oa56h01.r1 NCI CGAP GCB1 Homo saniens cDNA clone IMAGE:1308009.5	EST00596 Fetal brain. Stratagene (rettt036206) Home senions conv. 15030093	EST00596 Fetal brain, Stratagene (catt/036206) Home senions CDNA close HEBCCZ6	QV2-HT0698-020800-295-407 HT0698 Homo saniens CDNA	DKFZp761J2116 r1 761 (synonym hamno) Home saplens cDNA close DK EZ-264 18448	AU116988 HEMBA1 Homo canisars critical class and the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract	1/3-NT0104-200500-143-An7 NT0104 Home senions 20NA	PM0-HT0645-060500-002-E05 HT0645-Home segions control	PM0-HT0645-060500-002-LCO HT0645-Dome COINA	601439092F1 NIH MCC 72 Home control appears CUINA	HE-BND-ako-4-02-0-11 of MID MCC Follows	11 HE DND AND OF 11 AND AND AND AND SAPERS CON CIONE IMAGE: 3077019 5	COTH CONG-BAS-G-02-0-01.11 NIT MCC_30 Homo sapiens CDNA clone IMAGE:3077019 5'	20111011 MOC_Z INDINO SAPIENS CLINA CIONE IMAGE:3925403 5	acoust 11.X1 Schiller maningiums Homo sapiens cDNA clone IMAGE: 1952804 3'	HSBT76122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone.	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone	Homo saniens marrowin III (NIOXN 2) DATA	60187090781 NIH MGC 10 Home conjunction	H-BI2-ang-h01-0-11 of NICL COAD SILVE U	ROD-CITORROZ 2010 COLOS INC. CONT. 2014 HOMO REPIERS CLINA CIONE IMACE 2724312.3	RCO-CT0380-21010-032-210 CT0380 Homo sapiens cDNA	Homo sabiens mRNA for KIAA0777 motein modified al-	Homo sapiens mRNA for KIAA0717 protein partial cds	
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Page 409 of 413 Table 4 Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart	Top Hit Descriptor	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:076022 076022 E1B-55KDA-ASSOCIATED PROTEIN.	ba04d07.yf NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B- 55KDA-ASSOCIATED PROTEIN	Homo sapiens myosin, heavy polypeptide 4. skeletal muscle (MYH4) mRNA	QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA	zp95b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCI F (HUMAN)	UI-H-BI4-ack-b-10-0-UI-st NC CGAP Sub8 Home serviens CDNA clone IMAGE 3086026.2	U-H-BI4-aok-b-10-0-UI.s1 NCI CGAP Subs Homo saniens cONA clone IMA CE-20055002 2	AU135170 PLACE1 Homo sabiens cDNA clone PLACE1001381 51	601486828F1 NIH MGC 69 Home sabiens cDNA clore MAGE-3880207 F	01486828F1 NIH MGC 69 Homo sapiens cDNA clone IMAGE 3880307 F	601875630F1 NIH MGC 55 Home sapiens cDNA clone MAGE-4000710 5	Homo sapiens mRNA for KIAA1316 protein, partial cots	Homo saplens mRNA for KIAA1316 protein partial cots	Homo sapiens retinoblastoma-like 2 (p130) (RBI 2) mRNA	Homo sapiens retinoblastoma-like 2 (p130) (RBL2) mRNA	Homo sapiens eukaryotic translation Initiation factor 5A (EIF5A) mRNA	602134132F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE 4280502 5	dr04g05.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE.2847177 5	Human gamma actin-like pseudogene, complete cds	wf20e11.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351180 3' similar to ob-M87789 IG GAMMA-1 CHAIN C PECION (HIMAN).	601889823F1 NIH MGC 17 Homo saniens CINA clone IMAGE 4122049 F1	601889823F1 NIH MGC 17 Homo sapiens cDNA cline IMAGE 4123948 5	QVZ-NN0054-230800-333-e04 NN0054 Homo sapiens cDNA	601439605F1 NIH MGC 72 Homo sabiens cDNA clane IMAGE 3024577 57	Homo sapiens golgin-like protein (GLP), mRNA	601861947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE: 4081715 5	ba04d07.y1 NIH_MGC_7 Horno sapiens cDNA clone IMAGE.2823373 5' similar to TR:O76022 O76022 E1B 55KDA-ASSOCIATED PROTEIN.;
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Sin	Top Hit Acession No.	0.0E+00 BE206848.1	BE206846.1	11024711 NT	0.0E+00 BF093687.1	BE148076.1	0.0E+00 BE148076.1	0.0E+00 AA195905.1	BF507876.1	BF507876.1	AU135170.1	11.1		0.0E+00 BF240536.1	0.0E+00 AB037737.1		11430868 NT	11430868 NT	4503544 NT		73.1	.1	0.0E+00 AI660968.1	<u></u>	0.0E+00 BF306996.1	0.0E+00 BF362462.1		3698	0.0E+00 BF207662.1	0.0E+00 BE206846.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 BE2068	0.0E+00	0.0E+00	0.0E+00 BE1480	0.0E+00	0.0E+00	0.0E+00 BF50787	0.0E+00 BF50787	0.0E+00 AU1351	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M55083	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	2.59	2.59	2.85	2.01	2.9	2.9	6.47	4.47	4.47	2.16	5.62	5.62	10.32	3.05	3.05	3.49	3.49	6.1	2.49	5.44	120.65	3.18	3.64	3.64	26.88	4.07	2.89	2.24	4.61
	ORF SEQ ID NO:	28628	28629	28648	28651	28653	28654	28665	28687	28688	28692	28696	28697		28713	28714	28717	28718	28734	28741	28744		28750	28752	28753	28758		28793	_	28833
	Exon SEQ ID NO:	18363	18363	18383	18386	18390	18390	18398	18418	18418	18423	18427	18427	18435	18445	18445	18449	18449	18463	18470	18472	18475	18479	18481	18481	18486	18504	18512	18514	18550
	Probe SEQ (D NO:	8490	8490	8511	8514	8518	8518	8526	8546	8546	8553	8557	8557	8566	8577	8577	8581	8581	8596	8603	8605	8608	8612	8614	8614	8620	8639	8648	8650	8661

Page 410 of 413 Table 4 Single Exon Probes Expressed in Heart

Single Exon Flobes Explessed in Healt	Most Similar Top Hit Acession (Top) Hit Acession ID NO: Signal BLASTE No. Source Source	550 28834 4.61 0.0E+00 BE206846.1 EST_HUMAN 55KDA-ASSOCIATED PROTEIN.;	28836 3 0.0E+00 AW753028.1	2.36 0.0E+00 AA558707.1	24915 5 0.0E+00 AI934954.1 EST_HUMAN	28842 7.41 0.0E+00 AW327895.1 EST_HUMAN	28800 4.73 0.0E+00 BE185656.1 EST_HUMAN	28812 4.74 0.0E+00 AL046540.1 EST_HUMAN	28813 4.74 0.0E+00 AL046540.1 EST_HUMAN	28823 12.53 0.0E+00 AI923116.1 EST_HUMAN RECEPTOR (HUMAN);	28863 4.18 0.0E+00 AA760913.1 EST_HUMAN Q13686 ALKB HOMOLOG PROTEIN.;	28864 4.18 0.0E+00 AA760913.1	28869 2.33	28130 5.67 0.0E+00 BE676347.1 EST HUMAN	28875 2.78 0.0E+00 L39891.1 NT	28876 2.78 0.0E+00 L39891.1 NT	28888 4.02 0.0E+00 AU138211.1 EST_HUMAN	28902 1.91 . 0.0E+00 BE622317.1 EST_HUMAN	28924 10.47 0.0E+00 BE748899.1 EST_HUMAN	28925 10.47 0.0E+00 BE748899.1 EST_HUMAN	28937 2.97 0.0E+00 AU141882.1 EST_HUMAN	28938 2.97 0.0E+00 AU141882.1 EST_HUMAN	28941 2.35 0.0E+00 AW006022.1 EST_HUMAN	74 28943 3.84 0.0E+00 BF002333.1 EST HUMAN TRIO.	28962 3.19 0.0E+00 AW387776.1	28963 3.19 0.0E+00 AW387776.1 EST_HUMAN	28982 2.57 0.0E+00 11435244 NT
	ORF SEQ ID NO:																								L		
	Exon SEQ ID NO:	1 18550	3 18552	18557	9 15148	0 18558		2 18529	2 18529	2 18539	4 18580	18580	18584	7 17886	2 18589	2 18589				_		7 18650	0 18653	3 19474	1 18673		18690
	Probe SEQ ID NO:	8661	8663	8998	8669	8670	8700	8712	8712	8722	8724	8724	8728	8737	8772	8772	8784	8797	8827	8827	8837	8837	8840	8843	8861	8861	8878

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 | Human von Willebrand factor pseudogene corresponding to expres 23 through 34 | 601299403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE 3630544 57 | Homo sapiens protein kinase, AMP activated, alpha 2 cetalving sulpunit (PRKAAA) | Homo sapiens protein kinase, AMP-activated alpha 2 catalytic submit (DEKAAS)
 | Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic submit (PRKAA2), mRNA | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively splitted | 602155727E1 NIH MCC 82 Home comits - CNA - | 602155722F1 NIH MGC 83 Home septemble CDNA CLORE IMAGE: 4296725 5 | 601676357F1 NIH MGC 21 Homo saniens cDNA clone IMACE actions 2 | 601897524F1 NIH MGC 19 Homo sabiens cDNA clone IMAGE:4127050 5 | 601897524F1 NIH MGC 19 Homo sapiens cDNA clone IMAGE 4127069 5
 | Human lambda-immunoglobulin constant region complex (germline) | Human lambda-immunoglobulin constant region complex (germline) | 801890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131415 5' | RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA | NOTIVIOUSS-120000-010-007 (NV0029 Homo sapiens cDNA R0447740754 Nill 1900 4-11
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 | 2.93 | 6.35 | 1.93 | 1.93
 | 1.93 | 2:32 | 2.32 | 5.66 | 5.66 | 3.22 | 6.15 | 6.15
 | 3.02 | 3.02 | 20.36 | 1.98 | 31.56
 | 36.47 | 36.47 | 34.29 | 31.52 |
| ORF SEQ
ID NO: | 28983 | 28987 | 28989 | 28990 | 26434 | 26006 | 29005 | 29006

 | 29007 | 23014 | 23015 | 29016
 | 23017 | 29018 | 29019 | 29020 | 29021 | 29026 | 29034 | 29035
 | 29036 | 29037 | 20062 | 29063 | 29066
 | 29076 | 29077 | 29078 | 29081 |
| Exon
SEQ ID
NO: | | | | | 16272 | 15883 | 18710 | 18711

 | 18712 | 18723 | 18724 | 18724
 | 18724 | 18725 | 18725 | 18727 | 18727 | 18732 | 18741 | 18741
 | 18/42 | 18/42 | 18771 | 18771 | 18775
 | 18786 | 18786 | 18787 | 18792 |
| Probe
SEQ ID
NO: | 8878 | 8883 | 8885 | 8885 | 8896 | 8900 | 8902 | 8903

 | 8904 | 8915 | 8916 | 8916
 | 8916 | 8917 | 8917 | 8919 | 8919 | 8924 | 8933 | 8933
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Single Exon Probes Expressed in Heart

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Top Hit Descriptor	HTM1-654F HTM1 Homo sapiens cDNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE 182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);	yoS9008.r1 Soares breast 3NbHBst Homo sepiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN),	Human gamma-cytoplasmic actin (ACTGP9) pseudogene	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA	TCBAP1E4468 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens	cDNA clone TCBAP4466	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA	Horno sapiens G protein-coupled receptor 24 (GPR24), mRNA	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA	Homo sapiens chromosome 21 segment HS21C046	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA	Human endogenous retrovirus pHE.1 (ERV9)	Homo sapiens oxytocin receptor (OXTR), mRNA	RC1-HT0595-200400-012-f12 HT0595 Homo sapiens cDNA	DKFZp434J0618_r1 434 (synonym: htes3) Homo sapions cDNA clone DKFZp434J0618
Top Hit Database Source	EST_HUMAN	LN	LZ.	NT	EST_HUMAN	EST_HUMAN	LN	LZ	LZ		EST_HUMAN	L	LN	NT	NT	ΤN	NT	TN	LN	LN	TN	LN	EST HUMAN	EST HUMAN
Top Hit Acession No.	0.0E+00 BE439792.1	6912457 NT	6912457 NT	0.0E+00 AF036365.1	H30132.1	130132.1	50659.1	11418189 NT	11418189 NT		0.0E+00 BE246780.1	8922593 NT	11526291 NT	4885312 NT	0.0E+00 AB029900.1	9558724 NT	0.0E+00 AL163246.2	6806918 NT	7657020 NT	8567387 NT	(57147.1	11434874 NT	0.0E+00 BE177449.1	AL048911.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 H30132.1	0.0E+00 H30132.	0.0E+00 D50659.1	0.0E+00	0.0E+00	_	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X57147.1	0.0E+00	0.0E+00	0.0E+00 AL048911
Expression Signal	1.68	1.98	1.98	2.33	2.87	2.87	32.21	3.99	3.99		5.21	1.64	2.39	3.19	2.21	1.5	2.79	1.41	2.13	2.42	1.51	1.29	1.56	1.28
ORF SEQ ID NO:		21724	21725	25267	21426	21427		25244	25245		25214	24829		24886		25233		20354		25177				
Exen SEQ ID NO:	19596	11841	11841	19161	11561	11561	19179	19181	19181		19239	15089	19249	15092	19269	19291	19757	10546	19364	.19388	19407	19621	19591	19431
Probe SEQ ID NO:	9540	9551	9551	9571	9584	9584	9597	9539	9599		9685	3695	9698	9721	9734	9773	9794	0086	9878	9913	9938	9946	9966	9971

A spatially-addressable set of single exon nucleic-acid probes for measuring gene expression in a sample derived
 from human heart comprising a plurality single exon nucleic

- probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 9,980 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
- 3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
- 4. A spatially-addressable set of single exon nucleic acid 20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 9,981 - 19,771.
- 5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
- 6. A spatially-addressable set of single exon nucleic acid 30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
- 7. A spatially-addressable set of single exon nucleic acid 35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exc. nucleic acid probes is between 200 and 500 bp.

- 8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.
- 9. A spatially-addressable set of single exon nucleic acid 10 probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.
- 10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 9 characterised in that said set of probes is addressably disposed upon a substrate.
- 11. A spatially-addressable set of single exon nucleic acid 20 probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.
- 12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 11.
- 13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart

 30 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 9,980 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human heart.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 9,981 - 19,771 or a complementary sequence or a fragment thereof.

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- 15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 19,772 29,119, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.
- 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
- 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between $3-25~\mathrm{kb}$ in length.
 - 18. A single exon nucleic acid probe as claimed in any one of claims 13 17, wherein said probe is DNA, RNA or PNA.

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- 19. A single exon nucleic acid probe as claimed in any one of claims 13 18, wherein said probe is detectably labeled.
- 30 20. A single exon nucleic acid probe as claimed in any one of claims 13 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
- 21. A single exon nucleic acid probe as claimed in any one of claims 13 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human heart, comprising:

5 contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human heart; and then measuring the label detectably bound to each probe of said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

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24. A method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence according to the method of claim 23; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

35 wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

- 25. A nucleic acid sequence as set out in any of SEQ ID 5 NOs: 1 19,771 which encodes a peptide.
 - 26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 19,771.
- 10 27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 19,772 29,119.

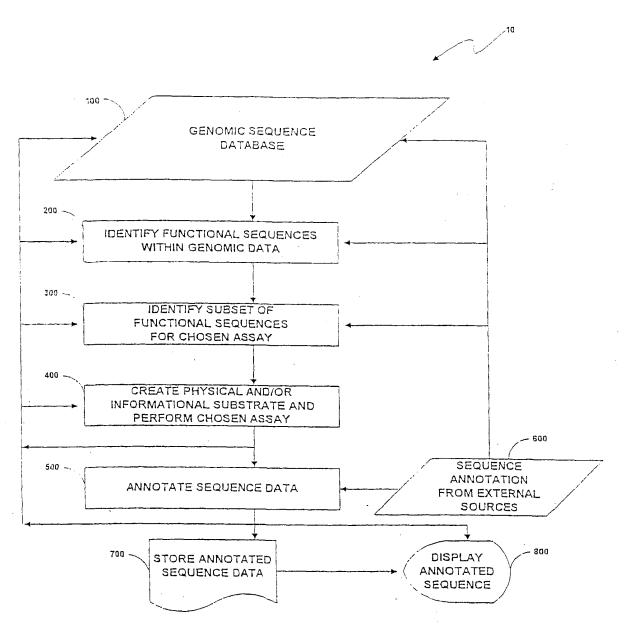


Fig. 1

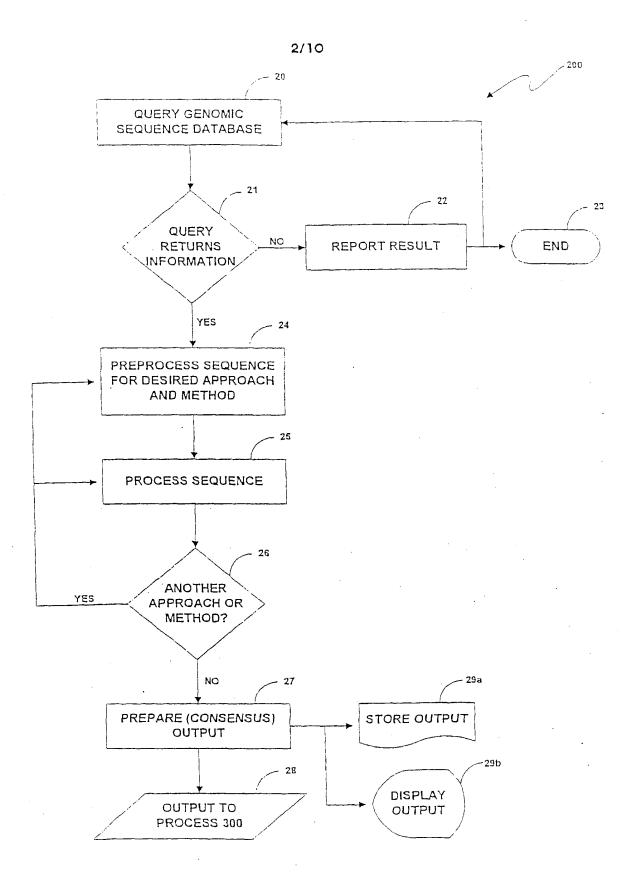


Fig. 2

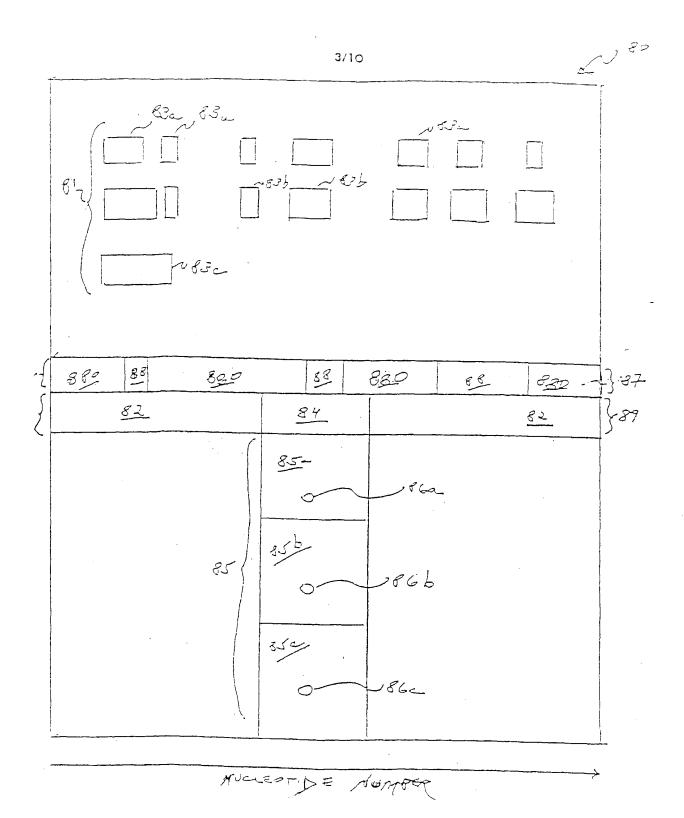


Fig. 3

4/10

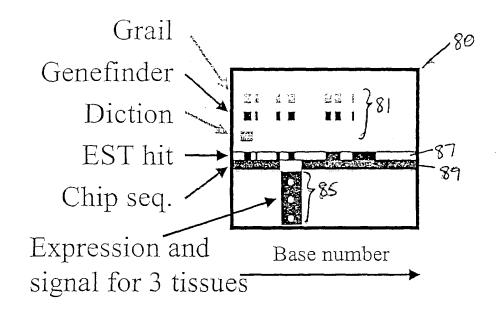


Fig. 4

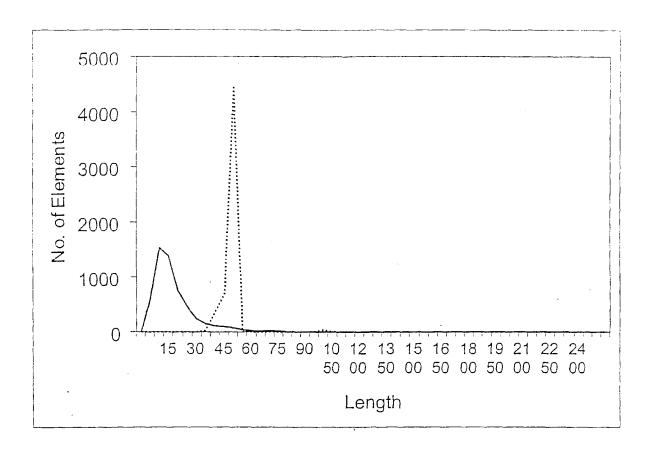


Fig. 5

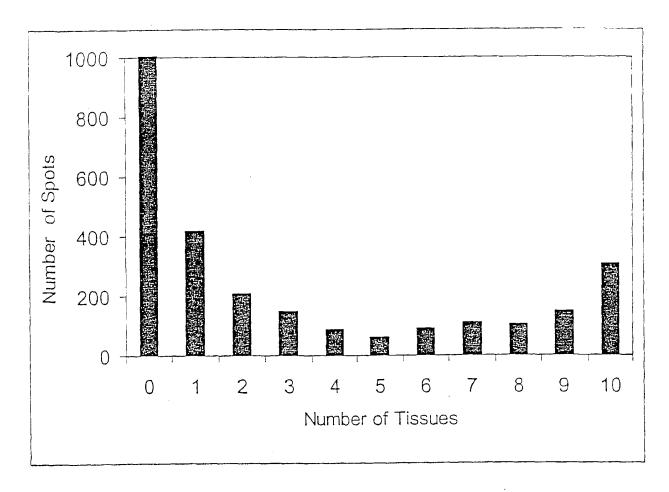
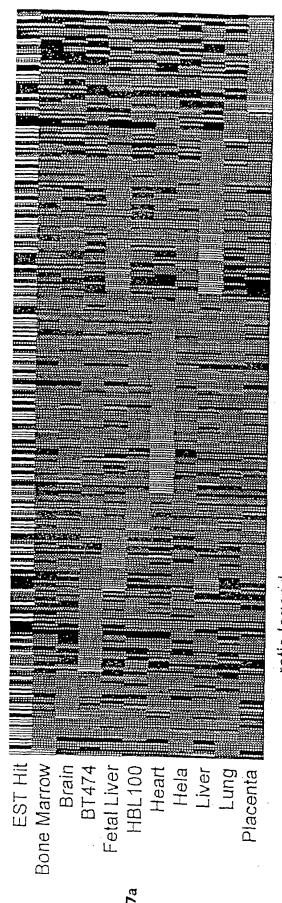


Fig. 6



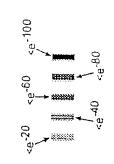


Fig. 7b

ratio legend

Fig. 7a

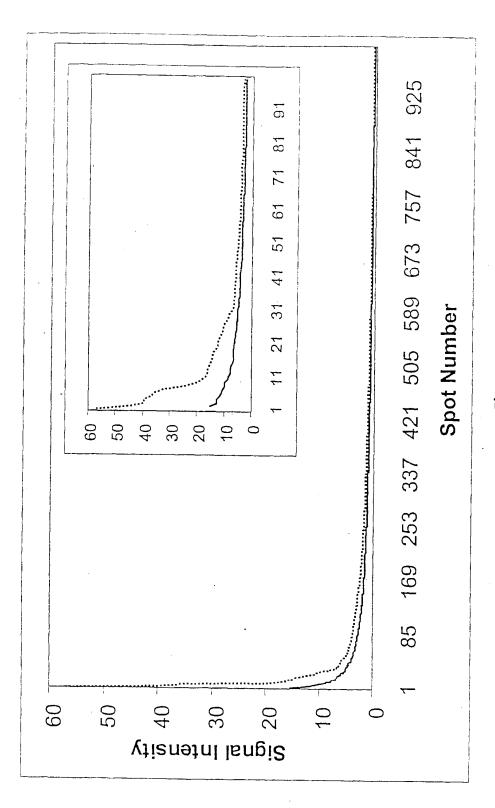


Fig. 8

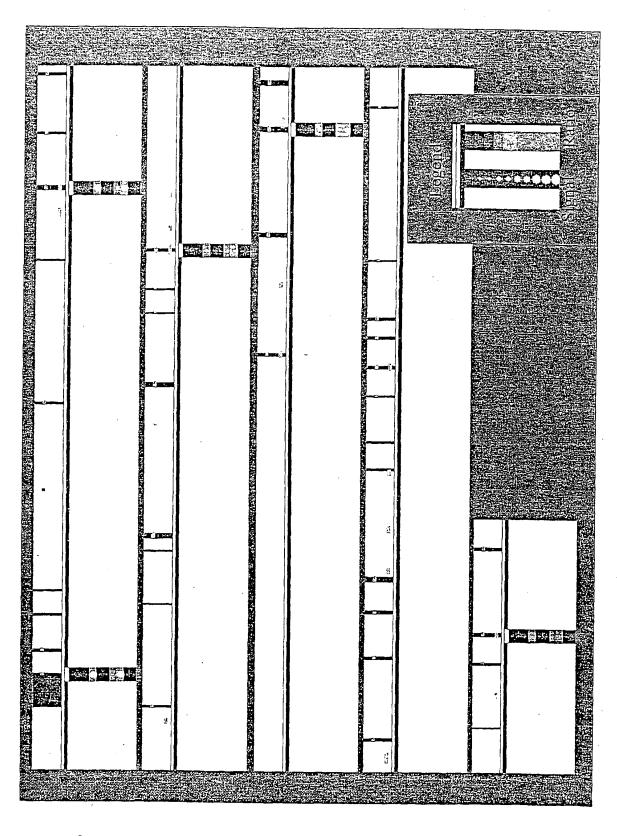
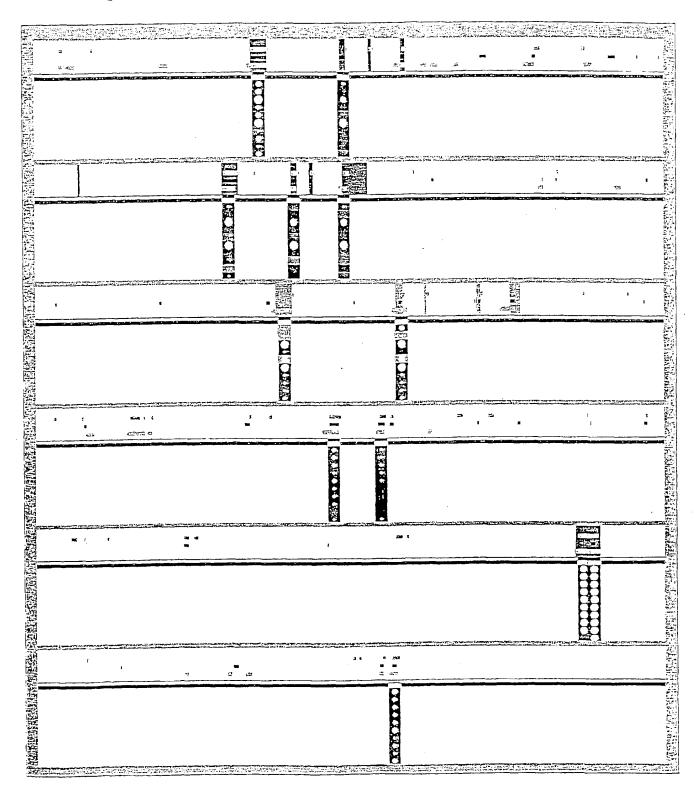


Fig. 9

Fig. 10



(19) World Intellectual Property Organization International Bureau





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0024263.6	4 October 2000 (04.10.2000)	GB

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- (74) Agent: RONNING, Royal, N., Jr.: Amersham Pharmacia Biotech. Inc., 800 Centennial Avenue, P.O. Box 1327, Piscataway, NJ 08855 (US).

(81) Designated States inationaly: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States tregionaly: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW). Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM). European patent (AT BE, CH, CY, DE, DK ES, FI, FR, GB, GR, IE, TT, LU, MC, NL, PT, SE, TR). OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

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- (15) Information about Correction: Previous Correction:

see PCT Gazette No. 51/2001 of 20 December 2001, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



1/057274 A3

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart is described. Also described are single exon nucleic acid probes expressed in the heart and their use in methods for detecting gene expression.

INTERNATIONAL SEARCH REPORT

ernational Application No PCT/US 01/00666

A. CLASSIFICATION OF SUBJECT MATTER IPC 7 C12Q1/68

C. DOCUMENTS CONSIDERED TO BE RELEVANT

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documenta are included. In the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

SEQUENCE SEARCH, EPO-Internal, PAJ, WPI Data, BIOSIS

Category °	Citation of document, with indication, where appropriate, of the	e relevant passages	Relevant to claim No.
X	DATABASE EBI 'Online! EMBL; Accession Number: AL049837, 11 May 1999 (1999-05-11) HEILIG ET AL.: "Human chromoson sequence BAC R-959A22 of librar from chromosome 14 of Homo sapi (Human)"	ry RPCI-11	13-21, 25,27
Y	XP002182997 the whole document 	-/	1-12, 22-24,26
X Furti	her documents are listed in the continuation of box C.	X Patent family members are listed	in annex.
"A" docume consid "E" earlier of filing of the docume which citation other of the country of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of the citation of citation of citation of citation of citation of citation of citation of citation of citation of citation of citation of citation of citation of citation of citation of citation of citation of c	tegories of cited documents: ent defining the general state of the art which is not defining the general state of the art which is not decument but published on or after the international date described by the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the st	"T" later document published after the inte or priority date and not in conflict with cited to understand the principle or the invention "X" document of particular relevance; the cannot be considered novel or cannot involve an inventive step when the document of particular relevance; the cannot be considered to involve an involve and document is combined with one or moments, such combination being obvious in the art. "&" document member of the same patent	the application but lony underlying the laimed invention be considered to cument is taken alone aimed invention rentive step when the re other such docu- is to a person stilled
	actual completion of the international search 2 July 2002	Date of mailing of the international sea	rch report
Name and r	mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Botz, J	

INTERNATIONAL SEARCH REPORT

ternational Application No PCT/US 01/00666

	ation) DOCUMENTS CONSIDERED TO BE RELEVANT	
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EBI 'Online! EMBL; AA414703, 9 May 1997 (1997-05-09) MARRA ET AL.: "The WashU-HHMI Mouse EST Project"	13-21, 25,27
Υ	XP002205620 the whole document	1-12, 22-24,26
X	DATABASE EBI 'Online! EMBL; Accession Number: 002711, 1 July 1997 (1997-07-01) BENIT ET AL.: "Cloning of a new murine endogenous retrovirus MuERV-L with strong similarity to the human HERV-L element and with a gag coding sequence closely related to the Fv1 restriction gene" XP002037954	15-21,27
Υ	the whole document	1-12, 22-24,26
Y	LIEW ET AL .: "A catalogue of genes in the cardiovascular system as identified by expressed sequence tags" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES, USA, vol. 91, October 1994 (1994-10), pages 10645-10649, XP002185728 table 2	1–27
Y	LIPSHUTZ ET AL.: "High density synthetic oligonucleotide arrays" NATURE GENETICS, vol. 21, January 1999 (1999-01), pages 20-24, XP002115232 NEW YORK, NY, US the whole document	1–27
Α	DATSON ET AL.: "Scanning for genes in large genomic regions: cosmid based exon trapping of multipleexpons in a single product" NUCLEIC ACIDS RESEARCH, OXFORD UNIVERSITY PRESS, vol. 24, no. 6, 1996, pages 1105-1111, XP002081565 Surrey, GB the whole document	
A	WO 98 30722 A (MACK DAVID H.) 16 July 1998 (1998-07-16) page 63, paragraph 2	

International application No. PCT/US 01/00666

INTERNATIONAL SEARCH REPORT

Boxi	Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)
This Intern	national Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1	Claims Nos.: pecause they relate to subject matter not required to be searched by this Authority, namely:
b a	Claims Nos.: 1-12, 15-21 (partially not searched) because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically: See FURTHER INFORMATION sheet PCT/ISA/210
з с	Claims Nos.: secause they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II C	Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
This intern	national Searching Authority found multiple inventions in this international application, as follows:
\$	see additional sheet
1. A	us all required additional search fees were timely paid by the applicant, this international Search Report covers all earchable claims.
	is all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment If any additional fee.
	as only some of the required additional search fees were timely paid by the applicant, this International Search Report overs only those claims for which fees were paid, specifically claims Nos.: 1-27 (partially)
4. N	to required additional search fees were timely paid by the applicant. Consequently, this International Search Report is estricted to the invention first mentioned in the claims, it is covered by claims Nos.:
Remark o	The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-12, 15-21 (partially not searched)

The following statements about the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject matter for which a search has been performed and identified as the first and second inventions in form 206 PCT.

Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising Seq. Id. 1 or 2 as well as microarrays comprising said sets. In fact, the claims contain so many possible permutations that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible. Consequently, the search for the sets of probes comprising Seq. Id. 1 or 2 has been limited to the Seq. Id. as such.

Claims 1-3, 5, 6, 8-15 and 18-24 relate to portions or fragments of nucleic acids defined by Seq. Id. 1 or 2. The length or other similar characterizing features of the portions or fragments is not disclosed, bringing the total number of possible prior art sequences to exceptionally high numbers. The shorter the length, the higher the possibility that an overflow of, in principle unrelated, sequences are retrieved, making the establishment of a meaningful International Search Report impossible. For this reason the search has been limited to portions or fragments of Seq. Id. 1 or 2 having a significant minimum length and being supported by the description, namely at least 15 contiguous nucleotides (se claim 16).

Claims 15-21 relate to an extremely large number of nucleic acid probes. The probes are defined solely by their potential to code for peptide Seq. Id. 19780. However, due to the degeneracy of the genetic code, every peptide is potentially coded by an extremely high number of nucleic acid sequences. In fact, the claims contain so many potential nucleic acid sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole scope of the claims impossible. The search has therefore been carried out for those parts of the claims which do appear to be clear and concise, namely the nucleic acid sequences disclosed in the application and identified as encoding the referred peptide in table 4 (Seq. Ids. 1 or 2 and 9989).

Likewise, claim 26, which refers to peptides encoded by Seq. Id. 1 or 2 and 9989, encompasses a high and undefined number of possible peptides. Besides three possible reading frames deriving from the encoding nucleic acid strand, as well as three additional reading frames deriving from the complementary nucleic acid strand, every possible fragment of these is being covered by the claim. This is due to the potential presence of stop codons within any of the six possible reading frames which can not be established a priori. Thus, claim 26 contains so many potential peptide sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

over the whole scope of the claim impossible. Consequently, the search has been carried out for those parts of the claim which do appear to be clear and concise, namely the peptide disclosed, identified by Seq. Id. 19780.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1 - 27 (partially)

Invention number 1:

A nucleic acid probe comprising SEQ ID 1, complementary sequences or fragments thereof (in particular comprising Seq. Id. 9989). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by Seq. Id. 1 (in particular the one defined by Seq. Id. 19780).

2. Claims: 1 - 27 (partially)

Invention 2

A nucleic acid probe comprising SEQ ID 2, complementary sequences or fragments thereof (in particular comprising Seq. Id. 9989). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by Seq. Id. 2 (in particular the one defined by Seq. Id. 19780).

3. Claims: 1 - 27 (partially)

Inventions 3 - 9980

A nucleic acid probe comprising SEQ ID n (where n ranges from 2 - 9980 according to the invention number above), complementary sequences or fragments thereof, in particular comprising the SEQ ID no. which is listed in the column "Exon Seq. Id. no." in the same row that contains Seq. Id. n in table 4. Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by Seq. Id. n, in particular the one defined by the Seq. Id. no. in the column "ORF Seq. Id. no." of the same row where Seq. Id. n is listed.

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(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart is described. Also described are single exon nucleic acid probes expressed in the heart and their use in methods for detecting gene expression.